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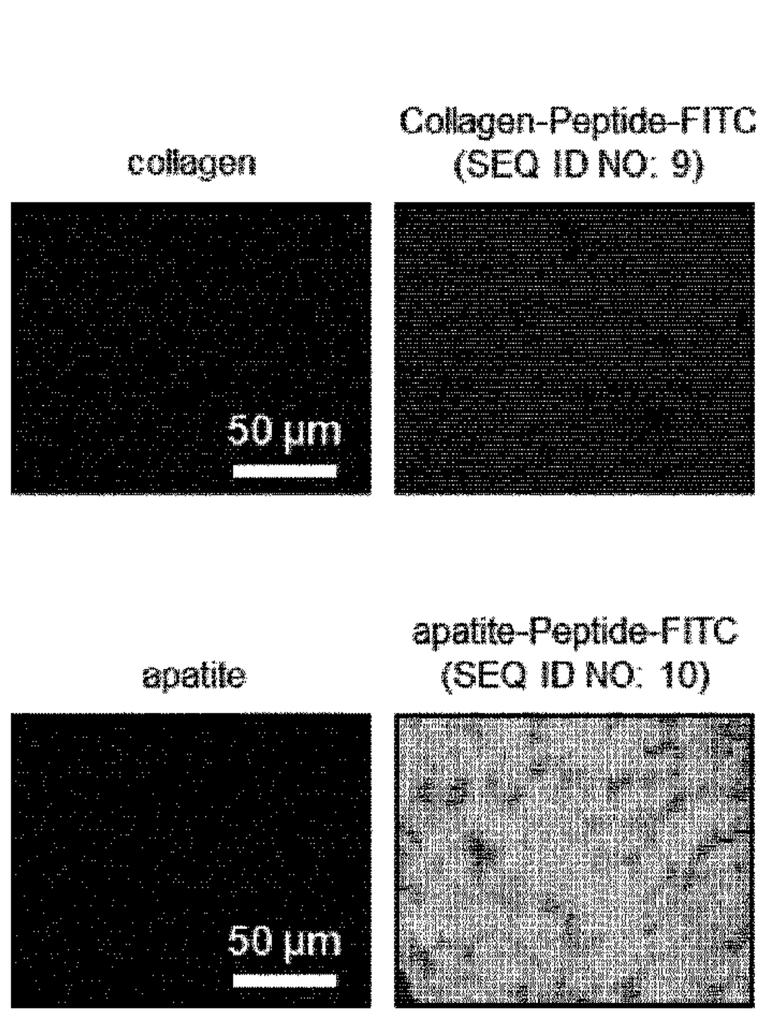
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(54) Titre : ASSOCIATION PHARMACEUTIQUE POUR CONVERTIR UNE CELLULE NEOPLASIQUE EN CELLULE NON-NEOPLASIQUE ET SES UTILISATIONS

(54) Title: PHARMACEUTICAL ASSOCIATION FOR CONVERTING A NEOPLASTIC CELL INTO A NON-NEOPLASTIC CELL AND USES THEREOF

FIGURE 1



(57) Abrégé/Abstract:
The present disclosure provides a pharmaceutical association for use in the treatment, prevention and/or diagnostic of a neoplastic disease, said association comprising at least one growth factor receptor-binding compound, which activates at least one growth factor receptor of a neoplastic cell, and at least one bioactive carrier forming at least one covalent or non-covalent interaction with said at least one growth factor receptor-binding compound, and wherein said association reduces or suppresses, in the neoplastic cell, the gene expression of at least one cyclin D and/or reduces or suppresses the formation of at least one complex formed between said at least one cyclin D and at least one of cyclin dependent-kinase 4 or 6.

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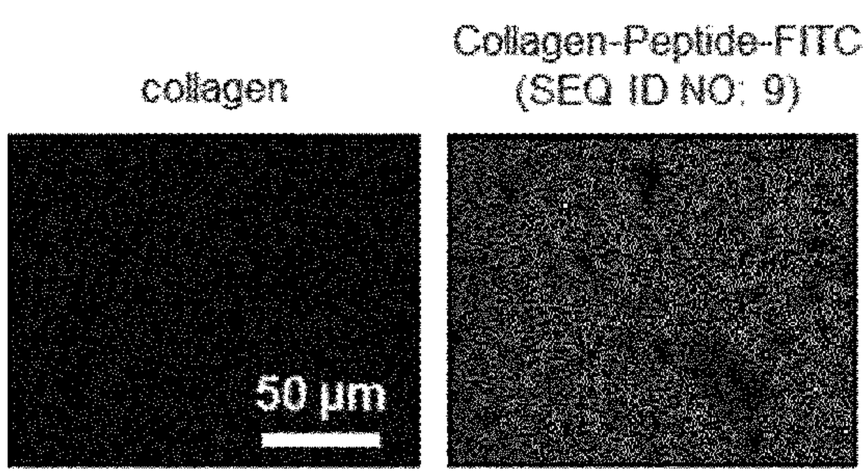
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[Continued on next page]

(54) Title: PHARMACEUTICAL ASSOCIATION COMPRISING A GROWTH FACTOR RECEPTOR AGONIST CONJUGATED TO A BIOACTIVE CARRIER FOR CONVERTING A NEOPLASTIC CELL INTO A NON-NEOPLASTIC CELL AND USES THEREOF

FIGURE 1



(57) Abstract: The present disclosure provides a pharmaceutical association for use in the treatment, prevention and/or diagnostic of a neoplastic disease, said association comprising at least one growth factor receptor-binding compound, which activates at least one growth factor receptor of a neoplastic cell, and at least one bioactive carrier forming at least one covalent or non-covalent interaction with said at least one growth factor receptor-binding compound, and wherein said association reduces or suppresses, in the neoplastic cell, the gene expression of at least one cyclin D and/or reduces or suppresses the formation of at least one complex formed between said at least one cyclin D and at least one of cyclin dependent-kinase 4 or 6.

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CONTENANT LES PAGES 1 À 240

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JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 240

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PHARMACEUTICAL ASSOCIATION FOR CONVERTING A NEOPLASTIC CELL INTO A NON-NEOPLASTIC CELL AND USES THEREOF

FIELD OF THE INVENTION

The invention relates to associations, combinations, compositions, kits, methods and processes for the design, preparation, manufacture and/or formulation thereof, and methods and uses thereof for converting or recoding a neoplastic cell into a non-neoplastic cell and treating and/or preventing a neoplastic disease.

BACKGROUND

Neoplastic cells, such as cancer cells, are generally characterized by abnormal and/or uncontrolled proliferation leading, in most cases, to the development of a neoplastic disease, such as cancer. Conventional methods for treating neoplastic diseases include surgical treatments, radiotherapy and chemotherapy.

Surgery is usually practised in order to extract localised (non-circulating) neoplastic cells from a patient's body and is most generally combined with radiotherapy treatments. As well as being limited to the treatment of very early stage, non-metastatic tumors, surgery is an invasive medical procedure which remains traumatic for the treated patient, involves the permanent removal of tissues or organs (which is sometimes not possible as some organs or organ parts are not accessible or cannot be removed due to life threatening consequences), in some cases has been shown to "unblock" dormant tumors, while only offering a "visual" selectivity to distinguish between healthy and tumor cells. Radiotherapy also presents some significant drawbacks for the treated patients including the high cost of the radiation therapy equipment, the high cost of the treatment itself, side effects associated with the damage or destruction of healthy cells, limited effectiveness against metastasized neoplastic diseases, skin rashes caused by external beam radiation, the potential deleterious impact on the functioning of tissues, glands or organs located near the site of treatment, and the possible development of secondary cancers as a result of exposure to the radiations.

Conventional chemotherapy methods generally involve the administration of small synthetic regulatory molecules which inhibit specific intracellular target proteins thought to be responsible for the neoplastic phenotype of the cell. One example is the inhibition of tyrosine kinase signal transduction by small molecule inhibitors to regulate uncontrolled cell proliferation. Typical chemotherapy methods also include treatments wherein DNA is covalently altered by *e.g.* DNA strands crosslinking, or treatments wherein the polymerisation and depolymerisation of microtubules is enhanced prevented thus provoking apoptosis of the damaged cell.

Another method for treating neoplastic diseases includes gene therapy wherein a missing or defective gene is replaced with a functional, healthy copy, which is delivered to the target dysfunctional cells using a "vector." Gene transfer therapy can be done outside the body (ex vivo) by extracting bone marrow or blood from the patient and growing the cells in a laboratory. The corrected copy of the gene is then introduced and allowed to penetrate the cells' DNA before being injected back into the body. Gene

transfers can also be done directly inside the patient's body (in vivo). Gene therapy has been applied to a few specific cases of blood cancers (chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL) and multiple myeloma) through a particular form thereof in which the genetically modified cells were not the neoplastic cells themselves but instead the immune T-cells. Modified T-cells could then target and destroy specific blood cells (neoplastic as well as healthy). The body of the patient is then able to produce healthy blood cells and eventually provide a treatment to certain blood cancer types. However, gene therapy is generally best suited for the treatment of diseases caused by a single defective gene, not neoplastic diseases, which often involve multiple defective genes. Overall, issues such as the correct integration of therapeutic DNA into the genome; the immune system response to the introduction of foreign DNA into the cell; the toxicity, immune and inflammatory responses; gene control and targeting issues of the vectors (usually viral) required to transport the DNA inside the cell; the difficulties associated with the treatment of multigene-associated neoplastic cells; the possibilities of inducing tumors if the DNA is integrated in the wrong place in the genome; and/or the significant cost usually involved with such a therapy, have greatly undermined the development of gene therapy.

Other intracellular therapies have been contemplated for the treatment of neoplastic diseases using, for instance, micro-ribonucleic acids (miRNAs) or small interfering ribonucleic acids (siRNA). Under these conditions, the neoplastic cell is generally forced to down-regulate or repress the expression of one or more specific target genes (*e.g.* oncogenes) thus inhibiting the expression of defective and/or defecting proteins (*e.g.* oncoproteins). One example is the repression of genes encoding key proteins in the proliferation of cancer cells such as vascular endothelial growth factor (VEGF) and kinesin spindle protein (KSP), thus controlling cancer proliferation.

Neoplastic diseases may also be treated using immunotherapy such as antibody therapies wherein the antibodies bind to a target antigen typically on the surface of the neoplastic cell. Cell surface receptors are common targets for antibody therapies and include the epidermal growth factor receptor, HER2, CD52, the vascular endothelial growth factor-A and CD30. Once bound to an antigen (*e.g.* a cancer antigen), antibodies can induce antibody-dependent cell-mediated cytotoxicity, activate the complement system, prevent a receptor interacting with its ligand or deliver a payload of chemotherapy or radiation, which may all lead to the induction of neoplastic cell death. For instance, Cetuximab (Erbitux) is a chimeric IgG1 monoclonal antibody that targets the extracellular domain of the epidermal growth factor receptor (EGFR). Once a ligand binds to the EGFR on the surface of the cell, signalling pathways are activated inside the cell that are associated with malignant characteristics such as cancer cell proliferation and invasion. Cetuximab competitively inhibits ligand binding, thereby preventing EGFR activation and subsequent cellular signalling. It also activates programmed cell death (apoptosis).

Other intracellular treatments such as messenger ribonucleic acids (mRNAs) –based therapies have also been used in the treatment of neoplastic disease wherein administration of mRNA material into a neoplastic cell causes the neoplastic cell *e.g.* to express specifically encoded antigens and causing the neoplastic cell to be eliminated by the host immune system.

Differentiation therapy is another technique which was developed on the concept that the acquisition of

the malignant phenotype (such as neoplasia) in a cell is considered as a progressive de-differentiation or a defective differentiation of that cell. Thus, as e.g. tumor cell populations evolve to greater degrees of malignancy, they usually lose more and more differentiation markers. This led to the suggestion that it may be possible to treat cancer by inducing differentiation of cancer cells. However, some scientific reports have shown that the differentiation therapy does not in fact induce cancer cells differentiation but instead restrains their growth thus allowing the application of more conventional therapies (such as chemotherapy) to eradicate the malignant cells. Examples of differentiation therapy involve the forced (re-expression of some specific micro-RNAs and thus rely on an intracellular action generally presenting the same drawbacks as in any other intracellular therapies such the siRNA and gene therapies.

A shortcoming of the medical therapies relying on previously reported methods of treatment are numerous and mainly resides in the incapacity of providing a sustainable therapeutic effect *i.e.* the treated cells are not healed but instead are either destroyed (*e.g.* through induced apoptosis) or their proliferation reduced or temporarily halted using a sustained administration of therapeutic molecules until, in most case scenarios, neoplastic cells are able to adapt themselves and render the therapy ineffective. Interrupting a known therapy will usually lead to resumption of the neoplastic cell state.

Other drawbacks associated with previously reported therapies are numerous. For example, they may be very invasive and traumatic for the patient; they may necessitate permanently removing neoplastic tissues or organs which may be in some cases not practicable or feasible (organs or organ parts not accessible) or not possible due to life-threatening consequences; they may not be applied to or have limited effectiveness against metastatic neoplastic cells; they may not possess the ability to remove or treat all neoplastic cell types (*i.e.* neoplastic cells having different invasiveness levels and/or of different lineage origins); they may potentially “unblock” dormant tumors; they are often expensive; they may damage or destroy healthy cells alongside neoplastic cells thereby causing adverse treatment side effects; they may cause skin rashes and skin sensitivity; they may not target cancer stem cells as these are not proliferating; they may have a mutagenic action even towards healthy cells; they may require sustained administration to maintain treatment therapeutic effects; they may display very high cytotoxicity; they may cause multi-drug resistance whereby a drug having an intracellular action is no longer imported inside the cancer cell or is systematically exported outside of the cell.

None of these previously known methods allows for the effective recoding of a neoplastic cell thus permitting conversion of a neoplastic cell into a non-neoplastic cell.

The present invention thus provides associations, combinations, compositions, kits, methods and processes for the design, preparation, manufacture and/or formulation thereof, and methods and uses thereof for converting a neoplastic cell into a non-neoplastic cell including converting or recoding the neoplastic cell to induce, provide and/or reintroduce self-recovery or self-healing capabilities thereto.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a representation of a fluorescence intensity of non-covalent pharmaceutical associations comprising GFR-binding compounds of the present disclosure and type-I collagen or apatite ceramics

bioactive carriers. The images represent surfaces non-covalently coated with GFR-binding compounds of the present disclosure labeled with FITC.

FIG. 2 is (a) a representation of a fluorescence intensity of pharmaceutical associations comprising various GFR-binding compounds of the present disclosure and type-I collagen immediately after association or 3, 7 and 10 days after association. The images represent surfaces non-covalently coated with GFR-binding compounds of the present disclosure labeled with FITC, (b) a total fluorescence intensity quantification of GFR-binding compounds of the present disclosure labeled with FITC associated with apatite ceramics after incubation in cell culture medium for the given indicated times (up to 10 days).

FIG. 3 is a representation of a Quantitative Real Time PCR analysis of the expression of DMP-1, Sclerostin and RANK-L in neoplastic cells (osteosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, ($P<0.001$).

FIG. 4 is a representation of Quantitative Real Time PCR analysis of the expression of MLC-1, GATA-4 and α-Sarcomeric actin in neoplastic cells (Rabdomiosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, ($P<0.005$).

FIG. 5 is a representation of Quantitative Real Time PCR analysis of the expression of Sox-9, IBSP and Collagen-IV in neoplastic cells (chondrosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, ($P<0.001$).

FIG. 6 is a representation of Quantitative Real Time PCR analysis of the expression of MMP-9, Vimentin and a-SMA in neoplastic cells (adenocarcinoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, ($P<0.005$).

FIG. 7 is (a) a diagram representing a relative quantification from western blot of the amount of p53 protein present in neoplastic cells (osteosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, (b) a diagram representing a relative quantification from western blot of the extent of phosphorylation of the pRB protein present in neoplastic cells cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture.

FIG. 8 is diagrams representing a relative quantification from western blot of the extent of phosphorylation of the ERK protein (a) and of the Src kinase (b) present in neoplastic cells (osteosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, (c) a diagram representing a relative quantification from western blot of the amount of PDK1 protein present in neoplastic cells cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture.

FIG. 9 is a representation of a Quantitative Real Time PCR analysis of the expression of Paxillin (a) and Vinculin (b) in neoplastic cells (osteosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure after 24 hours of culture, ($P<0.001$).

FIG. 10 is a representation of a Quantitative Real Time PCR analysis of the expression of Cyclin D (average gene expression of Cyclin D1, D2 and D3) at different time intervals during 24 hours in neoplastic cells (osteosarcoma cells) cultured on a native bioactive carrier (control) and on a bioactive carrier covalently associated with various GFR-binding compounds of the present disclosure.

FIG. 11 is a diagram representing the grafting or association density of various radiolabeled GFR-binding compounds of the present disclosure covalently associated with a bioactive carrier using radioactivity quantification.

FIG. 12 is (a) a representation of a Quantitative Real Time PCR analysis of the expression of DMP-1, SCT and RANK-L in neoplastic cells (osteosarcoma cells) cultured on a native polymer scaffold (control) and on a polymer scaffold grafted with a mixture comprising a GFR-binding compound as defined in the present disclosure and a RGD peptide, after 24 hours of culture, (b) immunofluorescence staining of a representative neoplastic cell (osteosarcoma cells) cultured on a polymer scaffold grafted with a mixture comprising a GFR-binding compound as defined in the present disclosure (ID SEQ NO: 2) and a RGD peptide, after 24 hours of culture. The actin filaments were immunostained by using Alexa 488-phalloidin. The focal adhesions were represented by immunostaining with anti-vinculin. The nucleus was stained with DAPI and is represented by a circle in the center of the cell. Scale bar: 5 µm. (c) is a diagram representing the grafting density of a radiolabeled GFR-binding compound as defined in the present disclosure covalently grafted on a polymer scaffold and of a radiolabeled GFR-binding compound and a non-labeled RGD peptide both grafted on a polymer scaffold. The measurements were performed by using radioactivity quantification (no significant difference was observed). (d) Relative cell spreading function as the presence of different integrin subunits (α and β) couples (anti-α3β1, anti- αvβ3 and anti-α5β3 in neoplastic cells cultured on a non-modified polymer scaffold, after 24h of culture.

FIG. 13 is (a) Western blot analysis of the expression integrin α3 and β1 before and after transduction with two independent integrin α3 and β1 shRNAs, which efficiently reduced endogenous integrin α3β1 protein levels. (b) Immunofluorescence visualization of a neoplastic cell (osteosarcoma cells) after silencing integrins α3β1 by using shRNAs, after 24 hours of culture on a polymer scaffold covalently grafted with RGD peptides. The silencing of these specific integrin proteins were shown to significantly reduce or suppress neoplastic cell adhesion on the RGD grafted polymers. The actin filaments were immunostained by using Alexa 488-phalloidin. The focal adhesions were represented by immunostaining with anti-vinculin. The nucleus was stained with DAPI and is represented by a circle in the center of the cell. Scale bar: 5 µm. (c) Immunofluorescence visualization of neoplastic cells cultured on a polymer scaffold covalently modified with a mixture comprising a GFR-binding compound as defined in the present disclosure (SEQ ID NO: 2) and a RGD peptide, after 24 hours of culture. Scale bar: 500 µm. A magnification of one region (right, Scale bar: 50 µm) indicates that Spheroid-like structures of neoplastic cells become predominant in this case as a result of the RGD induced integrin engagement. The actin filaments were immunostained by using Alexa 488-phalloidin. The focal adhesions were represented by immunostaining with anti-vinculin. The nucleus was stained with DAPI and is represented by a circle in the center of the cell.

FIG. 14 is a screen shot of the Standard Protein Blast online software used in the RMSD calculation procedure.

DETAILED DESCRIPTION

Neoplastic diseases start when a cell (or neoplastic cell) is somehow altered so that it multiplies out of control. Tumors and cancers are some examples of neoplastic diseases. A tumor is a mass composed of a cluster of such abnormal cells. Most cancers form tumors, but not all tumors are cancerous. Benign, or non-cancerous, tumors - such as freckles and moles - stop growing, do not spread to other parts of the body, and do not create new tumors. Malignant, or cancerous, tumors crowd out healthy cells, interfere with body functions, and draw nutrients from body tissues. Cancers continue to grow and spread by direct extension or through a process called metastasis, whereby the malignant cells travel through the lymphatic or blood vessels, eventually forming new tumors in other parts of the body.

The term "cancer" generally encompasses more than one hundred diseases affecting nearly every part of the body, and all are potentially life threatening. The major types of cancer are carcinoma, sarcoma, melanoma, lymphoma, and leukemia.

Carcinoma is a type of cancer that develops from epithelial cells. Specifically, a carcinoma is a cancer that begins in a tissue that lines the inner or outer surfaces of the body, and that generally arises from cells originating in the endodermal or ectodermal germ layer during embryogenesis.

Sarcoma is a cancer that arises from transformed cells of mesenchymal origin. Thus, malignant tumors made of cancerous bone, cartilage, fat, muscle, vascular or hematopoietic tissues are, by definition, considered sarcomas. This is in contrast to a malignant tumor originating from epithelial cells, which are termed carcinoma. Human sarcomas are quite rare. Common malignancies, such as breast, colon, and lung cancer, are almost always carcinoma.

Melanoma is a type of skin cancer, which forms from melanocytes (pigment-containing cells in the skin).

Lymphoma is a group of blood cell tumors that develop from lymphocytes. It is sometimes used to refer to just the cancerous ones rather than all tumors. There are two main types: Hodgkin lymphoma (HL) and non-Hodgkin lymphoma (NHL), with two others, multiple myeloma and immunoproliferative diseases, also included by the World Health Organization within the category. Non-Hodgkin lymphoma makes up about 90% of cases and includes a large number of sub-types. Lymphomas are part of the broader group of neoplasms called tumors of the hematopoietic and lymphoid tissues.

Leukemia is a group of cancers that usually begins in the bone marrow and results in high numbers of abnormal white blood cells. These white blood cells are not fully developed and are called blasts or leukemia cells. Symptoms may include bleeding and bruising problems, feeling very tired, and an increased risk of infections. These symptoms occur due to a lack of normal blood cells. Diagnosis is typically by blood tests or bone marrow biopsy.

Cancers include, but are not limited to, Adrenal Cancer, Anal Cancer, Bile Duct Cancer, Bladder Cancer, Bone Cancer, Brain/CNS Tumors In Adults, Brain/CNS Tumors In Children, Breast Cancer, Breast Cancer In Men, Cancer in Adolescents, Cancer in Children, Cancer in Young Adults, Cancer of Unknown

Primary, Castleman Disease, Cervical Cancer, Colon/Rectum Cancer, Endometrial Cancer, Esophagus Cancer, Ewing Family Of Tumors, Eye Cancer, Gallbladder Cancer, Gastrointestinal Carcinoid Tumors, Gastrointestinal Stromal Tumor (GIST), Gestational Trophoblastic Disease, Hodgkin Disease, Kaposi Sarcoma, Kidney Cancer, Laryngeal and Hypopharyngeal Cancer, Leukemia, Leukemia - Acute Lymphocytic (ALL) in Adults, Leukemia - Acute Myeloid (AML), Leukemia - Chronic Lymphocytic (CLL), Leukemia - Chronic Myeloid (CML), Leukemia - Chronic Myelomonocytic (CMML), Leukemia in Children, Liver Cancer, Lung Cancer, Lung Cancer - Non-Small Cell, Lung Cancer - Small Cell, Lung, Carcinoid Tumor, Lymphoma, Lymphoma of the Skin, Malignant Mesothelioma, Multiple Myeloma, Myelodysplastic Syndrome, Nasal Cavity and Paranasal Sinus Cancer, Nasopharyngeal Cancer, Neuroblastoma, Non-Hodgkin Lymphoma, Non-Hodgkin Lymphoma In Children, Oral Cavity and Oropharyngeal Cancer, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Penile Cancer, Pituitary Tumors, Prostate Cancer, Retinoblastoma, Rhabdomyosarcoma, Salivary Gland Cancer, Sarcoma - Adult Soft Tissue Cancer, Skin Cancer, Skin Cancer - Basal and Squamous Cell, Skin Cancer – Melanoma, Skin Cancer - Merkel Cell, Small Intestine Cancer, Stomach Cancer, Testicular Cancer, Thymus Cancer, Thyroid Cancer, Uterine Sarcoma, Vaginal Cancer, Vulvar Cancer, Waldenstrom Macroglobulinemia, Wilms Tumor.

The activation of growth factor receptors (GFR) is commonly known to promote neoplastic cell proliferation. For instance, many cancer treatments rely on the inhibition of growth factors, growth factors receptors and/or downstream signalling proteins such as protein kinases. Such inhibitors include, non-exhaustively, anti-Met (*e.g.* ARQ-197), anti-VEGF (*e.g.* Bevacizumab), anti-VEGFR (*e.g.* Sunitinib or Semaxinib), anti-Her2 (*e.g.* Trastuzumab), anti-EGFR (*e.g.* Cetuximab, Gefitinib or Erlotinib), anti-PDGFR (*e.g.* Imatinib), anti-IGF-1 (*e.g.* IMC-A12), anti-Ras (*e.g.* Tipifarnib), anti-Raf (*e.g.* Sorafenib), anti-src (*e.g.* Dastinib or Saracatinib), anti-Mek (*e.g.* C1040 or PD-0325901), anti-PI3K (*e.g.* LY294002), anti-PDK (*e.g.* UNC01), anti-HSP90 (*e.g.* 17-AGG or IPI-504), anti-CDK (*e.g.* Flavopiridol) and anti-mTOR (*e.g.* Everolimus).

Unlike previously reported treatments, it has been surprisingly demonstrated that the pharmaceutical associations, combinations and compositions disclosed herein can be used to treat, prevent and/or diagnose neoplasms (*e.g.* tumors or cancers) by activating growth factor receptors of vertebrate cells (such as mammalian cells, especially human cells).

The present invention also aims at providing mechanisms for solving and/or avoiding at least one of, preferably a plurality of, the problems, issues and/or shortcomings associated with previously reported neoplasm treatment therapies.

The present disclosure thus provides embodiments for:

- Converting or recoding a neoplastic cell to induce and/or promote and/or improve self-healing and/or self-recovery thereof, particularly within a shorter period of time
- Converting or recoding a neoplastic cell to induce and/or promote and/or improve self-healing and/or self-recovery thereof, particularly with a higher conversion yield;
- Restoring a neoplastic cell’s ability to undergo conversion into a physiologically functional and/or healthy cell, particularly within a shorter period of time;

- Restoring a neoplastic cell's ability to undergo differentiation, particularly within a shorter period of time;
- Converting and/or recoding a circulating or non-circulating neoplastic cell such as a cancer cell, into a non-neoplastic cell, particularly within a shorter period of time;
- Protecting a subject from a neoplastic disease, disorder, condition, or pathology such as cancer, or any symptoms thereof, particularly within a shorter period of time;
- Providing and/or producing a physiologically functional and/or healthy cell including an osteocyte and/or a chondrocyte and/or an adipocyte and/or a myocyte and/or a keratinocyte and/or a fibrocyte and/or a podocyte and/or a neurocyte and/or a mature endothelial cell and/or a osteoblast and/or a chondroblast and/or a neuroblast and/or a Sertoli cell and/or a Leydig cell and/or a germ cell and/or an endothelial cell and/or an angioblast and/or a fibroblast from a neoplastic cell, particularly within a shorter period of time;
- Re-establishing, restoring and/or reactivating a cell adhesion checkpoint of a neoplastic cell;
- Inducing and/or promoting and/or enhancing neoplastic cell differentiation, particularly within a shorter period of time;
- Inducing and/or promoting and/or enhancing a decrease in Cyclin D gene and protein expression;
- Inducing and/or promoting and/or enhancing a G1 to G0 cell cycle phase transition;
- Inducing and/or promoting and/or enhancing the inactivation of a protein complex between a Cyclin D and at least one of Cyclin-dependent kinase (CDK) 4 or 6;
- Preventing or reducing the phosphorylation of the retinoblastoma (Rb) protein thus activating its tumour suppressor functions;
- Increasing the phosphorylation of the p53 protein thus reducing its degradation and activating its tumor suppressor functions;
- Preventing or reducing the activation of the Ras/MAP kinase signalling cascade;
- Identifying and/or analysing the features and/or markers of a neoplastic cell;
- Regulating and/or activating growth factor receptors of a neoplastic cell;
- Modulating and/or regulating the adhesion between a cell (in particular a neoplastic cell) and its micro-environment *i.e.* the surrounding extracellular matrix;
- Treating, recoding or converting a neoplastic cell without temporarily or permanently damaging or killing said neoplastic cell and/or without permanently inducing a quiescent state thereof;
- Dampening and/or reducing or suppressing cell division and/or cell proliferation of a neoplastic cell;
- Activating and/or promoting and/or regulating anti-mitogen activity and/or tumor suppressor pathways in a neoplastic cell;
- Inhibiting and/or reducing anti-oncogenic activity in a neoplastic cell;
- Converting or recoding a neoplastic cell to induce and/or promote and/or improve self-healing and/or self-recovery thereof, and/or protecting a subject from a neoplastic disease, disorder, condition or pathology such as cancer using extracellular means;
- Converting or recoding a neoplastic cell to induce and/or promote and/or improve self-healing and/or self-recovery thereof, protecting a subject from a neoplastic disease, disorder, condition or pathology such as cancer without modifying the genome of said cell;

- Providing diagnostic tools for diagnosing neoplastic diseases in a subject.

I. Definitions

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the invention described herein. The scope of the present invention is not intended to be limited to the present description, but rather is as set forth in the appended claims.

In the claims, articles such as "a", "an", and "the" may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include "or" between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention includes embodiments in which more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process.

It is also noted that the term "comprising" is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term "comprising" is used herein, the terms "consisting of", “consisting essentially of”, “consisting substantially of” and “consisting exclusively of” are thus also encompassed and disclosed.

As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise indicated, self-evident or contradictory in context (*e.g.* except where such number would exceed 100% of a possible value).

As used herein and unless otherwise indicated or contradictory in context, the term “with” followed by a specific number of amino acids, when used to define a particular peptide, variant or analog thereof, such as in “a peptide with three amino acids”, means that such peptide, variant or analog thereof, contains exclusively the specific number of amino acids specified after this term.

As used herein and unless otherwise indicated or contradictory in context, the term “Ci-alkyl” is intended to specifically and individually disclose any branched or unbranched radical, moiety or functional group having “i" carbon atom(s).

The carbon atom content of the various hydrocarbon-containing moieties herein may be indicated by a prefix designating the minimum and maximum number of carbon atoms in the moiety. For example, in certain embodiments, (Ca-Cb)alkyl indicates an alkyl moiety of the integer "a" to the integer "b" carbon atoms, inclusive.

At various places in the present specification, substituents of compounds of the present disclosure may be disclosed in groups or in ranges. It is specifically intended that the present disclosure include each and every individual sub-combination of the members of such groups and ranges. For example, in certain embodiments, the term "C1-C5 alkyl" is an abbreviation for (and thus is specifically intended to individually disclose) C1-alkyl (*i.e.* methyl), C2-alkyl (*i.e.* ethyl), C3-alkyl (*i.e.* 1-propyl and 2-propyl), C4-alkyl (*i.e.* 1-butyl, *sec*-butyl, *iso*-butyl and *tert*-butyl), and C5-alkyl (*i.e.* 1-pentyl, 2-pentyl, 3-pentyl, 2-methyl-1-butyl, 3-methyl-1-butyl, 2-methyl-2-butyl, 3-methyl-2-butyl, 2,2-dimethyl-1-propyl and 1,1-dimethyl-1-propyl).

As used herein, unless indicated otherwise or contradictory in context, the terms "alkyl" and "(Ca-Cb)alkyl" refer to monovalent hydrocarbon radicals containing the requisite number of carbon atoms as described above, having straight or branched moieties or combinations thereof. As used herein, alkyl groups may be optionally substituted with between one to four substitutes. Non-limiting examples of alkyl groups include, *e.g.* methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, sec-butyl, t-butyl, etc. Of course, other alkyl groups will be readily apparent to those of skilled in the art given the benefit of the present disclosure.

Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or sub-range within the stated ranges in different embodiments of the invention, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise. For example, in certain embodiments, a disclosed 0-10 range would, for example, in certain embodiments, also specifically and individually disclose the following values and ranges: 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 0-1, 0-2, 0-3, 0-4, 0-5, 0-6, 0-7, 0-8, 0-9, 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 2-3, 2-4, 2-5, 2-6, 2-7, 2-8, 2-9, 2-10, 3-4, 3-5, 3-6, 3-7, 3-8, 3-9, 3-10, 4-5, 4-6, 4-7, 4-8, 4-9, 4-10, 5-6, 5-7, 5-8, 5-9, 5-10, 6-7, 6-8, 6-9, 6-10, 7-8, 7-9, 7-10, 8-9, 8-10, 9-10, 0-0.1, 0-0.2, 0-0.3, 0-0.4, 0-0.5, 0-0.6, 0-0.7, 0-0.8, 0-0.9, 0-1.1, 0-1.2, etc.

As used herein and unless otherwise indicated or contradictory in context, the term "substantially" refers to the qualitative condition of exhibiting total or near-total extent or degree of a characteristic or property of interest. One of ordinary skill in the biological arts will understand that biological and chemical phenomena rarely, if ever, go to completion and/or proceed to completeness or achieve or avoid an absolute result. The term "substantially" is therefore used herein to capture the potential lack of completeness inherent in many biological and chemical phenomena.

In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from any one or more of the claims using the appropriate

disclaimer(s) or proviso(s). Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the invention (e.g., any peptide or peptidomimetic; any method of production; any method of use; etc.) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

All cited sources, for example, in certain embodiments, references, publications, databases, database entries, and art cited herein, are incorporated into this application by reference in their entirety, even if not expressly stated in the citation. In case of conflicting statements of a cited source and the instant application, the statement in the instant application shall control.

As the case may be, and unless otherwise indicated or contradictory in context, macromolecules molecular weights should be understood in the present description as being number averaged molecular weights.

The peptides mentioned in the present description may not follow the usual representation conventions. For instance, the N-terminal amino acid of a peptide sequence may be the first amino acid in the sequence or the last amino acid. Likewise, the C-terminal amino acid of a peptide sequence may be the first amino acid in the sequence or the last amino acid. For example, in the peptide sequence NAIS, “N” may be N-terminal or C-terminal, and “S” may be N-terminal or C-terminal. Consequently, for the purpose of the present disclosure, e.g. NAIS also covers SIAN, SAIS also covers SIAS, SPIN also covers NIPS, etc.

In the present application, when reference is made to a certain peptide (*e.g.* a GFR-binding compound as provided herein) comprising one or more other peptide(s), said one or more other peptide(s) is(are) understood to be stably (in most cases, covalently) attached/bound to at least one part of said peptide. The attachment/binding may be located anywhere on the peptide unless indicated otherwise, contradictory in context or contradictory to general scientific rules. No specific attachment/binding location of said one or more other peptide(s) to said peptide shall be assumed unless specifically mentioned.

Peptide or polypeptide: As used herein, the term "peptide" or “polypeptide” are used interchangeably and refers to a polymer of less than or equal to 100 amino acids long, e.g., about 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 amino acids long. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, non-naturally occurring amino acid polymers, peptide analogs, peptide variants and peptide mimetics. Conventional techniques for synthesising peptides involve the activation of the carboxylic acid function of an amino acid or of a peptide, using a coupling agent. This activated acid is then contacted with an amino acid or a peptide in which the N-terminal amino acid is not protected, thus forming an amide bond also called peptide bond. Coupling reaction conditions together with coupling agents are well known in the art and described, for instance, in Greene, "Protective Groups in Organic Synthesis", Wiley, New York, 2007 4th edition. In addition, suitable peptide synthesis routes are described, for instance, in Hojo H., Recent

progress in the chemical synthesis of proteins, Curr Opin Struct Biol. 2014; 26C:16-23 and Saranya Chandrudu, *et al.*, Chemical Methods for Peptide and Protein Production, Molecules, 2013, 18, 4373-4388, each of which is incorporated herein by reference in its entirety. There are two main strategies for peptide synthesis i.e. liquid-phase peptide synthesis and solid-phase peptide synthesis (SPPS) which is now most commonly used for peptide synthesis. Instead of C-terminal protection with a chemical group, the C-terminus of the first amino acid is coupled to an activated solid support, such as polystyrene or polyacrylamide. This type of approach has a two-fold function: the resin acts as the C-terminal protecting group and provides a rapid method to separate the growing peptide product from the different reaction mixtures during synthesis. As with many different biological manufacturing processes, peptide synthesizers have been developed for automation and high-throughput peptide production. SPPS allows the synthesis of natural peptides which are difficult to express in bacteria, the incorporation of unnatural amino acids, peptide/protein backbone modification, and the synthesis of D-proteins, which consist of D-amino acids. Very long peptide can be accessed by using native chemical ligation to couple two peptides together with quantitative yields.

Peptide analogs: As used herein, unless indicated otherwise or contradictory in context, the term “peptide analogs” refers to polypeptide variants which differ by one or more amino acid alterations, e.g., substitutions, additions or deletions of amino acid residues that still maintain one or more of the properties of the parent or starting peptide.

Peptide variants: As used herein, unless indicated otherwise or contradictory in context, the term “peptide variants” refers to a peptide which has a certain identity with a native or reference compound sequence. In one example, the peptide variant refers to any post- administration, application, injection modified peptide. Such post- administration, application, injection modifications include, but are not limited to, phosphorylation, acetylation, glutamylation, tyrosination, palmitoylation, glycosylation, myristoylation, palmitoylation, isoprenylation, glypiation, lipoylation, phosphopantetheinylation, acylation, alkylation, amidation, arginylation, polyglutamylation, polyglycylation, butyrylation, gamma-carboxylation, glycosylation, polysialylation, malonylation, hydroxylation, iodination, nucleotide addition, oxidation, adenylylation, propionylation, pyroglutamate formation, S-glutathionylation, S-nitrosylation, succinylation, sulfation, glycation, biotinylation, pegylation, ISGylation, SUMOylation, ubiquitination, Neddylation, Pupylation, citrullination, deamidation, eliminylation, carbamylation, and racemization.

Peptido-mimetic: As used herein, unless indicated otherwise or contradictory in context, the term “peptido-mimetic” or “peptidomimetic” refers to a synthetic chemical compound which comprises amino acids but not only and that is able to mimic the biological action of a peptide, often because the mimetic has a basic structure that mimics the basic structure of the peptide and/or has the salient biological properties of that peptide. In one particular example, a peptidomimetic is a hybrid molecule containing both, at least one peptide, and at least one of a polysaccharide, a polynucleotide or a linear or branched, saturated or unsaturated, hydrocarbon chain.

Linear peptide: As used herein, unless indicated otherwise or contradictory in context, the term "linear peptide” means a peptide in which the C-terminal and the N-terminal amino acid residues do not

covalently interact with each other and none of the C-terminal or the N-terminal amino acid residues covalently interacts with another amino acid residue of the peptide chain.

Cyclic peptide: As used herein, unless indicated otherwise or contradictory in context, the term "cyclic peptide" means peptide in which the C-terminal and N-terminal amino acid residues do covalently interact with each other or the C-terminal and/or the N-terminal amino acid residues covalently interact with at least one other amino acid residue of the peptide chain so as to form a ring-like structure.

Amino acid: As used herein, unless indicated otherwise or contradictory in context, the term "amino acid" refers to naturally occurring and non-naturally occurring amino acids including amino acid analogs. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, [gamma]-carboxyglutamate, and O-phosphoserine. Naturally encoded amino acids are the 20 common amino acids glycine (Gly, G), alanine (Ala, A), valine (Val, V), leucine (Leu, L), isoleucine (Ile, I), serine (Ser, S), threonine (Thr, T), phenylalanine (Phe, F), tyrosine (Tyr, Y), tryptophane (Trp, W), cysteine (Cys, C), methionine (Met, M), proline (Pro, P), aspartic acid (Asp, D), asparagine (Asn, N), glutamine (Gln, Q), glutamic acid (Glu, E), histidine (His, H), arginine (Arg, R) et lysine (Lys, K) and pyrrolysine and selenocysteine. Non-naturally occurring amino acids include, but are not limited to, the dextrogyre (D) isomers of the above-cited naturally-occurring amino acids. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid *i.e.,* an [alpha] carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group (*i.e.* side chain), and which may be used in replacement thereof without substantially affecting the overall function of the peptide to which it belongs. Amino acid analogs (or non-naturally occurring amino acids) that may be suitable for implementing embodiments of the present invention include, but are not limited to, amino acids comprising a photoactivatable cross-linker, spin-labeled amino acids, fluorescent amino acids, metal binding amino acids, metal-containing amino acids, radioactive amino acids, amino acids with novel functional groups, amino acids that covalently or noncovalently interact with other molecules, photocaged and/or photoisomerizable amino acids, amino acids comprising biotin or a biotin analogue, glycosylated amino acids such as a sugar substituted serine, other carbohydrate modified amino acids, keto-containing amino acids, amino acids comprising polyethylene glycol or polyether, heavy atom substituted amino acids, chemically cleavable and/or photocleavable amino acids, amino acids with an elongated side chains as compared to natural amino acids, including but not limited to, polyethers or long chain hydrocarbons, including but not limited to, greater than about 5 or greater than about 10 carbons, carbon-linked sugar-containing amino acids, redox-active amino acids, amino thioacid containing amino acids, and amino acids comprising one or more toxic moiety. The term "**AA^{I}**" (AA roman numeral one) may be used in the description and refers to an amino acid which may be any amino acid as defined above in particular any naturally occurring and non-naturally occurring amino acids.

Amino acid side chain: As used herein, unless indicated otherwise or contradictory in context, the term "amino acid side chain" means the functional group of an amino acid that differentiates it from other amino acids. All amino acid structures have a carboxyl group, an amine group and a specific side chain.

AA^{II} (AA roman numeral two): As used herein, unless indicated otherwise or contradictory in context, the terms “polar amino acid” or “AA^{II}” means amino acids having a polar, non-charged group-containing side chain. Polar amino acids are protonated at physiological pH (about 7). Examples of polar amino acids include, but are not limited to, Cys (C), Asn (N), Gln (Q), Ser (S), Thr (T), or Tyr (Y).

AA^{III} (AA roman numeral three): As used herein, unless indicated otherwise or contradictory in context, the terms “acidic amino acid” or “AA^{III}” means amino acids having an acidic group-containing side chain. Acidic amino acid deprotonated forms predominate at physiological pH (about 7). Examples of acidic amino acids include, but are not limited to, Asn (N) and Glu (E).

AA^{IV} (AA roman numeral four): As used herein, unless indicated otherwise or contradictory in context, the terms “aliphatic amino acid” or “AA^{IV}” means amino acids having an aliphatic side chain. Examples of aliphatic amino acids include, but are not limited to, Ala (A), Leu (L), Ile (I), Gly (G), Val (V) and any analogs and derivatives thereof.

AA^{V} (AA roman numeral five): As used herein, unless indicated otherwise or contradictory in context, the terms “apolar amino acid” or “AA^{V}” means amino acids having an apolar side chain. Examples of apolar amino acids include, but are not limited to, Ala (A), Phe (F), Gly (G), Ile (I), Leu (L), Met (M), Pro (P), Val (V) or Trp (W).

AA^{VI} (AA roman numeral six): As used herein, unless indicated otherwise or contradictory in context, the term “aromatic amino acid” or “AA^{VI}” means amino acids having an aromatic group-containing side chain. Examples of aromatic amino acids include, but are not limited to, Trp (W), Tyr (Y) or Phe (F).

AA^{VII} (AA roman numeral seven): As used herein, unless indicated otherwise or contradictory in context, the term “basic amino acid” or “AA^{VII}” means amino acids having a basic group-containing side chain. Basic amino acid protonated forms predominate at physiological pH (about 7). Examples of basic amino acids include, but are not limited to, Arg (R), His (H), or Lys (K).

AA^{VIII} (AA roman numeral eight): As used herein, unless indicated otherwise or contradictory in context, the term “AA^{VIII}“ means Leu (L) or Ile (I) and any analogs and derivatives thereof.

AA^{IX} (AA roman numeral nine): As used herein, unless indicated otherwise or contradictory in context, the term “charged amino acid” or “AA^{IX}” means amino acids having either an acidic group-containing side chain or an basic group-containing side chain. Charged amino acid charged forms predominate at physiological pH (about 7). Examples of charged amino acids include, but are not limited to, Asn (N), Glu (E), His (H), Lys (K) or Arg (R).

AA^{n}: As used herein, unless indicated otherwise or contradictory in context, the term “AA^{n}”, in which n is a positive integer arbitrarily chosen to identify a specific position within the primary sequence of a peptide. For instance, AA^{13} means the amino acid of position 13. The terms “amino acid” and “AA” are interchangeably used in the present description.

N-terminal: As used herein, unless indicated otherwise or contradictory in context, the term “N-terminal” means the amine (-NH_2) function/group/moiety located at one (terminal) end of a protein or polypeptide. This functional group is the only amine group which is not engage in n amide peptide bond.

C-terminal: As used herein, unless indicated otherwise or contradictory in context, the term “C-terminal” means the carboxylate (-CO_2H) function/group/moiety located at one (terminal) end of a protein or polypeptide. This functional group is the only carboxylic acid group which is not engage in n amide peptide bond.

Naturally-occurring peptide: As used herein, unless indicated otherwise or contradictory in context, the terms "naturally-occurring peptide” or “natural peptide” means a peptide which may be found in nature without human direct intervention (except for its extraction and/or isolation).

Synthetic peptide: As used herein, unless indicated otherwise or contradictory in context, the terms "synthetic peptide” or “non-natural peptide” means a peptide which may not be found in nature without human direct intervention (except for its extraction and/or isolation). For example, in certain embodiments, a synthetic peptide may have the amino acid sequence of a natural peptide except for at least one amino acid deletion or substitution relative to the natural sequence. In the case of a substitution, an amino acid from the natural sequence is replaced by another, different, naturally-occurring or non-naturally occurring amino acid. For example, in certain embodiments, a synthetic peptide may not possess a post-translational modification of the natural peptide such as the attachment of an acetate group, a phosphate group, a lipid, a carbohydrate, or the formation of a disulfide bridge.

Covalent interaction: As used herein, unless indicated otherwise or contradictory in context, the term “interact covalently”, “covalent interaction” or “covalent bond” are interchangeably used and means a chemical bond or interaction that involves the sharing of electron pairs between atoms. Examples of such interactions are σ-bonding and π-bonding.

Non-covalent interaction: As used herein, unless indicated otherwise or contradictory in context, the term “interact non-covalently”, “non-covalent interaction” or “non-covalent bond” are interchangeably used and means a chemical bond or interaction that does not involve the sharing of electron pairs between atoms but rather involves more dispersed variations of electromagnetic interactions between molecules or within a molecule. Non-covalent interactions can be generally classified into four categories, electrostatic interactions, π-interactions, van der Waals forces, and hydrophobic interactions.

Electrophile: As used herein, unless indicated otherwise or contradictory in context, the term “electrophile” means an organic molecule attracted to electrons that participates in a chemical reaction by accepting an electron pair in order to bond to a nucleophile. Most electrophiles are positively charged, have an atom that carries a partial positive charge, or have an atom that does not have an octet of electrons.

Nucleophile: As used herein, unless indicated otherwise or contradictory in context, the term “nucleophile” means an organic molecule that donates an electron pair to an electrophile to form a chemical bond in relation to a reaction. All molecules or ions with a free pair of electrons or at least one pi bond can act as nucleophiles.

Polysaccharide: As used herein, unless indicated otherwise or contradictory in context, the term “polysaccharide” means polymeric carbohydrate molecules composed of long chains of monosaccharide units bound together by glycosidic linkages and which upon hydrolysis provide monosaccharides or oligosaccharides. They range in structure from linear to highly branched polymers.

Polynucleotide: As used herein, the term “polynucleotide” or “nucleic acid”, which are used interchangeably, refers to the phosphate ester polymeric form of ribonucleosides ("RNA molecules") or deoxyribonucleosides ("DNA molecules"), or any phosphoester analogs thereof, such as phosphorothioates and thioesters, in either single stranded form, or a double-stranded helix. The term "nucleic acid" includes double-stranded DNA round, inter alia, in linear (*e.g.,* restriction fragments) or circular DNA molecules. In particular, nucleic acids as used herein refer to nucleic acids such as RNAs encoding for agonist of growth factor receptors as defined herein.

Nucleoside: As used herein, the term “nucleoside” refers to a compound containing a sugar molecule (e.g., a pentose or ribose) or derivative thereof in combination with an organic base (e.g., a purine or pyrimidine) or a derivative thereof (also referred to herein as "nucleobase").

Nucleotide: As used herein, the term "nucleotide" refers to a nucleoside including a phosphate group.

Dendrimer: As used herein, unless indicated otherwise or contradictory in context, the term “dendrimer” means any repetitively branched molecules. Examples of dendrimers are phosphorous dendrimers, polylysine dendrimers, polypropylenimine dendrimers and PAMAM dendrimers, such as the ones described, for instance, in Scientific World Journal. 2013; 2013:732340; Curr Opin Chem Biol. 1998; 2(6):733-42; J Pept Sci. 1999; 5(5):203-20; and J Pept Sci. 2008; 14(1):2-43, which may be used for implementing embodiments of the present invention, each of which being herein incorporated by reference in its entirety.

Synthetic molecule: As used herein, unless indicated otherwise or contradictory in context, the term “synthetic molecule” means a molecule which may not be found in nature without human direct intervention (except for its extraction and/or isolation).

Synthetic polymers: As used herein, unless indicated otherwise or contradictory in context, the term “synthetic polymer” refers to a macromolecule or polymer which may not be found in nature without human direct intervention (except for its extraction and/or isolation).

Biocompatible: As used herein, unless indicated otherwise or contradictory in context, the term "biocompatible" means compatible with living cells, tissues, organs or systems posing little to no risk of

injury, toxicity or rejection by the immune system.

Biologically active: As used herein, unless indicated otherwise or contradictory in context, the term "biologically active" refers to a characteristic of any substance that has activity in a biological system and/or organism. For instance, a substance that, when administered to an organism, has a biological effect on that organism, is considered to be biologically active. In particular examples, a compound, substance or pharmaceutical composition of the present disclosure may be considered biologically active even if a portion of the compound, substance or pharmaceutical composition is biologically active or mimics an activity considered biologically relevant.

Stem cells: As used herein, unless indicated otherwise or contradictory in context, the term “stem cell” refers to the term as it is generally understood in the art. For example, in certain embodiments, stem cells, regardless of their source, are cells that are capable of dividing and renewing themselves for long periods, are at least to a degree unspecialized (undifferentiated), and can give rise to (differentiate into) specialized cell types (i.e., they are progenitor or precursor cells for a variety of different, specialized cell types).

Mesenchymal stem cells: As used herein, unless indicated otherwise or contradictory in context, the term “mesenchymal stem cells” generally means multipotent adult stromal cells that can differentiate into a variety of cell types, such as osteoblasts, chondrocytes, and adipocytes.

Stem cell-like: As used herein, unless indicated otherwise or contradictory in context, the term “Stem cell-like” refers to a cell which is not a stem cell by its origin but functions as a stem cell and presents similar characteristics such as, for example, the expression of stemness markers like Stro-1 and/or is multipotent thus has the ability to differentiate into various cell types.

Progenitor cells: As used herein, unless indicated otherwise or contradictory in context, the term “progenitor cells” generally means a biological cell that, like any stem cell, has a tendency to differentiate into a specific type of cell, but is already more specific than a stem cell and is pushed to differentiate into its "target" cell. Stem cells can generally replicate indefinitely, whereas progenitor cells can divide only a limited number of times.

Adult stem cells: As used herein, unless indicated otherwise or contradictory in context, the term “adult stem cells” means undifferentiated cells, found throughout the body after development, that multiply by cell division to replenish dying cells and regenerate damaged tissues. Also known as somatic stem cells, they can be found in juvenile as well as adult animals and human bodies.

Differentiation: As used herein, unless indicated otherwise or contradictory in context, the term “differentiation” refers to the process by which a less specialized cell becomes a more specialized cell type and involves a switch from one gene expression pattern to another.

Differentiated cells: As used herein, unless indicated otherwise or contradictory in context, the term

"differentiated cells" generally means any cell of a specific lineage at the exception of cells containing stem cell specific markers.

Non-terminally differentiated: As used herein, unless indicated otherwise or contradictory in context, the term "non-terminally differentiated", when used in relation to a cell, refers to a differentiated cell as defined herein which has not reached its final state of differentiation. For example, in certain embodiments, in the Osteoblast cell lineage, a non-terminally differentiated cell is any differentiated cell of the lineage at the exception of an osteocyte.

Terminally differentiated: As used herein, unless indicated otherwise or contradictory in context, the term "terminally differentiated", when used in relation to a cell, refers to a differentiated cell as defined herein which has reached its final state of differentiation. For example, in certain embodiments, in the Osteoblast cell lineage, a terminally differentiated cell is an osteocyte.

Methods for obtaining stem cells: Methods for obtaining such stem cells and providing initial culture conditions, such as a liquid culture or semi-solid culture medium, are known in the art. The cells are initially expanded in vivo or in vitro, by contacting the source of the stem cells with a suitable reagent that expands or enriches such cells in the tissue source or in culture. Preferably, adult stem cells are isolated from a tissue source and then expanded or enriched in vitro by exposure to a suitable agent. Cells are obtained from an individual by any suitable method for obtaining a cell sample from an animal, including, but not limited, to, collection of bone marrow collection of a bodily fluid (e.g., blood), collection of umbilical cord blood, tissue punch, and tissue dissection, including particularly, but not limited to, any biopsies of skin, intestine, cornea, spinal cord, brain tissue, scalp, stomach, breast, lung (*e.g.*, including lavage and bronchioschopy), fine needle aspirates of the bone marrow, amniotic fluid, placenta and yolk sac.

Cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "cell lineage" refers to the developmental history of a particular cell from its primary state in the fertilized egg or embryo through to its fully differentiated state. The different steps and phases involved in the development of a cell produces many intermediate cells which may be referred to as progenitor or precursor cells in the present application and form an integral part of the cell lineage.

Bone: It is conventionally known that mature osteoblasts are the cells responsible for bone formation and are derived from osteoblast precursors. Differentiation of human bone marrow mesenchymal stem cells and osteoblast precursors is one of the important processes for bone regeneration. Osteoblasts differentiate from mesenchymal stem cells. Mature osteoblasts differentiate from osteoblast precursors and into osteocytes which are non-dividing cells. Bone-related neoplastic diseases include, but are not limited to, bone primary tumors (benign tumors or cancers) such as osteoma, osteoid osteoma, osteochondroma, osteoblastoma, enchondroma, giant cell tumor of bone, aneurysmal bone cyst, fibrous dysplasia of bone, osteosarcoma, chondrosarcoma, Ewing's sarcoma, fibrosarcoma; and secondary tumors (*i.e.* metastasize) such as, for example, in certain embodiments, carcinomas of the prostate, breasts, lungs, thyroid, and kidneys.

Osteoblast cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "osteoblast cell lineage" refers to bone cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, osteoblasts, osteocytes or any precursors thereof.

Cartilage: Native chondrocytes are responsible for the synthesis and turnover of the cartilage extracellular matrix (ECM), which provides an environment of nutrition diffusion for chondrocytes and provides the joint surface with biomechanical competence. Chondrogenic cells arise from pluripotential adult mesenchymal stem cells (MSCs) through a series of differentiation pathways. Chondrogenic differentiation of MSCs is induced by various intrinsic and extrinsic factors. Growth factors play an important role in this process. For instance, in the hyaline cartilage, growth factors regulate homeostasis and integrity, as well as development. Cartilage-related neoplastic diseases include, but are not limited to, Chondroma/ecchondroma/enchondroma (Enchondromatosis, Extraskeletal chondroma), Chondrosarcoma (Mesenchymal chondrosarcoma, Myxoid chondrosarcoma), Osteochondroma (Osteochondromatosis), Chondromyxoid fibroma, and Chondroblastoma,

Chondrocytic cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "chondrocytic cell lineage" refers to cartilage cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, chondroblasts, chondrocytes or any precursors thereof.

Muscles: Skeletal muscle is a highly complex and heterogeneous tissue serving a multitude of functions in the organism. The process of generating muscle - myogenesis - can be divided into several distinct phases. During embryonic myogenesis, mesoderm-derived structures generate the first muscle fibers of the body proper, and in subsequent waves additional fibers are generated along these template fibers. In the perinatal phase, muscle resident myogenic progenitors initially proliferate extensively but, later on, decrease as the number of myonuclei reaches a steady state and myofibrillar protein synthesis peaks. Once the muscle has matured, these progenitors will enter quiescence and henceforth reside within it as satellite cells. Adult skeletal muscle, like all renewing organs, relies on a mechanism that compensates for the turnover of terminally differentiated cells to maintain tissue homeostasis. This type of myogenesis depends on the activation of satellite cells that have the potential to differentiate into new fibers. The most comprehensively studied form of myogenesis takes place when mature muscle is damaged and large cohorts of satellite cells expand mitotically and differentiate to repair the tissue and reestablish homeostasis. It is now generally accepted that satellite cells are closely related to progenitors of somitic origin. The activation of the network of transcription factors that controls skeletal muscle development depends on paracrine factors that are released by adjacent tissues, such as the neural tube, notochord, surface ectoderm and lateral mesoderm. Several secreted factors have been identified that determine the spatial and temporal onset of myogenesis. Signalling molecules, such as Noggin and bone morphogenetic proteins (BMPs) - which inactivate and activate receptors of the transforming growth factor-β (TGFβ) superfamily, respectively – are reported to participate in the orchestration of the activation of myogenesis. Muscle-related neoplastic diseases include, but are not limited to, Rhabdomyosarcoma, and Leiomyosarcoma.

Muscle cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "muscle cell lineage" refers to muscle cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, myoblasts, myocytes or any precursors thereof.

Vascular: The vasculature in the human body forms through two distinct processes: vasculogenesis and angiogenesis. Vasculogenesis is defined as the process of de novo blood vessel formation occurring when endothelial precursor cells (angioblasts) migrate and differentiate into endothelial cells which form the new vessel. These vascular trees are then extended through angiogenesis which is defined as the new vessel formation secondary to proliferation of endothelial cells from pre-existing vessels. Vasculogenesis as well as angiogenesis occur during the embryologic development of the circulatory system but also in the adult organism from circulating endothelial progenitor cells (derivatives of stem cells) able to contribute, albeit to varying degrees, to neovascularization. Vascular-related neoplastic diseases include, but are not limited to, Hemangiosarcoma, Kaposi's sarcoma, Lymphangiosarcoma, and Infantile hemangio-pericytoma.

Vascular cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "vascular cell lineage" refers to vascular cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, angioblast, pericytes and endothelial cells or any precursors thereof.

Neurons: It was recently reported that neural cells can be regenerated from neural stem cells (NSCs). These are self-renewing, multipotent adult stem cells that generate the main phenotype of the nervous system. They undergo asymmetric cell division into two daughter cells, one non-specialized and one specialized. NSCs primarily differentiate into neurons, astrocytes, and oligodendrocytes. NSCs are generated throughout an adult's life via the process of neurogenesis. NSCs can be differentiated to replace lost or injured neurons or in many cases even glial cells. NSCs are stimulated to begin differentiation via exogenous cues from their microenvironment, or the neural stem cell niche. This niche defines a zone in which stem cells are retained after embryonic development for the production of new cells of the nervous system. This continual supply of new neurons and glia then provides the postnatal and adult brain with an added capacity for cellular plasticity. Critical to the maintenance of the stem cell niche are microenvironmental cues and cell-cell interactions that act to balance stem cell quiescence with proliferation and to direct neurogenesis versus gliogenesis lineage decisions. Several proteins like different growth factors are involved in the mechanisms of the neural stem cell niche as well as in the maintenance and growth of the newly formed neurons. These include the BMPs, FGFs, PDGF, VEGF, TGF β, BDNF and others. Neuron-related neoplastic diseases include, but are not limited to, Anaplastic astrocytoma, Astrocytoma, Central neurocytoma, Choroid plexus carcinoma, Choroid plexus papilloma, Choroid plexus tumor, Dysembryoplastic neuroepithelial tumour, Ependymal tumor, Fibrillary astrocytoma, Giant-cell glioblastoma, Glioblastoma multiforme, Gliomatosis cerebri, Gliosarcoma, Hemangiopericytoma, Medulloblastoma, Medulloepithelioma, Meningeal carcinomatosis, Neuroblastoma, Neurocytoma, Oligoastrocytoma, Oligodendroglioma, Optic nerve sheath meningioma, Pediatric ependymoma, Pilocytic astrocytoma, Pinealoblastoma, Pineocytoma, Pleomorphic anaplastic neuroblastoma, Pleomorphic xanthoastrocytoma, Primary central nervous system lymphoma, Sphenoid

wing meningioma, Subependymal giant cell astrocytoma, Subependymoma, and Trilateral retinoblastoma.

Neuronal cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "neuron lineage" refers to brain cells at any stage of their development and thus include, but are not limited to, neural stem cells, neuroblast, neurocyte and neuroglial cells or any precursors thereof.

Eye retina: The vertebrate retina is a light-sensitive layer of tissue, lining the inner surface of the eye. Retinal development involves a complex progression of tissue induction, proliferation of retinal progenitor cell (RPC) populations and terminal differentiation of these cells into specific functional types. Bone morphogenetic protein (BMP), is a member of the transforming growth factor (TGF)-β family of signaling molecules plays an important role in the retinal cell development. BMP-2, -4, and -7 and their receptors (BMPRs) are expressed in the eye during embryogenesis and are essential for multiple aspects of retinal development. Retina-related neoplastic diseases include, but are not limited to, Retinoblastoma. It should also be noted that eye cancers can be primary (starts within the eye) and metastatic (spread to the eye from another organ). The two most common cancers that would spread to the eyes from another organ are breast cancer and lung cancer. Other, less common, sites of origin include prostate, kidney, thyroid, skin, colon and blood or bone marrow.

Retinal cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "retinal cell lineage" refers to eye retina cells at any stage of their development and thus include, but are not limited to, photoreceptor, bipolar cells, rod and cone cells or any precursors thereof.

Kidneys: The kidneys are composed of complex tissues consisting of several different cell types including glomerular podocytes, endothelial cells, mesangial cells, interstitial cells, tubular epithelial cells, and connecting duct cells. These cell types interact to establish a precise cellular environment that functions as an efficient tissue. Kidneys-related neoplastic diseases include, but are not limited to, Squamous cell carcinoma, Juxtaglomerular cell, tumor (reninoma), Angiomyolipoma, Renal oncocytoma, Bellini duct carcinoma, Clear-cell sarcoma of the kidney, Mesoblastic nephroma, Wilms' tumor, Mixed epithelial stromal tumor, Clear cell adenocarcinoma, Transitional cell carcinoma, Inverted papilloma, Renal lymphoma, Teratoma, Carcinosarcoma, and Carcinoid tumor.

Renal cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term "renal cell lineage" refers to renal cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, podocytes, or any precursors thereof.

Ligaments and Tendons: Tendons and ligaments (T/L) are dense connective tissues of mesodermal origin. They connect and transmit force from muscle to bone and bone to bone, respectively. Both tissues are able to store elastic energy and withstand hightensile forces, on which locomotion is entirely dependent. T/L are predominantly composed of collagen type I fibrils organized in a highly hierarchical manner that is unique for the T/L. Other collagens (types III–VI, XI, XII, XIV, and XV) and various proteoglycans (decorin, cartilage oligomeric matrix protein (COMP), byglican, lumican, fibromodulin,

tenascin-C, etc.) are building the remaining T/L substance. The cellular content of T/L is dominated by tendon-specific fibroblasts named tenocytes. During embryonic development, the tendon-specific cells descend from a sub-set of mesenchymal progenitors condensed in the syndetome, a dorsolateral domain of the sclerotome. L/T-related neoplastic diseases include, but are not limited to, Fibrosarcoma, Malignant fibrous, Hystiocytoma, and Dermatofibrosarcoma.

Ligament and tendon cell lineage: As used herein, unless indicated otherwise or contradictory in context, the term “ligament and tendon cell lineage” or “L/T cell lineage” refers to bone or cartilage cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, fibroblasts, fibrocytes, or any precursors thereof.

Skin: The skin constantly renews itself throughout adult life. Stem cells (SCs) residing in the epidermis ensure the maintenance of adult skin homeostasis, but they also participate in the repair of the epidermis after injuries. The skin protects the body from dehydration, injury and infection. The skin consists of an underlying dermis, separated by a basement membrane from the multilayered overlaying epidermis. The dermis is of mesodermal embryonic origin and contains as adult stem cells fibroblastic mesenchymal stem-cell-like cells. These cells have a multi-lineage differentiation potential, being also able to form adipose tissue or bones. Skin-related neoplastic diseases include, but are not limited to, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, dermatofibrosarcoma protuberans, Merkel cell carcinoma, Kaposi's sarcoma, keratoacanthoma, spindle cell tumors, sebaceous carcinomas, microcystic adnexal carcinoma, Paget's disease of the breast, atypical fibroxanthoma, leiomyosarcoma, and angiosarcoma.

Fibroblast lineage: As used herein, unless indicated otherwise or contradictory in context, the term “fibroblast lineage” refers to skin cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, fibroblasts, keratinocytes, Merkel cells, melanocytes, Langerhans cells, and any precursor cells thereof.

Reproduction: Reproduction (or procreation) is the biological process by which new offspring individual organisms are produced from their parents. Sexual reproduction is a biological process by which organisms create descendants that have a combination of genetic material contributed from two (usually) different members of the species. The development and physiological functions of basic structures in the mammalian reproductive system are influenced by the tissue-specific expression of members of different growth factors families like the BMP family. The establishment of the germ line is a fundamental aspect of reproduction. Germ cell determination is induced in epiblast cells by the extraembryonic ectoderm, and is not acquired through the inheritance of preformed germ plasma. There is some strong evidence that BMP-4 and -8b play a central role in determining primordial germ cell (PGC) formation in the embryo. The genes encoding BMP-4 and -8b have overlapping expression in the extraembryonic ectoderm before gastrulation, i.e., before PGCs are seen. Thus, PGC formation requires BMP-4 expression. There is also evidence from knockout mammals that BMP-8b is required for PGC formation. Furthermore, there is increasing evidence that locally produced BMPs play a major role in the differentiation of the pituitary gonadotrope. Reproduction-related neoplastic diseases include, but are not limited to, Prostate cancer,

Ovary cancer (adenocarcinoma, or glandular cancer) also known as carcinoma of the prostate or prostatic intraepithelial neoplasia.

Reproduction system lineage: As used herein, unless indicated otherwise or contradictory in context, the term “reproduction system lineage” refers to Sertoli cells, Leydig cell and Germ cell at any stage of their development, in particular, mesenchymal stem cells.

Blood: Blood is a bodily fluid in animals that delivers necessary substances such as nutrients and oxygen to the cells and transports metabolic waste products away from those cells. When it reaches the lungs, gas exchange occurs wherein carbon dioxide is diffused out of the blood into the alveoli and oxygen is diffused into the blood. This oxygenated blood is pumped to the left hand side of the heart in the pulmonary vein and enters the left atrium. From here it passes through the bicuspid valve, through the ventricle and taken all around the body by the aorta. Blood contains antibodies, nutrients, oxygen and much more to help the body work. In vertebrates, it is composed of blood cells suspended in blood plasma. Plasma, which constitutes 55% of blood fluid, is mostly water (92% by volume), and contains dissipated proteins, glucose, mineral ions, hormones, carbon dioxide (plasma being the main medium for excretory product transportation), and blood cells themselves. Albumin is the main protein in plasma, and it functions to regulate the colloidal osmotic pressure of blood. Hematopoietic stem cells (HSCs) are the blood cells that give rise to all the other blood cells and are derived from the mesoderm. They are located in the red bone marrow, which is contained in the core of most bones. The HSCs give rise to the myeloid lineage (monocytes and macrophages, neutrophils, basophils, eosinophils, erythrocytes, megakaryocytes/platelets, dendritic cells), and to the lymphoid lineages (T-cells, B-cells, NK-cells). The most abundant cells in the vertebrate blood are red blood cells (also called RBSs or erythrocytes). These contain hemoglobin, an iron-containing protein, which facilitates oxygen transport by reversibly binding to this respiratory gas and greatly increasing its solubility in blood. Blood-related neoplastic diseases include, but are not limited to, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL) and chronic myeloid leukemia (CML).

Blood cell lineages (myeloid lineage and lymphoid lineage): As used herein, unless indicated otherwise or contradictory in context, the term “blood cell lineages” refers to blood cells at any stage of their development from the myeloid or from the lymphoid lineage, and thus include, but are not limited to, hematopoietic stem cells (HSC), myeloid progenitors, lymphoid progenitors, mast cells, myeloblasts, monocytes, macrophages, neutrophils, basophils, eosinophils, erythrocytes, megakaryocytes, thrombocytes, dendritic cells, small lymphocytes, T-lymphocytes (T-cells), B-lymphocytes (B-cells), natural killer (NK)-cells, and any precursor cells thereof.

Adipose tissue: Adipose tissue is loose connective tissue composed mostly of adipocytes. In addition to adipocytes, adipose tissue contains the stromal vascular fraction (SVF) of cells including preadipocytes, fibroblasts, vascular endothelial cells and a variety of immune cells (i.e. adipose tissue macrophages (ATMs)). Adipose tissue is derived from preadipocytes. Its main role is to store energy in the form of lipids, although it also cushions and insulates the body. Pre-adipocytes are thought to be undifferentiated fibroblasts that can be stimulated to form adipocytes. The pre-adipocytes originate from mesenchymal

stem cells. Areolar connective tissue is composed of adipocytes. The term "lipoblast" is used to describe the precursor of the adult cell. The term "lipoblastoma" is used to describe a tumor of this cell type. Adipose tissue-related neoplastic diseases include, but are not limited to, lipoma, Adenolipomas, Angiolipoleiomyomas, Angiolipomas, Corpus callosum lipoma, Cerebellar pontine angle and internal auditory canal lipomas, Chondroid lipomas, Hibernomas, Intradermal spindle cell lipomas, Neural fibrolipomas, Pleomorphic lipomas, Spindle-cell lipomas, Superficial subcutaneous lipomas, Lipoblastoma, Liposarcoma.

Adipocyte lineage: As used herein, unless indicated otherwise or contradictory in context, the term “adipocyte cell lineage” refers to adipocyte cells at any stage of their development and thus include, but are not limited to, mesenchymal stem cells, areolar connective cells, adipocytes, pre-adipocytes/lipoblasts, and any precursor cells thereof.

Digestive system: The human digestive system is composed mainly of the gastrointestinal tract (including the esophagus, stomach, small intestine, large intestine, rectum and anus) and the accessory digestive glands (the liver, the gall bladder and the pancreas). To achieve the goal of providing energy and nutrients to the body, six major functions take place in the digestive system: ingestion, secretion, mixing and movement, digestion, absorption, excretion. The gastrointestinal wall refers to the specialized series of tissue layers surrounding the lumen of the gastrointestinal tract. The general structure involves the four following layers (ordered from the lumen outward): mucosa, submucosa, muscularis externa, serosa (if the tissue is intraperitoneal) / adventitia (if the tissue is retroperitoneal). Gastrointestinal cancer refers to malignant conditions of the gastrointestinal tract (GI tract) and accessory organs of digestion. The symptoms relate to the organ affected and can include obstruction (leading to difficulty swallowing or defecating), abnormal bleeding or other associated problems. Gastrointestinal tissue-related neoplastic diseases include, but are not limited to, Esophageal cancer, Stomach cancer, Pancreatic cancer, Liver cancer, Gallbladder cancer, MALT lymphoma, Gastrointestinal stromal tumors and Cancers of the biliary tree, including cholangiocarcinoma.

Gastrointestinal cell lineages: As used herein, unless indicated otherwise or contradictory in context, the term “ gastrointestinal cell lineages” refers to gastrointestinal cells and cells of the digestive accessory organs at any stage of their development and thus include, but are not limited to interstitial cells of Cajal, gastrointestinal epithelial cells, parietal cells, acinar cells, chief cells, mucus cells, goblet cells, G cells, endocrine I cells, endocrine S cells, endocrine K cells, endocrine M cells, ECL (enterochromaffin) cells, D cells, enteroendocrine cells, APUD cells, hepatocytes, sinusoidal hepatic endothelial cells, Kupffer cells, hepatic stellate cells, centroacinar cells, pancreatic stellate cells, α-cells, γ-cells, β-cells, δ-cells, centroacinar cells, basophilic cells, ductal cells, columnar cells, cholecystocytes and any precursor cells thereof.

Lung: The lung is the essential respiration organ in many air-breathing animals. In mammals the two lungs are located near the backbone on either side of the heart. Their principal function is to transport oxygen from the atmosphere into the bloodstream, and to release carbon dioxide from the bloodstream into the atmosphere. A large surface area is needed for this exchange of gases, which is accomplished

by the mosaic of specialized cells that form millions of tiny, exceptionally thin-walled air sacs called alveoli. Lung cells include, but are not limited to, type I pneumocytes, type II pneumocytes, clara cells and goblet cells. Lung tissue-related neoplastic diseases include, but are not limited to, lung cancer also known as carcinoma of the lung or pulmonary carcinoma, Epithelial cells or small-cell lung carcinoma (SCLC) and non-small-cell lung carcinoma (NSCLC).

Lung cell Lineages: As used herein, unless indicated otherwise or contradictory in context, the term "lung cell Lineage" refers to lung cells at any stage of their development and thus include, but are not limited to, epithelial cells, erythrocytes, alveolar cells and any precursor cells thereof.

Head and neck cancer: As used herein, unless indicated otherwise or contradictory in context, the term "head and neck cancer" refers to a group of cancers that usually starts in the lip, oral cavity, nasal cavity, paranasal sinuses, pharynx, and larynx. About 90% of head and neck cancers are squamous cell carcinomas. Thus, neoplastic diseases such as head and neck cancers include, but are not limited to, oral cancer, nasopharynx cancer, oropharyngeal cancer, hypopharynx cancer and laryngeal cancer.

The cell lineage involved in head and neck cancers includes all the cells involved in the formation of such cancers at any stage of their development and thus include, but are not limited to, cells of the oral cavity, cells of the pharynx, cells of the larynx, cells of the paranasal sinuses and nasal cavity, cells of the salivary glands and any precursor cells thereof.

Ratio: As used herein, unless indicated otherwise or contradictory in context, the term "ratio", when used in relation to GFR-binding compound with respect to the bioactive carrier in the pharmaceutical association or composition disclosed herein, refers to the (molar, weight or part as specified) ratio between the quantity of GFR-binding compound and the quantity of bioactive carrier. The ratio may be a molar ratio, a weight ratio or a part ratio and will be specified as needed on a case by case basis. Quantity units may conventionally be mole, millimole, gram, milligram or parts. For example, in certain embodiments, it is convenient to express the relative quantity between GFR-binding compounds and bioactive carriers using densities. It shall be understood that this ratio may be varied according to the neoplastic cell type to be treated.

Density: As used herein, unless indicated otherwise or contradictory in context, the term "density", when used in relation to GFR-binding compound with respect to the bioactive carrier in the pharmaceutical composition disclosed herein, refers to the quantity of GFR-binding compounds, expressed in *e.g.* mole, millimole, gram, or milligram, with respect to one standardised surface unit *e.g.* squared millimetre (mm^2), squared micrometre (μm^2), or squared nanometre (nm^2)). For example, in certain embodiments, the ratio between a GFR-binding compound and a bioactive carrier in the pharmaceutical association or composition disclosed herein may be expressed in pmol per mm^2 or pmol/mm^2.

Cell cycle: As used herein, unless indicated otherwise or contradictory in context, the term "cell cycle" refers to the process through which a vertebrate cell self-replicate. In eukaryote cells, cell cycle consists of four discrete phases: G1, S, G2, and M. Together, the G1, S, and G2 phases make up the period

known as interphase. During the S or “synthesis” phase, the cell replicates its DNA creating an exact copy of all of its chromosomes. In the M or “mitotic” phase, the cell division actually occurs and separates the chromosomes in its cell nucleus into two identical sets in two nuclei. The first phase within interphase, from the end of the previous M phase until the beginning of DNA synthesis, is called G1. During this phase the biosynthetic activities of the cell, which are considerably slowed down during M phase, resume at a high rate. This phase is marked by the formation of millions of proteins and later on enzymes that are required in S phase, mainly those needed for DNA replication. The G2 phase, or pre-mitotic phase, is the third and final sub-phase of Interphase in the cell cycle directly preceding Mitosis. It follows the successful completion of S phase and ends with the onset of prophase, the first phase of mitosis. In order to move from one phase of the cell cycle to the next, a cell must “validate” numerous checkpoints. At each checkpoint, specialized proteins determine whether the necessary conditions exist. If so, the cell is free to enter into the next phase. If not, progression through the cell cycle is halted. For example, in certain embodiments, during G1, the cell passes through a “validation” window punctuated by the restriction point R. During the “validation” phase, different checkpoints ensure that environmental conditions are favourable for replication. If conditions are not favourable, the cell may enter a resting state known as G0. The G0 phase or resting phase is a period in the cell cycle in which cells exist in a quiescent state. G0 phase is viewed as either an extended G1 phase, where the cell is neither dividing nor preparing to divide, or a distinct quiescent stage that occurs outside of the cell cycle. Typically, a healthy vertebrate cell undergoes cell division when needed *e.g.* to regenerate damaged tissues or simply replace old tissues by new ones, by switching from a G0 resting state into the G1 state of the cell cycle and resume cell division. In contrast, neoplastic cells (such as cancer cells) have lost their ability to suspend cell division and switch to the G0 phase therefore undergoing permanent cell division which is generally referred to uncontrolled cell division or proliferation. Another “validation” window takes place later in the cell cycle, just before a cell moves from G2 to mitosis. Here, a number of proteins scrutinize the cell's DNA ensuring proper replication has taken place. Finally, another cell cycle “validation” window takes place during mitosis in which different checkpoints determines whether chromosomes are correctly attached to the spindle, and to the network of microtubules that will separate them during cell division.

Quiescence: As used herein, unless indicated otherwise or contradictory in context, the term “quiescence”, when used in relation to a cell, refers to a resting state during which the cell does not divide, duplicate or proliferate. This state is also called the G0 state. As used herein, “inducing quiescence of a neoplastic cell” thus means to provoke the passage from G1 to G0 of a neoplastic cell which usually has lost the ability to do so. One method to detect the passage from G1 to G0 is, for instance, to monitor the state of phosphorylation of the protein Rb via Western Blot. The Rb protein is normally not phosphorylated during the G0 phase but becomes phosphorylated or even hyper-phosphorylated during the rest of the cell cycle. Consequently, observing the absence (or substantial reduction *i.e.* at least 90% reduction, in comparison with the quantity present in the G1 phase) of phosphorylated Rb protein on a western blot confirms that a neoplastic cell has undergone (at some point in time) a switch to the G0 phase.

Cell division or cell proliferation: As used herein, unless indicated otherwise or contradictory in context, the term “cell division” or “cell proliferation”, refers to the process by which a cell self-replicate, replicate or

is caused to replicate.

Proliferate: As used herein, unless indicated otherwise or contradictory in context, the term "proliferate" means to grow, expand or increase or cause to grow, expand or increase. "Proliferative" means having the ability to proliferate. "Anti-proliferative" means having properties to counter, reduce, or inhibit proliferation.

Hyperproliferation: As used herein, unless indicated otherwise or contradictory in context, the term “hyperproliferation” or “uncontrolled proliferation" means the abnormal growth, expansion or increase or causing the abnormal growth, expansion or increase. Abnormal growth typically originates from the abnormal regulation of the cell cycle preventing the cell to reach the G0 state and stop cell division and replication. One consequence of hyper or uncontrolled proliferation is the development of neoplastic diseases such as tumours and cancers.

Hyperproliferative diseases: As used herein, unless indicated otherwise or contradictory in context, the term “hyperproliferative diseases” is used interchangeably with “neoplastic diseases” and refers to diseases that are characterized by uncontrolled cellular proliferation and/or disruption in programmed cell death. The loss of a cell’s ability to control cellular proliferation is often caused by genetic damage to the cellular pathways responsible for regulating cellular functions, including but not limited to, for example, in certain embodiments, metabolism, cell cycle progression, cell adhesion, vascular function, apoptosis, and angiogenesis.

Anti-mitogen activity: As used herein, unless indicated otherwise or contradictory in context, the term “anti-mitogen activity”, refers to biological pathways that down-regulate, partially inhibit or suppress cell mitosis *i.e.* cell division. As used herein, a substance or pharmaceutical association which promotes, induces or favours anti-mitogen activity thus means a substance or pharmaceutical association which provides at least part of its effective biologic or therapeutic action by down-regulating, partially inhibiting or suppressing mitosis of the neoplastic cell to be treated.

Tumor suppressor pathways: As used herein, unless indicated otherwise or contradictory in context, the term “tumor suppressor pathways” refers to biological pathways that down-regulate, partially inhibit or suppress tumor activity *i.e.* protect the cell against cell defects which could cause tumors or cancers. As used herein, a substance or pharmaceutical association which promotes, induces or favours tumor suppressor pathways thus means a substance or pharmaceutical association which provides at least part of its effective biologic or therapeutic action by up-regulating, activating or promoting the tumor suppressor genes or proteins of the neoplastic cell to be treated. Known tumor suppressor proteins which have a dampening or repressive effect on the regulation of the cell cycle or promote apoptosis include, but are not limited to, p53, pRb, pVHL, APC, CD95, ST5, YPEL3, ST7, and ST14.

Anti-oncogenic activity: As used herein, unless indicated otherwise or contradictory in context, the term “anti-oncogenic activity” refers to any molecule having the ability to inhibit, repress or down-regulate the gene or protein expression of oncogenes. An oncogene is a gene that has the potential to cause

neoplastic diseases such as cancer. Examples of anti-oncogene molecules include tumor suppressor proteins.

By "**without temporarily or permanently damaging or killing a neoplastic cell**", is meant, unless indicated otherwise or contradictory in context, that a neoplastic disease, such as cancer, is treated without inducing the entry of the neoplastic cells into apoptosis as it may be assessed by the positive expression of proteins caspase 3, 6 and 7.

By "**without permanently inducing a quiescent state in a neoplastic cell**", is meant, unless indicated otherwise or contradictory in context, that a neoplastic disease, such as cancer, is treated by inducing a temporary quiescent state in the neoplastic cells (the cells enter the G0 phase) and then differentiate into a more specialised state.

Non-mutagenic: As used herein, unless indicated otherwise or contradictory in context, the term "non-mutagenic", when used in relation to a therapy or treatment, refers to a therapy which does not involve the alteration or modification of a cell's genome.

Recoding: As used herein, unless indicated otherwise or contradictory in context, the term "recoding" or "converting", when used in relation to a cell (in particular a neoplastic cell such as a cancer cell), refers to the action of providing, to a neoplastic cell to be treated, a suitable extracellular micro-environment (*e.g.* in the form of a pharmaceutical association or composition as defined herein) providing appropriate extracellular signals so that the cell may undergo self-recovery or -healing and be converted into a partially or fully differentiated non-neoplastic cell.

Recoding therapy: As used herein, unless indicated otherwise or contradictory in context, the term "recoding therapy" refers to a therapy that promotes and stimulates the cell's natural abilities to redirect its own fate by integrating accurate micro-environmental recoding signals.

Extracellular micro-environment: As used herein, unless indicated otherwise or contradictory in context, the term "extracellular micro-environment" refers to the environment surrounding (in functional proximity with) a specific cell which is characterized by biophysical, mechanical and biochemical properties specific for each tissue and is able to regulate cell behavior. Modification of the extracellular micro-environment of a neoplastic cell using, for instance, pharmaceutical associations or compositions as defined herein allows for the conversion or recoding of said neoplastic cell into a healthy, functional, non-neoplastic cell.

Self-recovery or self-healing: As used herein, unless indicated otherwise or contradictory in context, the term "self-recovery" or "self-healing", when used in relation to a neoplastic cell such as a cancer cell, means that the neoplastic cell operates its own internal biological changes once it has been recoded or treated using a pharmaceutical association or composition as defined herein, so that it becomes a functional, healthy, non-neoplastic cell. The cell heal itself when in contact with the pharmaceutical composition or association as defined herein and, in contrast with previously reported methods wherein

the neoplastic cell is forced to die or maintained in a temporarily reduced or non-proliferative state.

Physiologically functional cell: As used herein, unless indicated otherwise or contradictory in context, the term "physiologically functional cell" refers to a cell which is able to perform normally all of the cell functions associated with a particular cell type and necessary for the normal physiology of a cell. These functions include all of the intracellular molecular mechanisms but also all of the activities necessary for a normal communication between the cell and its microenvironment. One method which may be used to verify if a cell is physiologically functional is the grafting of the cell, after the introduction of fluorescent markers, in other mammalian model organisms such as mouse models. The cell is grafted in the tissue corresponding to its cell type. The cell characteristics and normal functions are monitored after a period of time with various methods such as in vivo microscopy or histological staining. The term "functional" when used in relation to a molecule, compound or substance refers to a biological molecule in a form in which it exhibits a property and/or activity by which it is characterized.

Healthy cell: As used herein, unless indicated otherwise or contradictory in context, the term "healthy cell" refers to a cell which presents a normal morphology, normal cell functions and normal cell growth which are not damaged, altered or inactivated by a neoplastic disease.

Shorter period of time: As used herein, unless indicated otherwise or contradictory in context, the term "shorter period of time", when used in relation to conversion or recoding duration, means substantially shorter to provide a substantial benefit for the treated patient in comparison with existing treatments. In certain embodiments, a shorter period of time includes at least 1.5-fold, at least 2-fold, at least 2.5-fold, at least 3-fold, at least 3.5-fold, at least 4-fold, at least 4.5-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold or at least 10-fold reduction with respect to an existing treatment.

Exogenous: As used herein, unless indicated otherwise or contradictory in context, the term “exogenous” refers to a substance coming from outside a living system such as a cell, an organ, or an individual organism. For example, in certain embodiments, exogenous factors in medicine include pathogens and therapeutics. DNA introduced into a cell via transfection or viral infection may be considered as an exogenous factor. Carcinogens are also commonly referred to as exogenous factors.

Endogenous: As used herein, unless indicated otherwise or contradictory in context, the term “endogenous” refers to substances that originate from within an organism, tissue, or cell.

Intracellular: As used herein, unless indicated otherwise or contradictory in context, the term “intracellular” generally means “inside the cell”. In vertebrates, such as animals, the cell membrane is the barrier between the inside of the cell and the outside of the cell (the extracellular milieu). Thus, treatments and therapies in which at least one substance, compound, pharmaceutical association, combination or composition penetrates the cell wall of a cell to be treated in order to produce/deliver its (effective) biological effect are considered as intracellular treatments and therapies.

Extracellular: As used herein, unless indicated otherwise or contradictory in context, the term

"extracellular" means "outside the cell". In vertebrates, such as animals, the cell membrane is the barrier between the inside of the cell (the intracellular milieu) and the outside of the cell. Thus, treatments and therapies in which no substance, compound, pharmaceutical association, combination or composition requires penetration of the cell membrane in order to produce/deliver its (effective) biological effect (*e.g.* by interacting with trans-membrane receptors) are considered as extracellular treatments and therapies. In other words, a therapy using a plurality of substances in order to provide the desired biological effect wherein one or more of these substances require the entry into the intracellular compartment to provide (or deliver) its biological effect is not considered as an extracellular therapy in the sense of the present disclosure.

Cytostatic: As used herein, unless indicated otherwise or contradictory in context, the term "cytostatic" refers to inhibiting, reducing, or suppressing the growth, division, or multiplication of a cell (*e.g.*, a mammalian cell (*e.g.*, a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

Cytotoxic: As used herein, unless indicated otherwise or contradictory in context, the term "cytotoxic" refers to killing or causing injurious, toxic, or deadly effect on a cell (*e.g.*, a mammalian cell (e.g., a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

In vitro: As used herein, unless indicated otherwise or contradictory in context, the term "in vitro" refers to events that occur in an artificial environment, *e.g.*, in a test tube or reaction vessel, in cell culture, in a Petri dish, etc., rather than within an organism (*e.g.*, animal, plant, or microbe).

In vivo: As used herein, unless indicated otherwise or contradictory in context, the term "in vivo" refers to events that occur within an organism (*e.g.*, animal, plant, or microbe or cell or tissue thereof).

Ex vivo: As used herein, unless indicated otherwise or contradictory in context, the term "ex vivo" refers to events that occur in an external environment on tissues sourced from an organism (*e.g.*, animal, plant, or microbe) in an attempt to replicate natural living conditions outside such an organism.

Syndecans: As used herein, unless indicated otherwise or contradictory in context, the term "syndecans" refers to single transmembrane domain proteins that are thought to act as co-receptors, especially for G protein-coupled receptors. These core proteins carry three to five heparan sulfate and chondroitin sulfate chains, which allow for interaction with a large variety of ligands including fibroblast growth factors, vascular endothelial growth factor, transforming growth factor-beta, fibronectin and antithrombin-1. Interactions between fibronectin and some syndecans can be modulated by the extracellular matrix protein tenascin C. The syndecan protein family has four members. Syndecans 1 and 3 and syndecans 2 and 4, making up separate subfamilies, arose by gene duplication and divergent evolution from a single ancestral gene. The syndecan numbers reflect the order in which the cDNAs for each family member were cloned. All syndecans have an N-terminal signal peptide, an ectodomain, a single hydrophobic transmembrane domain, and a short C-terminal cytoplasmic domain. All syndecans are anchored to plasma membrane via a 24-25 amino acid long hydrophobic transmembrane domain. In mammalian cells,

syndecans are expressed by unique genes located on different chromosomes. All members of the syndecan family have 5 exons. The difference in size of the syndecans is credited to the variable length of exon 3, which encodes a spacer domain. In humans, the amino acid length of syndecan 1, 2, 3 and 4 is 310, 201, 346 and 198 respectively. Glycosaminoglycan chains, a member of the heparan sulfate group, are an important component of syndecans and are responsible for a diverse set of syndecan functions. The addition of glycosaminoglycans to syndecan is controlled by a series of post- translational events.

Cyclin-dependent kinases: As used herein, unless indicated otherwise or contradictory in context, the term “Cyclin-dependent kinases” or “CDKs” refers to a family of protein involved in the regulation of the cell cycle. They are present in all known eukaryotes, and their regulatory function in the cell cycle has been evolutionarily conserved. By definition, a CDK binds a regulatory protein called a cyclin. It is reported that, without cyclin, CDK has little kinase activity; only the cyclin-CDK complex is considered to be an active kinase. CDKs phosphorylate their substrates on serines and threonines, so they can be said to belong to the serine-threonine kinase family. CDKs and cyclins are thus highly conserved across species and are present in all cell types including those having a neoplastic phenotype (*e.g.* cancer cells). Most of the known cyclin-CDK complexes regulate the progression through the cell cycle. Animal cells contain at least nine CDKs, four of which, CDK 1, 2, 3, 4 and 6, are reported to be directly involved in cell cycle regulation: CDK1 regulated by cyclin A, cyclin B; CDK2 regulated by cyclin A, cyclin E; CDK3 regulated by cyclin C; CDK4 regulated by cyclin D1, cyclin D2, cyclin D3; CDK5 regulated by CDK5R1, CDK5R2; CDK6 regulated by cyclin D1, cyclin D2, cyclin D3; CDK7 regulated by cyclin H; CDK8 regulated by cyclin C; CDK9 regulated by cyclin T1, cyclin T2a, cyclin T2b, cyclin K.

Cyclins: As used herein, unless indicated otherwise or contradictory in context, the term “cyclins” refers to a family of proteins that control the progression of cells through the cell cycle by activating cyclin-dependent kinase (CDK) enzymes. Cyclin D is one of the major cyclins produced in terms of its functional importance. It is known to interact with four CDKs: CDK2, 4, 5, and 6. In proliferating cells, cyclin D-CDK4/6 complex accumulation is of great importance for cell cycle progression. For instance, cyclin D-CDK4/6 complexes partially phosphorylates retinoblastoma tumor suppressor protein (Rb), whose inhibition can induce expression of some genes important for S phase progression.

Patient/subject: As used herein, unless indicated otherwise or contradictory in context, the term "patient" or "subject", which are used interchangeably, refers to any organism to which a composition in accordance with the invention may be administered, e.g., for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include animals (e.g., mammals such as mice, rats, rabbits, non-human primates, and humans) and/or plants. As used herein, patients/subjects include those individuals who may seek or be in need of treatment, requires treatment, is receiving treatment, will receive treatment, or a subject who is under care by a trained professional for a particular disease or condition.

Purified: As used herein, unless indicated otherwise or contradictory in context, the term "purify," "purified," "purification" means to make substantially pure or clear from unwanted components, material defilement, admixture or imperfection.

Targeted Cells: As used herein, unless indicated otherwise or contradictory in context, the term "targeted cells" refers to any one or more cells of interest. The cells may be found in vitro, in vivo, in situ or in the tissue or organ of an organism. The organism may be an animal, preferably a mammal, more preferably a human and most preferably a patient.

Molecule length: As used herein, unless indicated otherwise or contradictory in context, the term molecule or peptide “length” or “size” means the longest 2D or 3D distance which may possibly be measured within the molecule. For cyclic molecules, “length” or “size” means the longest measurable distance across the cyclic structure. Throughout the present disclosure, when a molecule size or length is given (in general using the nanometre, nm, unit), the following procedures were used to calculate them:

- The so-called « 2D » procedure: a 2D chemical structure was drawn in e.g. the ChemDraw® Software. Then, size measurement was carried out via the available ChemDraw length measurement tools. The length value given herein corresponds to the longest 2D length of the molecule using the default settings 2D bond sizes and angles of the software.
- Alternatively, the so-called “3D” procedure may be followed:

(1) Drawing of the chemical structure of the molecule using suitable softwares (such as ChemDraw).
(2) Creating a 3D structure model of the molecule hereby drawn using SCWRL (Protein Sci. 2003; 12(9):2001-14) or MODELLER (Current Protocols in Bioinformatics. 15:5.6:5.6.1–5.6.30), each of which is hereby incorporated by reference in its entirety.
(3) Incubating the obtained 3D structure model in a box simulation containing water for few milliseconds using AMBER (J. Computat. Chem. 2005; 26, 1668-1688), which is hereby incorporated by reference in its entirety.
(4) Measuring the size of the molecule hereby obtained using softwares such as Pymol® using available Pymol length measurement tools (DeLano Scientific LLC, http://www.pymol.org).

Root Mean Square Deviation: As used herein, unless indicated otherwise or contradictory in context, the term “Root Mean Square Deviation” or “RMSD” is well known in the art and means the square root of the arithmetic mean of the square of the distances between certain matched atoms. One can represent a molecular conformation as a vector whose components are the Cartesian coordinates of the molecule's atoms. Therefore, a conformation for a molecule with N atoms can be represented as a 3N-dimensional vector of real numbers. To calculate the RMSD of a pair of peptides or peptidomimetics (e.g. x and y), each one of them must be represented as a 3N-length (assuming N atoms) vector of coordinates. The RMSD is therefore the square root of the arithmetic mean of the square of the distances between corresponding atoms of x and y. It is a measure of the average atomic displacement between the conformations of the two structures:

$$\sqrt{\frac{1}{N}\sum_{i=1}^{N}|xi - yi|1^2}$$

In other words, the RMSD is the measure of the average distance between the atoms (usually the backbone atoms) of superimposed polypeptides or peptidomimetics. In the study of globular protein

conformations, one customarily measures the similarity in three-dimensional structure by the RMSD of the Cα atomic coordinates after optimal rigid body superposition.

The RMSD value of a given peptide or peptidomimetic with respect to a specifically selected reference structure (hereinafter may also be referred to as “PEPREF”) may be calculated using various methods all well know by the skilled person. However, for the purpose of the present disclosure and for the avoidance of doubts, the RMSD of a given peptide or peptidomimetic as used in the present disclosure is obtained precisely using the following procedure:

STEP 1: Creating a 3-dimensional model of (i.e. obtaining 3D structure coordinates for) a peptide or peptidomimetic for which the RMSD is to be calculated, by:

STEP 1.1: Obtaining a set of polypeptide 3D structure coordinates based on the alignment with the sequence of a peptide or peptidomometic for which the RMSD value is to be calculated, using the BLAST algorithm according to the following procedure:

1. Open the following link to access the “Standard Protein Blast” tool: **http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome**
2. Enter the amino acid sequence of the peptide or peptidomimetic of interest in the “Enter Query Sequence” section. The alignment is performed one sequence after the other (this is not a multiple alignment tool).
3. In the section “Choose Search Set”, choose the following database: Protein Data Bank Proteins (pdb).
4. In the section “Choose Search Set”, do not exclude « Models (XM/XP) » and do not Exclude « Uncultured /environmental sample sequences ».
5. In the section “Program Selection”, choose the following algorithm: blastp (protein-protein BLAST)
6. Leave other fields as shown on the screenshot in Figure 20.
7. Run BLAST.
8. The results obtained from the query are presented in the form of several pdb files.
9. From this output results, the first ten (10) PDB files corresponding to the best sequence alignments are retained. This set of 10 PDB files or structures will be used in the next step (Step 2: structural alignments with STAMP).
10. Finally, clean up the 10 structures contained in the 10 PDB files by removing all *e.g.* additional small molecules, receptors or portions thereof, dimers or portions thereof, so as to retain only the polypeptide chain of interest.

The set of pdf files contains the polypeptide 3D structure coordinates of the 10 structures having the highest sequence homology with the peptide or peptidomometic for which the RMSD value is to be calculated.

STEP 1.2: Performing the structural alignment of the set of 3D structure coordinates obtained in STEP 1.1, thereby obtaining a set of aligned polypeptide 3D structure coordinates, by using STAMP (Structural

Alignment of Multiple Proteins Version 4.2) according to the following procedure:

1. Open the following link to access the "STAMP superposition" tool: **http://www.russelllab.org/cgi-bin/pdc/stamp.pl**
2. In the section entitled "Structure A", input the PDB file corresponding to the first structure from the set of ten 3D structure ccordinates obtained in STEP 1.1, which corresponds to the best sequence alignment with BLAST.
3. In the section entitled "Structure B", input the PDB file corresponding to the second structure from the set of ten 3D structure ccordinates obtained in STEP 1.1, which corresponds to the second best sequence alignment with BLAST.
4. Run STAMP.
5. Repeat steps 2 to 4 with the other eight pdb files from the set of ten 3D structure coordinates identified in STEP 1.1 by successively entering the PDB files in the field "Structure B".
6. As a result, the structural alignment of the 10 structures contained in the set of PDB files obtained in STEP 1.1 is obtained in the form of 9 disctinct PDB files each containing a pair of aligned polypeptide 3D structure (structure 1 with structure 2, structure 1 with structure 3, structure 1 with structure 4, … , structure 1 with structure 10).
7. From these 9 "pair" PDB files, 10 PDB files each containing one of structures 1 to 10 are created.
8. 10 PDB files containing the aligned 3D structure coordinates are thus obtained from STEP 1.2. for use in the next step.

STEP 1.3: Modelling the sequence of peptide or peptidomometic for which the RMSD value is to be calculated against the set of aligned polypeptide 3D structure coordinates obtained in STEP 1.2, thereby obtaining a set of 3D structure coordinates for the peptide or peptidomometic for which the RMSD value is to be calculated, using SCWRL (reference: "SCWRL and MolIDE: computer programs for side-chain conformation prediction and homology modeling", Nature Protocols VOL.3 NO.12 2008, Qiang Wang et al.; which is hereby incorporated by reference in its entirety) according to the following procedure:

1. Insert the input sequence of a peptide or peptidomometic for which the RMSD value is to be calculated in Fasta format.
2. Import the first PDB file containing the aligned polypeptide 3D structure coordinates obtained in STEP 1.2.
3. Run SCWRL by typing the following command for Unix based systems: "scwrl_path/scwrl3 -i inputpdbfile -o outputpdbfile -s sequencefile 4 logfile".
4. As a result, a first PBD file is obtained containing the predicted 3D structure coordinates of the peptide or peptidomometic for which the RMSD value is to be calculated.
5. Repeat steps 1 to 3 using the 9 remaining PDB files obtained in STEP 1.2.
6. 10 PDB files are obtained from STEP 1.3 for use in the following STEP 1.4.

STEP 1.4: Minimizing the free energy (ΔG) of the set of 3D structure coordinates for the peptide or peptidomometic for which the RMSD value is to be calculated obtained in STEP 1.3 using GROMACS (Reference: Hess B, Kutzner C, Van Der Spoel D, Lindahl E (2008). "GROMACS 4: Algorithms for Highly

Efficient, Load-Balanced, and Scalable Molecular Simulation". **J Chem Theory Comput** 4 (2): 435; which is hereby incorporated by reference in its entirety) according to the following procedure:

1. Create a Gromacs topology (gmx) file from the first PDB file of the modeled peptide or peptidomometic for which the RMSD value is to be calculated obtained in STEP 1.3, by using the command « pdb2gmx -f NOMDUFICHIERPDB.pdb –water spc». "NOMDUFICHIERPDB" is the name of the input PDB file.
2. Create a box around the imported modeled peptide or peptidomometic by using the command « editconf -f conf.gro –bt cubic d 0.7 o box.gro».
3. Add solvent (water) molecules into the box by using the command « genbox –cp box.gro –cs spc216.gro –p topol.top – o solvated.gro».
4. Prepare the input for the molecular dynamics (MD) run with the command « vim em.mdp ». Default run is set to 1000 nsteps.
5. Create an input for the MD run by using the command « grompp -f em.mdp –p topol.top –c solvated.gro –o em.tpr».
6. Run the command « mdrun –v –deffnm em» to perform the actual energy minimization.
7. Run the command « g energy –f em.edr –s em.tpr –o em.xvg » and then run option « 7 ».
8. As a result, a first XMG file is obtained. To view the XMG file run the command « xmgrace em.xvg ».
9. Repeat steps 1 to 8 with the 9 remaining structures obtained in STEP 1.3. 10 XMG files are thus obtained.
10. The structure of lowest energy is obtained from each XMG file in the form of a PDB file. 10 PDB files each containing one structure of lowest energy are thus obtained from STEP 1.4 for use in the next step.

STEP 2: Calculating the RMSD of the peptide or peptidomimetic for which the RMSD value is to be calculated by comparing the 3D structure coordinates of the peptide or peptidomimetic obtained in STEP 1.4 with the 3D structure coordinates of PEPREF to obtain the lowest possible RMSD value using FATCAT (Flexible structure AlignmenT by Chaining Aligned fragment pairs allowing Twists) according to the following procedure:

1. Open the following link to access the "FATCAT" software: **http://fatcat.burnham.org**
2. Open the "pairwise alignment" tool.
3. Import the PDB file containing the structure coordinates of PEPREF in the "Get the 1st structure" section.
4. Import the first PDB file of the peptide or peptidomimetic for which the RMSD value is to be calculated with minimized energy obtained in STEP 1.4.
5. Run FATCAT.
6. As a result, a first RMSD value of the first structure of the peptide or peptidomimetic for which the RMSD value is to be calculated as obtained in STEP 1.4 will be obtained in the output report.
7. Repeat steps 1 to 5 with the 9 remaining structures (PDB files) obtained from STEP 1.4.
8. The peptide or peptidomimetic structure with the lowest RMSD (out of the ten RMSD values successively obtained) is the value taken into account in the present application.

3D structure coordinates of PEPREF: As used herein, unless indicated otherwise or contradictory in context, the 3D structure coordinates of PEPREF are as follows:

ATOM	511	N	LYS	A	1	-14.570	46.437	27.424
ATOM	512	CA	LYS	A	1	-13.512	45.748	28.151
ATOM	513	C	LYS	A	1	-13.655	44.259	27.884
ATOM	514	O	LYS	A	1	-12.769	43.463	28.197
ATOM	515	CB	LYS	A	1	-13.605	46.029	29.652
ATOM	516	CG	LYS	A	1	-13.640	47.509	29.991
ATOM	517	CD	LYS	A	1	-12.615	48.297	29.183
ATOM	518	CE	LYS	A	1	-12.625	49.768	29.575
ATOM	519	NZ	LYS	A	1	-13.994	50.369	29.497
ATOM	520	N	ILE	A	2	-14.792	43.890	27.309
ATOM	521	CA	ILE	A	2	-15.051	42.499	26.967
ATOM	522	C	ILE	A	2	-14.911	42.370	25.444
ATOM	523	O	ILE	A	2	-15.531	43.125	24.683
ATOM	524	CB	ILE	A	2	-16.466	42.065	27.401
ATOM	525	CG1	ILE	A	2	-16.630	42.238	28.915
ATOM	526	CG2	ILE	A	2	-16.710	40.629	26.985
ATOM	527	CD1	ILE	A	2	-15.631	41.478	29.30
ATOM	528	N	PRO	A	3	-14.085	41.411	24.989
ATOM	529	CA	PRO	A	3	-13.789	41.109	23.588
ATOM	530	C	PRO	A	3	-14.998	40.695	22.768
ATOM	531	O	PRO	A	3	-15.969	40.164	23.305
ATOM	532	CB	PRO	A	3	-12.785	39.968	23.688
ATOM	533	CG	PRO	A	3	-12.156	40.166	25.007
ATOM	534	CD	PRO	A	3	-13.330	40.506	25.867
ATOM	535	N	LYS	A	4	-14.937	40.937	21.463
ATOM	536	CA	LYS	A	4	-16.023	40.529	20.590
ATOM	537	C	LYS	A	4	-15.886	39.015	20.391
ATOM	538	O	LYS	A	4	-14.903	38.415	20.831
ATOM	539	CB	LYS	A	4	-15.926	41.244	19.245
ATOM	540	CG	LYS	A	4	-15.802	42.751	19.355
ATOM	541	CD	LYS	A	4	-16.292	43.433	18.083
ATOM	542	CE	LYS	A	4	-16.162	44.943	18.177
ATOM	543	NZ	LYS	A	4	-16.825	45.628	17.019
ATOM	544	N	ALA	A	5	-16.85	38.393	19.759
ATOM	545	CA	ALA	A	5	-16.811	36.955	19.507
ATOM	546	C	ALA	A	5	-15.772	36.771	18.416
ATOM	547	O	ALA	A	5	-15.727	37.534	17.455
ATOM	548	CB	ALA	A	5	-18.168	36.419	19.043
ATOM	549	N	CYS	A	6	-14.935	35.756	18.562
ATOM	550	CA	CYS	A	6	-13.887	35.518	17.584
ATOM	551	C	CYS	A	6	-14.347	34.765	16.338
ATOM	552	O	CYS	A	6	-15.327	34.018	16.368
ATOM	553	CB	CYS	A	6	-12.743	34.768	18.241
ATOM	554	SG	CYS	A	6	-11.198	34.959	17.353
ATOM	555	N	CYS	A	7	-13.623	34.973	15.243
ATOM	556	CA	CYS	A	7	-13.931	34.328	13.969
ATOM	557	C	CYS	A	7	-13.091	33.071	13.798
ATOM	558	O	CYS	A	7	-11.961	33.123	13.302
ATOM	559	CB	CYS	A	7	-13.653	35.290	12.824
ATOM	560	SG	CYS	A	7	-13.930	34.633	11.154
ATOM	561	N	VAL	A	8	-13.654	31.941	14.209
ATOM	562	CA	VAL	A	8	-12.949	30.684	14.110
ATOM	563	C	VAL	A	8	-13.653	29.733	13.157
ATOM	564	O	VAL	A	8	-14.759	30.016	12.687

ATOM	565	CB	VAL	A	8	-12.814	30.038	15.492
ATOM	566	CG1	VAL	A	8	-11.807	30.825	16.337
ATOM	567	CG2	VAL	A	8	-14.161	30.006	16.170
ATOM	568	N	PRO	A	9	-13.003	28.601	12.828
ATOM	569	CA	PRO	A	9	-13.593	27.615	11.918
ATOM	570	C	PRO	A	9	-14.726	26.886	12.631
ATOM	571	O	PRO	A	9	-14.581	26.476	13.780
ATOM	572	CB	PRO	A	9	-12.423	26.676	11.601
ATOM	573	CG	PRO	A	9	-11.204	27.487	11.925
ATOM	574	CD	PRO	A	9	-11.620	28.226	13.163
ATOM	575	N	THR	A	10	-15.847	26.721	11.942
ATOM	576	CA	THR	A	10	-16.999	26.060	12.527
ATOM	577	C	THR	A	10	-17.334	24.767	11.804
ATOM	578	O	THR	A	10	-18.097	23.943	12.303
ATOM	579	CB	THR	A	10	-18.211	27.010	12.523
ATOM	580	OG1	THR	A	10	-18.491	27.445	11.185
ATOM	581	CG2	THR	A	10	-17.902	28.230	13.375
ATOM	582	N	GLU	A	11	-16.750	24.586	10.627
ATOM	583	CA	GLU	A	11	-16.980	23.377	9.848
ATOM	584	C	GLU	A	11	-15.643	22.935	9.246
ATOM	585	O	GLU	A	11	-15.029	23.666	8.464
ATOM	586	CB	GLU	A	11	-17.981	23.624	8.715
ATOM	587	CG	GLU	A	11	-19.421	23.807	9.163
ATOM	588	CD	GLU	A	11	-19.686	25.166	9.770
ATOM	589	OE1	GLU	A	11	-19.478	26.175	9.073
ATOM	590	OE2	GLU	A	11	-20.111	25.227	10.939
ATOM	591	N	LEU	A	12	-15.183	21.749	9.622
ATOM	592	CA	LEU	A	12	-13.923	21.254	9.104
ATOM	593	C	LEU	A	12	-14.062	19.912	8.386
ATOM	594	O	LEU	A	12	-15.136	19.299	8.359
ATOM	595	CB	LEU	A	12	-12.893	21.144	10.230
ATOM	596	CG	LEU	A	12	-12.660	22.422	11.054
ATOM	597	CD1	LEU	A	12	-13.475	22.350	12.337
ATOM	598	CD2	LEU	A	12	-11.181	22.586	11.399
ATOM	599	N	SER	A	13	-12.971	19.476	7.771
ATOM	600	CA	SER	A	13	-12.964	18.218	7.046
ATOM	601	C	SER	A	13	-11.568	17.628	7.164
ATOM	602	O	SER	A	13	-10.613	18.320	7.550
ATOM	603	CB	SER	A	13	-13.346	18.435	5.578
ATOM	604	OG	SER	A	13	-12.404	19.261	4.923
ATOM	605	N	ALA	A	13	-11.449	16.352	6.818
ATOM	606	CA	ALA	A	13	-10.179	15.665	6.949
ATOM	607	C	ALA	A	13	-9.421	15.471	5.652
ATOM	608	O	ALA	A	13	-9.941	15.720	4.563
ATOM	609	CB	ALA	A	13	-10.413	14.306	7.626
ATOM	610	N	ILE	A	14	-8.171	15.046	5.783
ATOM	611	CA	ILE	A	14	-7.343	14.746	4.623
ATOM	612	C	ILE	A	14	-6.475	13.559	5.004
ATOM	613	O	ILE	A	14	-6.212	13.316	6.183
ATOM	614	CB	ILE	A	14	-6.401	15.916	4.183
ATOM	615	CG1	ILE	A	14	-5.284	16.106	5.200
ATOM	616	CG2	ILE	A	14	-7.188	17.211	3.982
ATOM	617	CD1	ILE	A	14	-4.173	16.973	4.696
ATOM	618	N	SER	A	15	-6.045	12.806	3.999
ATOM	619	CA	SER	A	15	-5.187	11.662	4.242
ATOM	620	C	SER	A	15	-3.740	12.089	4.217
ATOM	621	O	SER	A	15	-3.360	13.020	3.508
ATOM	622	CB	SER	A	15	-5.416	10.584	3.185
ATOM	623	OG	SER	A	15	-6.667	9.971	3.401
ATOM	624	N	MET	A	16	-2.933	11.409	5.012

ATOM	625	CA	MET	A	16	-1.518	11.700	5.047
ATOM	626	C	MET	A	16	-0.778	10.414	5.244
ATOM	627	O	MET	A	16	-1.137	9.594	6.078
ATOM	628	CB	MET	A	16	-1.170	12.694	6.164
ATOM	629	CG	MET	A	16	-1.848	14.042	5.974
ATOM	630	SD	MET	A	16	-1.017	15.431	6.760
ATOM	631	CE	MET	A	16	-0.799	14.823	8.475
ATOM	632	N	LEU	A	17	0.238	10.231	4.426
ATOM	633	CA	LEU	A	17	1.077	9.065	4.508
ATOM	634	C	LEU	A	17	2.289	9.610	5.264
ATOM	635	O	LEU	A	17	2.939	10.565	4.818
ATOM	636	CB	LEU	A	17	1.461	8.608	3.100
ATOM	637	CG	LEU	A	17	2.324	7.355	2.955
ATOM	638	CD1	LEU	A	17	1.553	6.145	3.445
ATOM	639	CD2	LEU	A	17	2.723	7.190	1.492
ATOM	640	N	TYR	A	18	2.581	9.029	6.418
ATOM	641	CA	TYR	A	18	3.706	9.501	7.196
ATOM	642	C	TYR	A	18	4.434	8.333	7.835
ATOM	643	O	TYR	A	18	4.081	7.186	7.603
ATOM	644	CB	TYR	A	18	3.222	10.458	8.281
ATOM	645	CG	TYR	A	18	2.386	9.782	9.346
ATOM	646	CD1	TYR	A	18	1.029	9.527	9.147
ATOM	647	CD2	TYR	A	18	2.961	9.379	10.550
ATOM	648	CE1	TYR	A	18	0.273	8.894	10.128
ATOM	649	CE2	TYR	A	18	2.218	8.745	11.526
ATOM	650	CZ	TYR	A	18	0.877	8.508	11.317
ATOM	651	OH	TYR	A	18	0.134	7.922	12.318
ATOM	652	N	LEU	A	19	5.439	8.651	8.650
ATOM	653	CA	LEU	A	19	6.255	7.661	9.347
ATOM	654	C	LEU	A	19	6.210	7.946	10.847
ATOM	655	O	LEU	A	19	6.685	8.992	11.288
ATOM	656	CB	LEU	A	19	7.701	7.763	8.871
ATOM	657	CG	LEU	A	19	7.901	7.850	7.359
ATOM	658	CD1	LEU	A	19	9.300	8.379	7.039
ATOM	659	CD2	LEU	A	19	7.669	6.482	6.748
ATOM	660	N	ASP	A	20	5.652	7.035	11.639
ATOM	661	CA	ASP	A	20	5.594	7.282	13.071
ATOM	662	C	ASP	A	20	7.001	7.289	13.662
ATOM	663	O	ASP	A	20	7.985	7.185	12.932
ATOM	664	CB	ASP	A	20	4.714	6.244	13.786
ATOM	665	CG	ASP	A	20	5.292	4.837	13.752
ATOM	666	OD1	ASP	A	20	6.533	4.678	13.775
ATOM	667	OD2	ASP	A	20	4.491	3.882	13.732
ATOM	668	N	GLU	A	21	7.089	7.413	14.981
ATOM	669	CA	GLU	A	21	8.375	7.451	15.669
ATOM	670	C	GLU	A	21	9.250	6.212	15.463
ATOM	671	O	GLU	A	21	10.459	6.246	15.738
ATOM	672	CB	GLU	A	21	8.164	7.699	17.171
ATOM	673	CG	GLU	A	21	7.220	6.731	17.868
ATOM	674	CD	GLU	A	21	5.828	6.726	17.257
ATOM	675	OE1	GLU	A	21	5.347	7.810	16.856
ATOM	676	OE2	GLU	A	21	5.210	5.640	17.185
ATOM	677	N	ASN	A	22	8.646	5.133	14.966
ATOM	678	CA	ASN	A	22	9.377	3.889	14.727
ATOM	679	C	ASN	A	22	9.682	3.647	13.249
ATOM	680	O	ASN	A	22	10.095	2.554	12.853
ATOM	681	CB	ASN	A	22	8.591	2.707	15.299
ATOM	682	CG	ASN	A	22	8.384	2.827	16.794
ATOM	683	OD1	ASN	A	22	9.349	2.930	17.560
ATOM	684	ND2	ASN	A	22	7.125	2.819	17.221

ATOM	685	N	GLU	A	23	9.485	4.672	12.435
ATOM	686	CA	GLU	A	23	9.749	4.558	11.015
ATOM	687	C	GLU	A	23	8.790	3.603	10.299
ATOM	688	O	GLU	A	23	9.145	2.996	9.292
ATOM	689	CB	GLU	A	23	11.203	4.129	10.784
ATOM	690	CG	GLU	A	23	12.232	5.210	11.082
ATOM	691	CD	GLU	A	23	12.072	6.410	10.166
ATOM	692	OE1	GLU	A	23	12.108	6.218	8.928
ATOM	693	OE2	GLU	A	23	11.907	7.541	10.677
ATOM	694	N	LYS	A	24	7.580	3.459	10.826
ATOM	695	CA	LYS	A	24	6.583	2.624	10.175
ATOM	696	C	LYS	A	24	5.815	3.540	9.228
ATOM	697	O	LYS	A	24	5.553	4.692	9.552
ATOM	698	CB	LYS	A	24	5.602	2.039	11.182
ATOM	699	CG	LYS	A	24	6.163	0.963	12.058
ATOM	700	CD	LYS	A	24	5.068	0.387	12.947
ATOM	701	CE	LYS	A	24	5.648	-0.511	14.031
ATOM	702	NZ	LYS	A	24	4.577	-1.091	14.886
ATOM	703	N	VAL	A	25	5.455	3.037	8.057
ATOM	704	CA	VAL	A	25	4.713	3.849	7.116
ATOM	705	C	VAL	A	25	3.237	3.737	7.444
ATOM	706	O	VAL	A	25	2.657	2.659	7.383
ATOM	707	CB	VAL	A	25	4.969	3.396	5.681
ATOM	708	CG1	VAL	A	25	4.250	4.317	4.708
ATOM	709	CG2	VAL	A	25	6.462	3.393	5.422
ATOM	710	N	VAL	A	25	2.637	4.864	7.800
ATOM	711	CA	VAL	A	25	1.231	4.916	8.170
ATOM	712	C	VAL	A	25	0.418	5.778	7.213
ATOM	713	O	VAL	A	25	0.871	6.841	6.774
ATOM	714	CB	VAL	A	25	1.062	5.531	9.577
ATOM	715	CG1	VAL	A	25	-0.341	5.253	10.115
ATOM	716	CG2	VAL	A	25	2.128	5.006	10.506
ATOM	717	N	LEU	A	26	-0.779	5.306	6.887
ATOM	718	CA	LEU	A	26	-1.706	6.048	6.040
ATOM	719	C	LEU	A	26	-2.862	6.358	6.992
ATOM	720	O	LEU	A	26	-3.679	5.497	7.297
ATOM	721	CB	LEU	A	26	-2.201	5.189	4.876
ATOM	722	CG	LEU	A	26	-3.204	5.898	3.952
ATOM	723	CD1	LEU	A	26	-2.519	7.077	3.262
ATOM	724	CD2	LEU	A	26	-3.755	4.925	2.929
ATOM	725	N	LYS	A	27	-2.910	7.584	7.489
ATOM	726	CA	LYS	A	27	-3.952	7.965	8.430
ATOM	727	C	LYS	A	27	-4.831	9.082	7.881
ATOM	728	O	LYS	A	27	-4.374	9.924	7.103
ATOM	729	CB	LYS	A	27	-3.305	8.409	9.738
ATOM	730	CG	LYS	A	27	-4.265	8.720	10.859
ATOM	731	CD	LYS	A	27	-3.509	9.382	11.994
ATOM	732	CE	LYS	A	27	-4.397	9.654	13.186
ATOM	733	NZ	LYS	A	27	-4.839	8.377	13.816
ATOM	734	N	ASN	A	28	-6.098	9.078	8.279
ATOM	735	CA	ASN	A	28	-7.045	10.095	7.843
ATOM	736	C	ASN	A	28	-7.147	11.103	8.979
ATOM	737	O	ASN	A	28	-7.815	10.842	9.969
ATOM	738	CB	ASN	A	28	-8.408	9.455	7.560
ATOM	739	CG	ASN	A	28	-9.518	10.485	7.364
ATOM	740	OD1	ASN	A	28	-9.360	11.444	6.597
ATOM	741	ND2	ASN	A	28	-10.653	10.288	8.050
ATOM	742	N	TYR	A	29	-6.473	12.241	8.837
ATOM	743	CA	TYR	A	29	-6.470	13.278	9.869
ATOM	744	C	TYR	A	29	-7.680	14.204	9.836

ATOM	745	O	TYR	A	29	-7.928	14.870	8.835
ATOM	746	CB	TYR	A	29	-5.197	14.130	9.768
ATOM	747	CG	TYR	A	29	-3.913	13.420	10.155
ATOM	748	CD1	TYR	A	29	-3.378	12.394	9.363
ATOM	749	CD2	TYR	A	29	-3.220	13.792	11.306
ATOM	750	CE1	TYR	A	29	-2.181	11.765	9.713
ATOM	751	CE2	TYR	A	29	-2.032	13.171	11.665
ATOM	752	CZ	TYR	A	29	-1.516	12.167	10.869
ATOM	753	OH	TYR	A	29	-0.319	11.603	11.231
ATOM	754	N	GLN	A	30	-8.408	14.254	10.950
ATOM	755	CA	GLN	A	30	-9.606	15.088	11.089
ATOM	756	C	GLN	A	30	-9.287	16.541	11.431
ATOM	757	O	GLN	A	30	-8.213	16.847	11.925
ATOM	758	CB	GLN	A	30	-10.500	14.541	12.202
ATOM	759	CG	GLN	A	30	-10.807	13.074	12.104
ATOM	760	CD	GLN	A	30	-11.744	12.749	10.969
ATOM	761	OE1	GLN	A	30	-11.900	11.582	10.602
ATOM	762	NE2	GLN	A	30	-12.385	13.773	10.405
ATOM	763	N	ASP	A	31	-10.238	17.430	11.173
ATOM	764	CA	ASP	A	31	-10.085	18.851	11.495
ATOM	765	C	ASP	A	31	-8.867	19.494	10.842
ATOM	766	O	ASP	A	31	-8.195	20.335	11.442
ATOM	767	CB	ASP	A	31	-10.000	19.025	13.019
ATOM	768	CG	ASP	A	31	-11.247	18.520	13.742
ATOM	769	OD1	ASP	A	31	-12.349	18.587	13.155
ATOM	770	OD2	ASP	A	31	-11.130	18.069	14.908
ATOM	771	N	MET	A	32	-8.582	19.113	9.606
ATOM	772	CA	MET	A	32	-7.426	19.662	8.918
ATOM	773	C	MET	A	32	-7.780	20.808	7.987
ATOM	774	O	MET	A	32	-7.021	21.768	7.855
ATOM	775	CB	MET	A	32	-6.741	18.559	8.125
ATOM	776	CG	MET	A	32	-6.037	17.540	8.980
ATOM	777	SD	MET	A	32	-4.559	18.231	9.714
ATOM	778	CE	MET	A	32	-3.406	18.041	8.318
ATOM	779	N	VAL	A	33	-8.942	20.707	7.351
ATOM	780	CA	VAL	A	33	-9.381	21.719	6.401
ATOM	781	C	VAL	A	33	-10.579	22.536	6.858
ATOM	782	O	VAL	A	33	-11.586	21.988	7.292
ATOM	783	CB	VAL	A	33	-9.701	21.056	5.027
ATOM	784	CG1	VAL	A	33	-10.388	22.040	4.087
ATOM	785	CG2	VAL	A	33	-8.423	20.561	4.412
ATOM	786	N	VAL	A	34	-10.465	23.855	6.739
ATOM	787	CA	VAL	A	34	-11.553	24.745	7.113
ATOM	788	C	VAL	A	34	-12.610	24.835	6.016
ATOM	789	O	VAL	A	34	-12.373	25.403	4.950
ATOM	790	CB	VAL	A	34	-11.057	26.176	7.407
ATOM	791	CG1	VAL	A	34	-12.240	27.097	7.601
ATOM	792	CG2	VAL	A	34	-10.222	26.186	8.655
ATOM	793	N	GLU	A	35	-13.779	24.266	6.282
ATOM	794	CA	GLU	A	35	-14.870	24.311	5.321
ATOM	795	C	GLU	A	35	-15.702	25.565	5.572
ATOM	796	O	GLU	A	35	-16.011	26.303	4.645
ATOM	797	CB	GLU	A	35	-15.733	23.054	5.447
ATOM	798	CG	GLU	A	35	-14.969	21.782	5.128
ATOM	799	CD	GLU	A	35	-14.515	21.732	3.676
ATOM	800	OE1	GLU	A	35	-15.036	22.519	2.858
ATOM	801	OE2	GLU	A	35	-13.643	20.902	3.344
ATOM	802	N	GLY	A	36	-16.053	25.811	6.829
ATOM	803	CA	GLY	A	36	-16.834	26.990	7.152
ATOM	804	C	GLY	A	36	-16.322	27.785	8.341

ATOM	805	O	GLY	A	36	-15.671	27.249	9.237
ATOM	806	N	CYS	A	37	-16.616	29.077	8.360
ATOM	807	CA	CYS	A	37	-16.177	29.917	9.466
ATOM	808	C	CYS	A	37	-17.347	30.502	10.249
ATOM	809	O	CYS	A	37	-18.467	30.628	9.741
ATOM	810	CB	CYS	A	37	-15.301	31.058	8.967
ATOM	811	SG	CYS	A	37	-13.785	30.558	8.098
ATOM	812	N	GLY	A	38	-17.079	30.867	11.494
ATOM	813	CA	GLY	A	38	-18.129	31.430	12.309
ATOM	814	C	GLY	A	38	-17.622	32.176	13.518
ATOM	815	O	GLY	A	38	-16.425	32.235	13.791
ATOM	816	N	CYS	A	39	-18.564	32.753	14.245
ATOM	817	CA	CYS	A	39	-18.253	33.505	15.439
ATOM	818	C	CYS	A	39	-18.543	32.670	16.665
ATOM	819	O	CYS	A	39	-19.620	32.084	16.794
ATOM	820	CB	CYS	A	39	-19.068	34.779	15.442
ATOM	821	SG	CYS	A	39	-18.539	35.799	14.053

Structure coordinates: As used herein, unless indicated otherwise or contradictory in context, the "structure coordinates" refers to Cartesian coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a protein, protein complex or peptide in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are then used to establish the positions of the individual atoms of the molecule or molecular complex.

STAMP: STAMP (Structural Alignment of Multiple Proteins) is a tool for aligning protein sequences based on a three-dimensional structure. Its algorithm minimizes the Cα distance between aligned residues of each molecule by applying globally optimal rigid-body rotations and translations. This program provides some information on the equivalence of the residues between the selected models.

SCWRL: This program predicts and optimizes the protein side-chain conformations. It is using the backbone of a support protein and a backbone-dependent rotamer library. The possible conformations are explored by minimizing the steric hindrance between the side-chains and between the side-chains and the backbone.

GROMACS: GROMACS is a molecular dynamics package. The ”gmx rms“ tool included in GROMACS compares two structures by computing the root mean square deviation (RMSD).

For the avoidance of doubts, the term “pharmaceutical association” or “pharmaceutical combination” as used herein refers to a compound or substance comprising at least two components, *i.e.* a (modified) GFR-binding compound and a bioactive carrier, linked, connected or bound through at least one covalent or non-covalent link, connection or bond.

In one aspect, the present disclosure provides for non-mutagenic extracellular therapies having the ability to direct cell fate. It is thus possible to convert or recode a neoplastic cell by modifying its surrounding extracellular micro-environment, in-vitro, ex-vivo or in-vivo, so that the cell operates self-recovery or self-healing and a subject possessing such a neoplastic cell may be protected from a neoplastic disease.

In one example, a neoplastic cell may operate self-recovery or self-healing *e.g.* by inducing a quiescence state so that the neoplastic cell may remain inactive or dormant for seconds, minutes, hours, days, weeks, months or years, in particular, will never resume neoplasia; and/or by preventing, reducing or suppressing cell division and/or cell proliferation, preferably uncontrolled cell division and/or cell proliferation of said neoplastic cell; and/or by regulating or promoting anti-mitogen activity and/or tumour suppressor pathways and/or anti-oncogenic activity in said neoplastic cell; and/or by inducing cytostaticity and not cytotoxicity in the neoplastic cell; and/or by inducing differentiation; and/or by regulating and/or modulating the adhesion or interactions between the cell and its micro-environment (i.e. the surrounding ECM) so as activate, reactivate or restore cell adhesion checkpoints in said neoplastic cell.

In one aspect, the present disclosure provides a pharmaceutical association or combination having the ability to convert or recode, extracellularly, a neoplastic cell, in-vitro, ex-vivo or in-vivo, so that it may be used in the treatment, prevention and/or diagnostic of a neoplastic disease, said association comprising at least one growth factor receptor-binding compound which activates at least one growth factor receptor of a neoplastic cell and at least one bioactive carrier which forms at least one covalent or non-covalent association with said at least one growth factor receptor-binding compound, and wherein said association reduces or suppresses (i) the gene expression of at least one cyclin D in the neoplastic cell and/or (ii) reduces or suppresses the formation of at least one complex formed between said at least one cyclin D and at least one of cyclin dependent-kinase (CDK) 4 or 6 in the neoplastic cell.

II. Growth factor receptor-binding compounds

In one aspect, the present disclosure provides for pharmaceutical associations or combinations comprising at least one growth factor receptor-binding compound as defined herein and a bioactive carrier as defined herein, said associations or combinations having the ability to convert or recode a neoplastic cell into a non-neoplastic cell.

As used herein, the term “Growth factor receptor-binding compound” or “GFR-binding compound” refers to an exogenous or endogenous compound, molecule or substance (a) having an (binding) affinity for a growth factor receptor as defined herein, (b) comprising the ability to associate or combine with a bioactive carrier as defined herein, and (c) comprising the ability to activate a growth factor receptor as defined herein.

There are many ways to test, measure and present the binding affinity of a given substance for a given receptor, but for the purpose of the present disclosure, and for the avoidance of any doubts, the (binding) affinity values of a given GFR-binding compound to a given GFR are provided using the method of fluorescence anisotropy. In this method, a GFR-binding compound is fluorescently labelled using technics well established in the art. Binding of the resulting labelled compound to a growth factor receptor results in a fluctuation of fluorescence anisotropy which is used to construct an affinity binding curve from which the GFR-binding compound binding affinity value is derived. Using this technique, binding affinity values are given in the form of dissociation constants Kd. In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 1 (one)

picomolar (pM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 1 (one) nanomolar (nM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 10 (ten) nanomolar (nM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 100 (one hundred) nanomolar (nM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 1 (one) micromolar (μM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 10 (ten) micromolar (μM). In certain embodiments, GFR-binding compounds of the present disclosure have Kd values as measured by fluorescence anisotropy of more than 100 (one hundred) micromolar (μM).

There are many ways to test and measure the ability of a given substance to activate a given receptor, but for the purpose of the present disclosure, and for the avoidance of any doubts, a given GFR-binding compound activates a growth factor receptor if it induces growth factor receptor phosphorylation as measured by the western blot method. There are many distinct phosphorylation sites on growth factor receptors and they may widely vary according to the type of growth factor receptor as reported in the published scientific article from Mark A. Lemmon and Joseph Schlessinger, “Cell Signaling by Receptor Tyrosine Kinases”, Cell. 2010; 141(7), 1117-1134, which is hereby incorporated by reference in its entirety.

A GFR-binding compound is said to possess the ability to associate or combine with a bioactive carrier if it comprises a functional chemical element, function or group allowing for the covalent or non-covalent assembly of the GFR-binding compound and the bioactive carrier. Such a functional chemical element, function or group, also referred to as a bioactive carrier-affinity-contaning group or bioactive carrier-high-affinity-containing group, include, but is not limited to, a thiol-containing compound, a cysteine-containing compound, a cysteine, or a GTPGP or a WWFWG peptide fragment.

Growth factor receptor: As used herein, unless indicated otherwise or contradictory in context, the term “growth factor receptor” or “GFR” is a receptor which binds to growth factors which are naturally occurring substances capable of stimulating, for instance, cellular growth, proliferation, healing, and cellular differentiation. Suitable as growth factor receptors for implementing embodiments of the present invention include epidermal growth factor receptors (EGFR), fibroblast growth factor receptors (FGFR), vascular endothelial growth factor receptors (VEGFR), nerve growth factor receptors (NGFR), Insulin receptor family, Trk receptor family, Eph receptor family, AXL receptor family, LTK receptor family, TIE receptor family, ROR receptor family, DDR receptor family, RET receptor family, KLG receptor family, RYK receptor family, MuSK receptor family, hepatocyte growth factor receptors (HGFR), somatomedin or insulin-like growth factor receptors (SGFR), platelet-derived growth factor receptors (PDGFR), transforming growth factor beta (TGF-β) superfamily proteins such as AMH, ARTN, BMP10, BMP15, BMP2, BMP3, BMP4, BMP5, BMP6, BMP7, BMP8A, BMP8B, GDF1, GDF10, GDF11, GDF15, GDF2, GDF3, GDF3A, GDF5, GDF6, GDF7, GDF8, GDF9, GDNF, INHA, INHBA, INHBB, INHBC, INHBE, LEFTY1, LEFTY2, MSTN, NODAL, NRTN, PSPN, TGFB1, TGFB2 and TGFB3, and any combination

thereof.

Growth factor: As used herein, unless indicated otherwise or contradictory in context, the term “growth factor” refers to any substance(s) having the ability to bind to a growth factor receptor and produce (a) biological effect(s) or reaction(s), such as promoting the growth of tissues, by activating such a growth factor receptor. Exemplary growth factors include, but are not limited to, platelet-derived growth factor (PDGF), platelet-derived angiogenesis factor (PDAF), vascular endotheial growth factor (VEGF), platelet-derived epidermal growth factor (PDEGF), transforming growth factor beta (TGF-β), transforming growth factor A (TGF-A), epidermal growth factor (EGF), fibroblast growth factor (FGF), acidic fibroblast growth factor (FGF-A), basic fibroblast growth factor (FGF-B), insulin-like growth factors 1 and 2 (IGF-I and IGF-2), keratinocyte growth factor (KGF), tumor necrosis factor (TNF), fibroblast growth factor (FGF) and interleukin-1 (IL-I), Keratinocyte Growth Factor-2 (KGF-2), and combinations thereof.

Activation of growth factor receptors: As used herein, unless indicated otherwise or contradictory in context, the term “activating” or “activation of”, when used in relation to a growth factor receptor, refers to the phosphorylation of the tyrosine kinase domain of such a growth factor receptor.

In one aspect, the present disclosure provides a GFR-binding compound, as part of a pharmaceutical association, combination or composition as defined herein, as an active principle for use in methods and uses described herein.

In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is an epidermal growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a fibroblast growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a vascular endothelial growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a nerve growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a hepatocyte growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a somatomedin or insulin-like growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a platelet-derived growth factor receptor. In one particular example, the growth factor receptor involved in the interaction with said GFR-binding compound is a protein from the transforming growth factor beta (TGF-β) superfamily.

In one particular example, the growth factor receptor(s) involved in the interaction with said GFR-binding compound is (are) preferably selected from epidermal growth factor receptors, fibroblast growth factor receptors, vascular endothelial growth factor receptors, nerve growth factor receptors, hepatocyte growth factor receptors, somatomedin or insulin-like growth factor receptors, platelet-derived growth factor receptors, and transforming growth factor beta (TGF-β) superfamily proteins.

In one particular example, the gene expression of cyclin-D, in a neoplastic cell, is reduced, down-

regulated, inhibited or suppressed during phase G1 of the cell cycle. In one particular example, the gene expression of cyclin-D is reduced or suppressed for substantially at least the entire duration of phase G1 of a cell cycle. In one particular example, the gene expression of cyclin-D is reduced by at least 20%. In one particular example, the gene expression of cyclin-D is reduced by at least 30%. In one particular example, the gene expression of cyclin-D is reduced by at least 40%. In one particular example, the gene expression of cyclin-D is reduced by at least 50%. In one particular example, the gene expression of cyclin-D is reduced by at least 60%. In one particular example, the gene expression of cyclin-D is reduced by at least 70%. In one particular example, the gene expression of cyclin-D is reduced by at least 80%. At least 40% is particularly preferred. Reduction of cyclin D gene expression is assessed with respect to the wild-type gene expression of cyclin-D and is measured by Quantitative Real Time Polymerase Chain Reaction (Q-PCR or RT-PCR) by (i) extracting RNA from the treated cells, (ii) converting the extracted RNA into the corresponding cDNA, (iii) subjecting the obtained cDNA to a real-time PCR amplification, (iv) analysing the data obtained from the real-time PCR amplification and comparing them with the data obtained by the ΔΔCt method, and (v) comparing the obtained values to the wild-type value.

In more details, Quantitative Real Time Polymerase Chain Reaction is carried out by (i) extracting RNA from the treated cells using the RNeasy total RNA kit from Qiagen®, (ii) converting the extracted RNA into the corresponding cDNA using a reverse transcription reaction (Gibco Brl®) and random primers from Invitrogen®, (iii) subjecting the obtained cDNA to a real-time PCR amplification in the presence of SYBR green reagents from Bio-Rad® in a thermocycler (iCycler, Biorad®), (iv) analysing the data obtained from the real-time PCR amplification with the iCycler IQ™ software following the iCycler iQ™ Real-Time PCR Detection System's instruction manual (Catalog Number 170-8740) and using weighted mean as a digital filter, PCR Baseline Subtracted Curve Fit as the analysis mode, FAM/490 as a fluorophore, the automatic calculation of the baseline cycles and the threshold, and the default settings for all other parameters, and comparing them with the data obtained by the ΔΔCt method as reported and described in Livak, K. J. and T. D. Schmittgen. "Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method", Methods (2001) 25(4): 402-408, hereby incorporated by reference in its entirety, and (v) comparing the obtained values to the wild-type value.

In one particular example, the gene expression of cyclin-D is maintained at such a reduced level (at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, or at least 80%) during phase G1 of a cell cycle of the treated neoplastic cell. In one example, the gene expression of cyclin-D is maintained at such a reduced level during substantially the entire duration of the G1 phase. In one example, the gene expression of cyclin-D is maintained at such a reduced level during substantially the entire duration of the G1 and S phases. In one example, the gene expression of cyclin-D is maintained at such a reduced level during substantially the entire duration of the G1, S and G2 phases. In one example, the gene expression of cyclin-D is maintained at such a reduced level during substantially the entire duration of the G1, S, G2 and M phases *i.e.* during substantially the entire duration of a cell cycle of a treated neoplastic cell. Reduction of the gene expression level of cyclin D during substantially the entire duration of G1 is preferred.

As used herein, unless indicated otherwise or contradictory in context, the term "wild-type expression" of

a protein or a gene, refers to the expression of a protein or a gene observed in normal, standard biological conditions i.e., in the present disclosure, without the presence of, or prior to the provision or administration to a neoplastic cell of a pharmaceutical association, combination or composition as defined herein. In-vitro, ex-vivo or in-vivo natural expression level of a protein or a gene in a neoplastic cell may thus be used as a comparative data (or control) to assess and quantify the effect of the presence or administration of a pharmaceutical association, combination or composition as defined herein on the expression level of such a protein or gene in that cell.

Suitable GFR-binding compounds for implementing certain embodiments of the invention include, without being limited to, linear (i.e. non-cyclic) GFR-binding compounds such as peptides, or variants or analogs thereof, or peptidomimetics, and cyclic GFR-binding compounds such as cyclic peptides, or variants or analogs thereof, or cyclic peptidomimetics.

II.1. Non-cyclic GFR-binding compounds

In one example, said (non-cyclic) GFR-binding compound has a molecular weight of less than 8,000 Daltons. In one particular example, said (non-cyclic) GFR-binding compound has a molecular weight of less than 6,000 Daltons. In one particular example, said (non-cyclic) GFR-binding compound has a molecular weight comprised between 2,000 and 8,000 Daltons. In one particular example, said (non-cyclic) GFR-binding compound has a molecular weight comprised between 2,000 and 6,000 Daltons. Between 2,000 and 6,000 Daltons is particularly preferred.

In one particular example, said GFR-binding compound is a (non-cyclic) peptide, a variant or analog thereof, as defined herein, with (exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having growth factor receptor-binding capability or capabilities.

In one particular example, said GFR-binding compound is a (non-cyclic) peptidomimetic as defined herein, having growth factor receptor-binding capability or capabilities, comprising (consecutively or non consecutively) between 20-60 amino acids, in particular between 20-50 or 20-45 amino acids, and more particularly, between 23-60, 23-50 or 23-45 amino acids; wherein said GFR-binding compound has a molecular weight comprised between 2,000 and 8,000 Daltons (in particular, between 2,000 and 6,000 Da).

In one particular example, said GFR-binding compound is a peptidomimetic as defined herein, having growth factor receptor-binding capability or capabilities, comprising (consecutively or non consecutively) between 20-60 amino acids, in particular between 20-50 or 20-45 amino acids, and more particularly, between 23-60, 23-50 or 23-45 amino acids; and containing at least one peptide portion or fragment with between 5-20 amino acids (in particular containing two peptide portions or fragments, each of which with between 5-20 amino acids); wherein said GFR-binding compound has a molecular weight comprised between 2,000 and 8,000 Daltons (in particular, between 2,000 and 6,000 Da).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a

peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having growth factor receptor-binding capability or capabilities, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3) and a peptide with three amino acids (PEP4).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3) and a peptide with three amino acids (PEP4).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5) and a peptide with between five and seven amino acids (PEP6).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5) and a peptide with between five and seven amino acids (PEP6).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2);

wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9) and a peptide with between six and eleven amino acids (PEP10).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9) and a peptide with between six and eleven amino acids (PEP10).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3) and a peptide with between five and seven amino acids (PEP6).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3) and a peptide with between five and seven amino acids (PEP6).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with eight amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3) and a peptide with between six and eleven amino acids (PEP10).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2);

wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5) and a peptide with three amino acids (PEP4).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5) and a peptide with three amino acids (PEP4).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9) and a peptide with three amino acids (PEP4).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5) and a peptide with between six and eleven amino acids (PEP10).

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wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9) and a peptide with between five and seven amino acids (PEP6).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3), an amino acid or a peptide with between two and seven amino acids (PEP7), and a peptide with three amino acids (PEP4).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with three amino acids (PEP4), and an amino acid or a peptide with between two and six amino acids (PEP8).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a

peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with three amino acids (PEP3), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with between five and seven amino acids (PEP6), and an amino acid or a peptide with between two and six amino acids (PEP8).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), and a peptide with three amino acids (PEP4).

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In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of)

between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), and a peptide with between six and eleven amino acids (PEP10).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), and a peptide with between six and eleven amino acids (PEP10).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with three amino acids (PEP4), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with three amino acids (PEP4), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with between five and seven amino acids (PEP6), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino

acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with five amino acids (PEP5), an amino acid or a peptide with between two and seven amino acids (PEP7), a peptide with between five and seven amino acids (PEP6), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9), a peptide with three amino acids (PEP4), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9), a peptide with three amino acids (PEP4), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9), a peptide with between five and seven amino acids (PEP6), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP12) and a peptide with five amino acids (PEP2); wherein said GFR-binding compound further comprises a peptide with between six and twelve amino acids (PEP9), a peptide with between five and seven amino acids (PEP6), and an amino acid or a peptide with between two and six amino acids (PEP8).

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having the following general formula (Ia) (hereinafter may also be referred to as compound (Ia) or

peptide (Ia)):

PEP(A)-LINKER-PEP(B) (Ia)

wherein one end of LINKER interacts covalently with one end of PEP(A); wherein another end of LINKER interacts covalently with one end of PEP(B); wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da, in particular, between about 300 and about 1000 Da.

In the present description, the molecular weight of LINKER refer to the calculated molecular weight prior to being connected to / reacted with any of the elements it is configured to connect to or react with e.g. PEP(A), PEP(B) or any other groups defined herein.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having the following general formula (Ia) (hereinafter may also be referred to as compound (Ia) or peptide (I)):

PEP(A)-LINKER-PEP(B) (Ia)

wherein one end of LINKER interacts covalently with one end of PEP(A); wherein another end of LINKER interacts covalently with one end of PEP(B); wherein PEP(A) comprises PEP12; wherein PEP(B) comprises PEP2; wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da, in particular, between about 300 and about 1000 Da.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP3; wherein PEP(B) further comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP12; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP3; wherein PEP(B) further comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP5; wherein PEP(B) further comprises PEP6.

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wherein PEP(B) further comprises PEP6.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP9; wherein PEP(B) further comprises PEP10.

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In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP3 and PEP7; wherein PEP(B) further comprises PEP4.

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wherein PEP(B) further comprises PEP4 and PEP8.

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In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP12; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP5 and PEP7; wherein PEP(B) further comprises PEP4 and PEP8.

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In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP9; wherein PEP(B) further comprises PEP4 and PEP8.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP12; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP9; wherein PEP(B) further comprises PEP4 and PEP8.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP1; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP9; wherein PEP(B) further comprises PEP6 and PEP8.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (Ia), wherein PEP(A) comprises PEP12; wherein PEP(B) comprises PEP2; wherein PEP(A) further comprises PEP9; wherein PEP(B) further comprises PEP6 and PEP8.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having the following general formula (IIa) (hereinafter may also be referred to as compound (IIa) or peptide (IIa)):

PEP(C)-PEP12-LINKER-PEP2-PEP(D) (IIa)

wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da, in particular, between about 300 and about 1000 Da; wherein PEP12 is a peptide with 8 amino acids of formula PEP1-AA^{17}-PEP11 as defined herein; wherein PEP2 is a peptide with five amino acids as already defined herein; wherein one end of PEP(C) interacts covalently with PEP12 via one end of PEP1; wherein one end of PEP(D) interacts covalently with one end of PEP2; wherein one end of LINKER interacts covalently with one end of PEP12

via one end of PEP11; wherein another end of LINKER interacts covalently with another end of PEP2; wherein PEP(C) is a peptide with at least 5 amino acids, in particular a peptide with between 5 and 12 amino acids; wherein PEP(D) is a peptide with at least 5 amino acids, in particular a peptide with between 5 and 11 amino acids.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3; wherein PEP(D) comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP5; wherein PEP(D) comprises PEP6. In one particular example, PEP(C) is PEP5; and PEP(D) is PEP6.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP9; wherein PEP(D) comprises PEP10. In one particular example, PEP(C) is PEP9; and PEP(D) is PEP10.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3; wherein PEP(D) comprises PEP6. In one particular example, PEP(C) comprises PEP3 and PEP(D) is PEP6.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3; wherein PEP(D) comprises PEP10. In one particular example, PEP(C) comprises PEP3 and PEP(D) is PEP10.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP5; wherein PEP(D) comprises PEP4. In one particular example, PEP(C) is PEP5 and PEP(D) comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP9; wherein PEP(D) comprises PEP4. In one particular example, PEP(C) is PEP9 and PEP(D) comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP5; wherein PEP(D) comprises PEP10. In one particular example, PEP(C) is PEP5 and PEP(D) is PEP10.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP9; wherein PEP(D) comprises PEP6. In one particular example, PEP(C) is PEP9 and PEP(D) is PEP6.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3 and PEP7; wherein PEP(D) comprises PEP4.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3 and PEP7; wherein PEP(D) comprises PEP6. In one particular example, PEP(C) comprises PEP3 and PEP7, and PEP(D) is PEP6.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP3 and PEP7; wherein PEP(D) comprises PEP10. In one particular example, PEP(C) comprises PEP3 and PEP7, and PEP(D) is PEP10.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP7; wherein PEP(D) comprises PEP4 and PEP8.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP7; wherein PEP(D) comprises PEP6 and PEP8.

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In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) comprises PEP9; wherein PEP(D) comprises PEP6 and PEP8.

In one aspect, the present disclosure provides a GFR-binding compound of general formula (IIa), wherein PEP(C) is PEP5 or PEP9 and wherein PEP(D) is PEP6 or PEP10.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino

acids, having the following general formula (IIIa) (hereinafter may also be referred to as compound (IIIa) or peptide (IIIa)):

PEP7-PEP5-PEP12-LINKER-PEP2-PEP6-PEP8 (IIIa)

wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da, in particular, between about 300 and about 1000 Da; wherein PEP12 is a peptide with 8 amino acids of formula PEP1-AA^{17}-PEP11 as defined herein; wherein PEP2 is a peptide with five amino acids as already defined herein; wherein PEP5 is a peptide with five amino acids as already defined herein; wherein PEP6 is a peptide with between five and seven amino acids as already defined herein; wherein PEP7 an amino acid or a peptide with between two and seven amino acids as already defined herein; wherein PEP8 an amino acid or a peptide with between two and six amino acids as already defined herein; wherein one end of LINKER interacts covalently with one end of PEP12 via AA^{20}; wherein another end of LINKER interacts covalently with one end of PEP2 via AA^{21}; wherein one end of PEP5 interacts covalently with another end of PEP12 via AA^{12}; wherein another end of PEP5 interacts covalently with one end of PEP7 via AA^{8}; wherein one end of PEP6 interacts covalently with another end of PEP2 via AA^{26}; wherein another end of PEP6 interacts covalently with one end of PEP8 via AA^{32}.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with (comprising, or exclusively consisting of, or constituted of) between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, having the following general formula (IVa) (hereinafter may also be referred to as compound (IVa) or peptide (IVa)):

AA^{1}-AA^{2}-AA^{3}-AA^{4}-AA^{5}-AA^{6}-AA^{7}-AA^{8}-AA^{9}-AA^{10}-AA^{11}-AA^{12}-AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20}-LINKER-AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25}-AA^{26}-AA^{27}-AA^{28}-AA^{29}-AA^{30}-AA^{31}-AA^{32}-AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} (IVa)

wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da, in particular, between about 300 and about 1000 Da; wherein AA^{1}-AA^{2}-AA^{3}-AA^{4}-AA^{5}-AA^{6}-AA^{7} is PEP7 as defined herein; wherein AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20} is PEP12 as defined herein; wherein AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25} is PEP2 as already defined herein; wherein AA^{8}-AA^{9}-AA^{10} is PEP3 as defined herein; wherein AA^{30}-AA^{31}-AA^{32} is PEP4 as defined herein; wherein AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} is PEP8 as defined herein; wherein AA^{11}, AA^{12}, AA^{26}, AA^{27}, AA^{28}, and AA^{29} are as defined herein; wherein one end of LINKER interacts covalently with AA^{20}; wherein another end of LINKER interacts covalently with AA^{21}; wherein AA^{1} and AA^{21} may be both N-terminal amino acids or both C-terminal amino acids; wherein AA^{38} and AA^{20} may be both N-terminal amino acids or both C-terminal amino acids.

In certain embodiments, PEP1 is selected from the group consisting of SAIS, SSLS, NAIS, SATS, SPIS, EPIS, SPIN, KPLS, EPLP, EPLT, SNIT, RSVK and RPVQ.

In certain embodiments, PEP2 is selected from the group consisting of LKNYQ, LKVYP, LKKYR, LRKHR, LKYHY, KFKYE, YGKIP, YKQYE, DHHKD, EQLSN, IGEMS, LGEMS, KEVQV and KKATV.

In certain embodiments, the pair PEP1:PEP2 is selected from the group consisting of SAIS:LKNYQ, SSLS:LKVYP, NAIS:LKKYR, SATS:LRKHR, SPIS:LKYHY, EPIS:KFKYE, SPIN:YGKIP, SPIS:YKQYE, KPLS:DHHKD, EPLP:EQLSN, EPLT:EQLSN, SNIT:IGEMS, SNIT:LGEMS, RSVK:KEVQV and RPVQ:KKATV.

In certain embodiments, PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV.

In certain embodiments, PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH.

In certain embodiments, PEP5 is a peptide of general formula PEP3-AA^{11}-AA^{12}; wherein PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H. In one particular example, PEP5 is selected from the group consisting of VPTEL, VPEKM, APTKL, APTQL, VPTKL, TPTKM, VPARL, VPTRL, APVKT, VPQAL, VSQDL, VPQDL, VPTEE, VPTGQ, SRVHH and TQVQL.

In certain embodiments, PEP6 is a peptide of general formula AA^{26}-AA^{27}-AA^{28}-AA^{29}-PEP4; wherein PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S. In one particular example, PEP6 is selected from the group consisting of DMVVE, NMTVE, EMVVE, NMVVR, NMVVK, EGMSVAE, GMAVS, GMVVD, MIVEE, MIVRS, MIVKS, MVVKS, FLQHN, LEEHS, RLEEH and TLEDH.

In certain embodiments, PEP7 is an amino acid or a peptide with between two and seven amino acids of general formula AA^{1}-AA^{2}-AA^{3}-AA^{4}-AA^{5}-AA^{6}-AA^{7}; wherein wherein AA^{1}, AA^{2}, AA^{3}, AA^{4}, and AA^{5} are independently absent or AA^{I} as defined herein; wherein AA^{6} is absent or selected from the group consisting of S, T, C, E, Q, P and R; wherein AA^{7} is absent or is selected from the group consisting of S, T, C, E, Q, P and R, and wherein at least one of AA^{1}, AA^{2}, AA^{3}, AA^{4}, AA^{5}, AA^{6} or AA^{7} is not absent. In one particular example, PEP7 is selected from the group consisting of KIPKAXX, GIPEPXX, SIPKAXX, HVTKPTX, YVPKPXX, TVPKPXX, AVPKAXX, KVGKAXX, KASKAXX, GSAGPXX, AAPASXX, STPPTXX, HVPKPXX, RVPSTXX, ASAAPXX, ASASPXX, NDEGLEX, SSVKXQP and RNVQXRP, wherein X is C or S throughout the present description.

In certain embodiments, PEP8 is an amino acid or a peptide with between two and six amino acids of

general formula AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38}; wherein AA^{33} is absent or is selected from the group consisting of AA^{I} amino acids at the exception of AA^{VI} amino acids; AA^{34} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{35} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{36} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{37} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{38} is absent or is selected from the group consisting of AA^{I}; and wherein at least one of AA^{33}, AA^{34}, AA^{35}, AA^{36}, AA^{37} or AA^{38} is not absent. In one particular example, PEP8 is selected from the group consisting of GXGXR, SXAXR, SXGXH, AXGXH, XGXR, EXGXR, RXGXS, AXGXR, SXGXR, XGXL, XKXS, KXEXR, QXEXR, LEXAXA and LAXKXE.

In certain embodiments, PEP9 is a peptide of general formula PEP7-PEP5; wherein PEP5 is a peptide of formula PEP3-AA^{11}-AA^{12}; wherein PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H; wherein PEP7 is an amino acid or a peptide with between two and seven amino acids of general formula AA^{1}-AA^{2}-AA^{3}-AA^{4}-AA^{5}-AA^{6}-AA^{7}; wherein AA^{1}, AA^{2}, AA^{3}, AA^{4}, and AA^{5} are independently absent or AA^{I} as defined herein; wherein AA^{6} is absent or selected from the group consisting of S, T, C, E, Q, P and R; wherein AA^{7} is absent or is selected from the group consisting of S, T, C, E, Q, P and R. In one particular example, PEP9 is selected from the group consisting of KIPKAXXVPTEL, GIPEPXXVPEKM, SIPKAXXVPTEL, HVTKPTXAPTKL, YVPKPXXAPTKL, TVPKPXXAPTQL, AVPKAXXAPTKL, KVGKAXXVPTKL, KASKAXXVPTKL, GSAGPXXTPTKM, AAPASXXVPARL, STPPTXXVPTRL, HVPKPXXAPTKL, RVPSTXXAPVKT, ASAAPXXVPQAL, ASASPXXVSQDL, ASASPXXVPQDL, NDEGLEXVPTEE, NDEGLEXVPTGQ, SSVKXQPSRVHH and RNVQXRPTQVQL, wherein X is C or S throughout the present description.

In certain embodiments, PEP10 is a peptide of general formula PEP6-PEP8; wherein PEP6 is a peptide of formula AA^{26}-AA^{27}-AA^{28}-AA^{29}-PEP4; wherein PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S; wherein PEP8 is an amino acid or a peptide with between two and six amino acids of general formula AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38}; AA^{33} is absent or is selected from the group consisting of AA^{I} amino acids at the exception of AA^{VI} amino acids; AA^{34} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{35} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{36} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{37} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{38} is absent or is selected from the group consisting of AA^{I}. In one particular example, PEP10 is selected from the group consisting of DMVVEGXGXR, NMTVESXAXR, EMVVEGXGXR, NMVVRSXGXH, NMVVRAXGXH, NMVVKAXGXH, EGMSVAEXGXR, GMAVSEXGXR, GMVVDRXGXS, DMVVEAXGXR, DMVVESXGXR, MIVEEXGXL, MIVRSXKXS, MIVKSXKXS, MVVKSXKXS, FLQHNKXEXR, LEEHSQXEXR, RLEEHLEXAXA and TLEDHLAXKXE.

In certain embodiments, PEP12 is a peptide of general formula PEP1-AA^{17}-PEP11; wherein AA^{17} is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T); wherein PEP1 is selected from the group consisting of SAIS, SSLS, NAIS, SATS, SPIS, EPIS, SPIN, KPLS, EPLP, EPLT, SNIT, RSVK and RPVQ.

In certain embodiments, the pair PEP12:PEP2 is selected from the group consisting of SAIS-AA^{17}-LYL:LKNYQ, SSLS-AA^{17}-LFF:LKVYP, NAIS-AA^{17}-LYF:LKKYR, SATS-AA^{17}-LYY:LRKHR, SPIS-AA^{17}-LYK:LKYHY, EPIS-AA^{17}-LYL:KFKYE, SPIN-AA^{17}-LYF:YGKIP, SPIS-AA^{17}-LYI:YKQYE, SPIS-AA^{17}-LFI:YKQYE, KPLS-AA^{17}-LYV:DHHKD, EPLP-AA^{17}-VYY:EQLSN, EPLT-AA^{17}-LYY:EQLSN, SNIT-AA^{17}-QIM:IGEMS, SNIT-AA^{17}-QIM:LGEMS, RSVK-AA^{17}-AKV:KEVQV and RPVQ-AA^{17}-RKI:KKATV ; wherein AA^{17} is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In certain embodiments, PEP11 is a peptide with 3 amino acids of general formula AA^{18}-AA^{19}-AA^{20}; wherein AA^{18} is selected from the group consisting of L, V, Q, A and R; wherein AA^{19} is selected from the group consisting of F, W, H, Y, I and K; wherein AA^{20} is selected from the group consisting of L, F, Y, K, I, V and M. In one particular example, PEP11 is selected from the group consisting of LYL, LFF, LYF, LYY, LYK, LYI, LFI, LYV, VYY, QIM, AKV and RKI.

In certain embodiments, PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV; PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH; and wherein the pair PEP3:PEP4 is selected from the group consisting of VPT:VVE, VPE:TVE, APT:VVR, APT:VVK, VPT:VAE, VPT:AVS, TPT:VVD, VPA:VVE, APV:VEE, VPQ:VRS, VSQ:VKS, VPQ:VKS, VPT:QHN, VPT:EHS, SRV:EEH and TQV:EDH.

In certain embodiments, PEP5 is selected from the group consisting of VPT-AA^{11}-AA^{12}, VPE-AA^{11}-AA^{12}-AA^{11}-AA^{12}, APT-AA^{11}-AA^{12}, TPT-AA^{11}-AA^{12}, VPA-AA^{11}-AA^{12}, VPT-AA^{11}-AA^{12}, APV-AA^{11}-AA^{12}, VPQ-AA^{11}-AA^{12}, VSQ-AA^{11}-AA^{12}, VPQ-AA^{11}-AA^{12}, SRV-AA^{11}-AA^{12} and TQV-AA^{11}-AA^{12}; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H; PEP6 is selected from the group consisting of AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVE, AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVE, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVK, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAE, AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVD, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEE, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHN, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEH and AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDH; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S; wherein the pair PEP5:PEP6 is selected from the group consisting of VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVE, VPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVE, APT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVR, APT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVK, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAE, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVS, TPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVD, VPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVE, APV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-

AA^{28}-AA^{29}-VEE, VPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRS, VSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKS, VPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKS, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHN, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHS, SRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEH and TQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDH.

In certain embodiments, PEP5 is selected from the group consisting of VPTEL, VPEKM, APTKL, APTQL, VPTKL, TPTKM, VPARL, VPTRL, APVKT, VPQAL, VSQDL, VPQDL, VPTEE, VPTGQ, SRVHH and TQVQL; PEP6 is selected from the group consisting of DMVVE, NMTVE, EMVVE, NMVVR, NMVVK, EGMSVAE, GMAVS, GMVVD, MIVEE, MIVRS, MIVKS, MVVKS, FLQHN, LEEHS, RLEEH and TLEDH; and wherein the pair PEP5:PEP6 is selected from the group consisting of VPTEL:DMVVE, VPEKM:NMTVE, VPTEL:EMVVE, APTKL:NMVVR, APTQL:NMVVR, APTKL:NMVVK, VPTKL:EGMSVAE, VPTKL:GMAVS, TPTKM:GMVVD, VPARL:DMVVE, VPTRL:DMVVE, APVKT:MIVEE, VPQAL:MIVRS, VSQDL:MIVKS, VPQDL:MVVKS, VPTEE:FLQHN, VPTGQ:LEEHS, SRVHH:RLEEH and TQVQL:TLEDH.

In certain embodiments, PEP7 is selected from the group consisting of KIPKAXX, GIPEPXX, SIPKAXX, HVTKPTX, YVPKPXX, TVPKPXX, AVPKAXX, KVGKAXX, KASKAXX, GSAGPXX, AAPASXX, STPPTXX, HVPKPXX, RVPSTXX, ASAAPXX, ASASPXX, NDEGLEX, SSVKXQP and RNVQXRP; wherein PEP8 is selected from the group consisting of GXGXR, SXAXR, SXGXH, AXGXH, XGXR, EXGXR, RXGXS, AXGXR, SXGXR, XGXL, XKXS, KXEXR, QXEXR, LEXAXA and LAXKXE; and wherein the pair PEP7:PEP8 is selected from the group consisting of KIPKAXX:GXGXR, GIPEPXX:SXAXR, SIPKAXX:GXGXR, HVTKPTX:SXGXH, YVPKPXX:SXGXH, TVPKPXX:AXGXH, AVPKAXX:AXGXH, KVGKAXX:XGXR, KASKAXX:EXGXR, GSAGPXX:RXGXS, AAPASXX:AXGXR, STPPTXX:SXGXR, HVPKPXX:SXGXH, RVPSTXX:XGXL, ASAAPXX:XKXS, ASASPXX:XKXS, NDEGLEX:KXEXR, NDEGLEX:QXEXR, SSVKXQP:LEXAXA and RNVQXRP:LAXKXE.

In certain embodiments, PEP9 is selected from the group consisting of KIPKAXXVPT-AA^{11}-AA^{12}, GIPEPXXVPE-AA^{11}-AA^{12}, SIPKAXXVPT-AA^{11}-AA^{12}, HVTKPTXAPT-AA^{11}-AA^{12}, YVPKPXXAPT-AA^{11}-AA^{12}, TVPKPXXAPT-AA^{11}-AA^{12}, AVPKAXXAPT-AA^{11}-AA^{12}, KVGKAXXVPT-AA^{11}-AA^{12}, KASKAXXVPT-AA^{11}-AA^{12}, GSAGPXXTPT-AA^{11}-AA^{12}, AAPASXXVPA-AA^{11}-AA^{12}, STPPTXXVPT-AA^{11}-AA^{12}, HVPKPXXAPT-AA^{11}-AA^{12}, RVPSTXXAPV-AA^{11}-AA^{12}, ASAAPXXVPQ-AA^{11}-AA^{12}, ASASPXXVSQ-AA^{11}-AA^{12}, ASASPXXVPQ-AA^{11}-AA^{12}, NDEGLEXVPT-AA^{11}-AA^{12}, NDEGLEXVPT-AA^{11}-AA^{12}, SSVKXQPSRV-AA^{11}-AA^{12} and RNVQXRPTQV-AA^{11}-AA^{12}; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H; PEP10 is selected from the group consisting of AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA and AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or

is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S; and wherein the pair PEP9:PEP10 is selected from the group consisting of KIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, GIPEPXXVPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR, SIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, HVTKPTXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, YVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, TVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH, AVPKAXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH, KVGKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR, KASKAXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR, GSAGPXXTPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS, AAPASXXVPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR, STPPTXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR, HVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, RVPSTXXAPV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL, ASAAPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS, ASASPXXVSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, ASASPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR, SSVKXQPSRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA and RNVQXRPTQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE.

In certain embodiments, PEP9 is selected from the group consisting of KIPKAXXVPTEL, GIPEPXXVPEKM, SIPKAXXVPTEL, HVTKPTXAPTKL, YVPKPXXAPTKL, TVPKPXXAPTQL, AVPKAXXAPTKL, KVGKAXXVPTKL, KASKAXXVPTKL, GSAGPXXTPTKM, AAPASXXVPARL, STPPTXXVPTRL, HVPKPXXAPTKL, RVPSTXXAPVKT, ASAAPXXVPQAL, ASASPXXVSQDL, ASASPXXVPQDL, NDEGLEXVPTEE, NDEGLEXVPTGQ, SSVKXQPSRVHH and RNVQXRPTQVQL; PEP10 is selected from the group consisting of DMVVEGXGXR, NMTVESXAXR, EMVVEGXGXR, NMVVRSXGXH, NMVVRAXGXH, NMVVKAXGXH, EGMSVAEXGXR, GMAVSEXGXR, GMVVDRXGXS, DMVVEAXGXR, DMVVESXGXR, MIVEEXGXL, MIVRSXKXS, MIVKSXKXS, MVVKSXKXS, FLQHNKXEXR, LEEHSQXEXR, RLEEHLEXAXA and TLEDHLAXKXE; and wherein the pair PEP9:PEP10 is selected from the group consisting of KIPKAXXVPTEL:DMVVEGXGXR, GIPEPXXVPEKM:NMTVESXAXR, SIPKAXXVPTEL:EMVVEGXGXR, HVTKPTXAPTKL:NMVVRSXGXH, YVPKPXXAPTKL:NMVVRSXGXH, TVPKPXXAPTQL:NMVVRAXGXH, AVPKAXXAPTKL:NMVVKAXGXH, KVGKAXXVPTKL:EGMSVAEXGXR, KASKAXXVPTKL:GMAVSEXGXR, GSAGPXXTPTKM:GMVVDRXGXS, AAPASXXVPARL:DMVVEAXGXR, STPPTXXVPTRL:DMVVESXGXR, HVPKPXXAPTKL:NMVVRSXGXH, RVPSTXXAPVKT:MIVEEXGXL, ASAAPXXVPQAL:MIVRSXKXS, ASASPXXVSQDL:MIVKSXKXS, ASASPXXVPQDL:MVVKSXKXS, NDEGLEXVPTEE:FLQHNKXEXR, NDEGLEXVPTGQ:LEEHSQXEXR, NDEGLEXVPTEE:FLQHNKXEXR, NDEGLEXVPTEE:FLQHNKXEXR, SSVKXQPSRVHH:RLEEHLEXAXA and RNVQXRPTQVQL:TLEDHLAXKXE.

In certain embodiments, PEP5 is selected from the group consisting of VPTEL, VPEKM, APTKL, APTQL, VPTKL, TPTKM, VPARL, VPTRL, APVKT, VPQAL, VSQDL, VPQDL, VPTEE, VPTGQ, SRVHH and TQVQL; PEP6 is selected from the group consisting of DMVVE, NMTVE, EMVVE, NMVVR, NMVVK,

EGMSVAE, GMAVS, GMVVD, MIVEE, MIVRS, MIVKS, MVVKS, FLQHN, LEEHS, RLEEH and TLEDH; wherein the pair PEP5:PEP6 is selected from the group consisting of VPTEL:DMVVE, VPEKM:NMTVE, VPTEL:EMVVE, APTKL:NMVVR, APTQL:NMVVR, APTKL:NMVVK, VPTKL:EGMSVAE, VPTKL:GMAVS, TPTKM:GMVVD, VPARL:DMVVE, VPTRL:DMVVE, APVKT:MIVEE, VPQAL:MIVRS, VSQDL:MIVKS, VPQDL:MVVKS, VPTEE:FLQHN, VPTGQ:LEEHS, SRVHH:RLEEH and TQVQL:TLEDH; and wherein the pair PEP5:PEP6 is not VPTEL:DMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein the pair PEP5:PEP6 is not VPEKM:NMTVE when PEP1 is SSLS and PEP2 is LKVYP; wherein the pair PEP5:PEP6 is not VPTEL:EMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein the pair PEP5:PEP6 is not APTKL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein the pair PEP5:PEP6 is not APTQL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein the pair PEP5:PEP6 is not APTKL:NMVVK when PEP1 is SATS and PEP2 is LRKHR; wherein the pair PEP5:PEP6 is not VPTKL:EGMSVAE when PEP1 is SPIS and PEP2 is LKYHY; wherein the pair PEP5:PEP6 is not VPTKL:GMAVS when PEP1 is EPIS and PEP2 is KFKYE; wherein the pair PEP5:PEP6 is not TPTKM:GMVVD when PEP1 is SPIN and PEP2 is YGKIP; wherein the pair PEP5:PEP6 is not VPARL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein the pair PEP5:PEP6 is not VPTRL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein the pair PEP5:PEP6 is not APVKT:MIVEE when PEP1 is KPLS and PEP2 is DHHKD; wherein the pair PEP5:PEP6 is not VPQAL:MIVRS when PEP1 is EPLP and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VSQDL:MIVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VPQDL:MVVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VPTEE:FLQHN when PEP1 is SNIT and PEP2 is IGEMS; wherein the pair PEP5:PEP6 is not VPTGQ:LEEHS when PEP1 is SNIT and PEP2 is LGEMS; wherein the pair PEP5:PEP6 is not SRVHH:RLEEH when PEP1 is RSVK and PEP2 is KEVQV; and wherein the pair PEP5:PEP6 is not TQVQL:TLEDH when PEP1 is RPVQ and PEP2 is KKATV.

In certain embodiments, PEP9 is selected from the group consisting of KIPKAXXVPT-AA^{11}-AA^{12}, GIPEPXXVPE-AA^{11}-AA^{12}, SIPKAXXVPT-AA^{11}-AA^{12}, HVTKPTXAPT-AA^{11}-AA^{12}, YVPKPXXAPT-AA^{11}-AA^{12}, TVPKPXXAPT-AA^{11}-AA^{12}, AVPKAXXAPT-AA^{11}-AA^{12}, KVGKAXXVPT-AA^{11}-AA^{12}, KASKAXXVPT-AA^{11}-AA^{12}, GSAGPXXTPT-AA^{11}-AA^{12}, AAPASXXVPA-AA^{11}-AA^{12}, STPPTXXVPT-AA^{11}-AA^{12}, HVPKPXXAPT-AA^{11}-AA^{12}, RVPSTXXAPV-AA^{11}-AA^{12}, ASAAPXXVPQ-AA^{11}-AA^{12}, ASASPXXVSQ-AA^{11}-AA^{12}, ASASPXXVPQ-AA^{11}-AA^{12}, NDEGLEXVPT-AA^{11}-AA^{12}, NDEGLEXVPT-AA^{11}-AA^{12}, SSVKXQPSRV-AA^{11}-AA^{12} and RNVQXRPTQV-AA^{11}-AA^{12}; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H; PEP10 is selected from the group consisting of AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR, AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA and AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino

acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S; and wherein the pair PEP9:PEP10 is selected from the group consisting of KIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, GIPEPXXVPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR, SIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, HVTKPTXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, YVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, TVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH, AVPKAXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH, KVGKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR, KASKAXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR, GSAGPXXTPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS, AAPASXXVPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR, STPPTXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR, HVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, RVPSTXXAPV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL, ASAAPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS, ASASPXXVSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, ASASPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR, SSVKXQPSRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA and RNVQXRPTQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE; and wherein PEP9:PEP10 is not KIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ ; wherein PEP9:PEP10 is not GIPEPXXVPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR when PEP1 is SSLS and PEP2 is LKVYP; wherein PEP9:PEP10 is not SIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ; wherein PEP9:PEP10 is not HVTKPTXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not YVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not TVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not AVPKAXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH when PEP1 is SATS and PEP2 is LRKHR; wherein PEP9:PEP10 is not KVGKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR when PEP1 is SPIS and PEP2 is LKYHY; wherein PEP9:PEP10 is not KASKAXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR when PEP1 is EPIS and PEP2 is KFKYE; wherein PEP9:PEP10 is not GSAGPXXTPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS when PEP1 is SPIN and PEP2 is YGKIP; wherein PEP9:PEP10 is not AAPASXXVPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not STPPTXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not HVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not RVPSTXXAPV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL when PEP1 is KPLS and PEP2 is DHHKD; wherein PEP9:PEP10 is not ASAAPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS when PEP1 is EPLP and PEP2 is EQLSN; ASASPXXVSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not ASASPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR when PEP1 is SNIT and PEP2 is LGEMS; wherein PEP9:PEP10 is not SSVKXQPSRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA when PEP1 is RSVK and PEP2 is KEVQV; and wherein PEP9:PEP10 is not RNVQXRPTQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE when

PEP1 is RPVQ and PEP2 is KKATV.

In certain embodiments, PEP9 is selected from the group consisting of KIPKAXXVPTEL, GIPEPXXVPEKM, SIPKAXXVPTEL, HVTKPTXAPTKL, YVPKPXXAPTKL, TVPKPXXAPTQL, AVPKAXXAPTKL, KVGKAXXVPTKL, KASKAXXVPTKL, GSAGPXXTPTKM, AAPASXXVPARL, STPPTXXVPTRL, HVPKPXXAPTKL, RVPSTXXAPVKT, ASAAPXXVPQAL, ASASPXXVSQDL, ASASPXXVPQDL, NDEGLEXVPTEE, NDEGLEXVPTGQ, SSVKXQPSRVHH and RNVQXRPTQVQL; PEP10 is selected from the group consisting of DMVVEGXGXR, NMTVESXAXR, EMVVEGXGXR, NMVVRSXGXH, NMVVRAXGXH, NMVVKAXGXH, EGMSVAEXGXR, GMAVSEXGXR, GMVVDRXGXS, DMVVEAXGXR, DMVVESXGXR, MIVEEXGXL, MIVRSXKXS, MIVKSXKXS, MVVKSXKXS, FLQHNKXEXR, LEEHSQXEXR, RLEEHLEXAXA and TLEDHLAXKXE; and wherein the pair PEP9:PEP10 is selected from the group consisting of

KIPKAXXVPTEL:DMVVEGXGXR, GIPEPXXVPEKM:NMTVESXAXR, SIPKAXXVPTEL:EMVVEGXGXR, HVTKPTXAPTKL:NMVVRSXGXH, YVPKPXXAPTKL:NMVVRSXGXH, TVPKPXXAPTQL:NMVVRAXGXH, AVPKAXXAPTKL:NMVVKAXGXH, KVGKAXXVPTKL:EGMSVAEXGXR, KASKAXXVPTKL:GMAVSEXGXR, GSAGPXXTPTKM:GMVVDRXGXS, AAPASXXVPARL:DMVVEAXGXR, STPPTXXVPTRL:DMVVESXGXR, HVPKPXXAPTKL:NMVVRSXGXH, RVPSTXXAPVKT:MIVEEXGXL, ASAAPXXVPQAL:MIVRSXKXS, ASASPXXVSQDL:MIVKSXKXS, ASASPXXVPQDL:MVVKSXKXS, NDEGLEXVPTEE:FLQHNKXEXR, NDEGLEXVPTGQ:LEEHSQXEXR, NDEGLEXVPTEE:FLQHNKXEXR, SSVKXQPSRVHH:RLEEHLEXAXA and RNVQXRPTQVQL:TLEDHLAXKXE; and wherein PEP9:PEP10 is not KIPKAXXVPTEL:DMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ ; wherein PEP9:PEP10 is not GIPEPXXVPEKM:NMTVESXAXR when PEP1 is SSLS and PEP2 is LKVYP; wherein PEP9:PEP10 is not SIPKAXXVPTEL:EMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ; wherein PEP9:PEP10 is not HVTKPTXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not YVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not TVPKPXXAPTQL:NMVVRAXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not AVPKAXXAPTKL:NMVVKAXGXH when PEP1 is SATS and PEP2 is LRKHR; wherein PEP9:PEP10 is not KVGKAXXVPTKL:EGMSVAEXGXR when PEP1 is SPIS and PEP2 is LKYHY; wherein PEP9:PEP10 is not KASKAXXVPTKL:GMAVSEXGXR when PEP1 is EPIS and PEP2 is KFKYE; wherein PEP9:PEP10 is not GSAGPXXTPTKM:GMVVDRXGXS when PEP1 is SPIN and PEP2 is YGKIP; wherein PEP9:PEP10 is not AAPASXXVPARL:DMVVEAXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not STPPTXXVPTRL:DMVVESXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not HVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not RVPSTXXAPVKT:MIVEEXGXL when PEP1 is KPLS and PEP2 is DHHKD; wherein PEP9:PEP10 is not ASAAPXXVPQAL:MIVRSXKXS when PEP1 is EPLP and PEP2 is EQLSN; ASASPXXVSQDL:MIVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not ASASPXXVPQDL:MVVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPTGQ:LEEHSQXEXR when PEP1 is SNIT and PEP2 is LGEMS ; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is

IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not SSVKXQPSRVHH:RLEEHLEXAXA when PEP1 is RSVK and PEP2 is KEVQV; and wherein PEP9:PEP10 is not RNVQXRPTQVQL:TLEDHLAXKXE when PEP1 is RPVQ and PEP2 is KKATV.

In certain embodiments, PEP1 is selected from the group consisting of SAIS, SSLS, NAIS, SATS, SPIS, EPIS, SPIN, KPLS, EPLP, EPLT, SNIT, RSVK and RPVQ; PEP11 is selected from the group consisting of LYL, LFF, LYF, LYY, LYK, LYI, LFI, LYV, VYY, QIM, AKV and RKI; and the pair PEP1:PEP11 is selected from the group consisting of SAIS:LYL, SSLS:LFF, NAIS:LYF, SATS:LYY, SPIS:LYK, SPIS:LYI, SPIS:LFI, EPIS:LYL, SPIN:LYF, KPLS:LYV, EPLP:VYY, EPLT:LYY, SNIT:QIM, RSVK:AKV and RPVQ:RKI.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) or a peptide with eight amino acids (PEP12), a peptide with five amino acids (PEP2), and optionally a pair of peptides selected form the group consisting of PEP3:PEP4, PEP3:PEP6, PEP3:PEP10, PEP5:PEP4, PEP9:PEP4, PEP5:PEP6, PEP5:PEP10, PEP9:PEP6 and PEP9:PEP10; wherein said GFR-binding compound does not comprise the pair of peptides VPTEL:DMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein said GFR-binding compound does not comprise the pair of peptides VPEKM:NMTVE when PEP1 is SSLS and PEP2 is LKVYP; wherein said GFR-binding compound does not comprise the pair of peptides VPTEL:EMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein said GFR-binding compound does not comprise the pair of peptides APTKL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides APTQL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides APTKL:NMVVK when PEP1 is SATS and PEP2 is LRKHR; wherein said GFR-binding compound does not comprise the pair of peptides VPTKL:EGMSVAE when PEP1 is SPIS and PEP2 is LKYHY; wherein said GFR-binding compound does not comprise the pair of peptides VPTKL:GMAVS when PEP1 is EPIS and PEP2 is KFKYE; wherein said GFR-binding compound does not comprise the pair of peptides TPTKM:GMVVD when PEP1 is SPIN and PEP2 is YGKIP; wherein said GFR-binding compound does not comprise the pair of peptides VPARL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein said GFR-binding compound does not comprise the pair of peptides VPTRL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein said GFR-binding compound does not comprise the pair of peptides APVKT:MIVEE when PEP1 is KPLS and PEP2 is DHHKD; wherein said GFR-binding compound does not comprise the pair of peptides VPQAL:MIVRS when PEP1 is EPLP and PEP2 is EQLSN; wherein said GFR-binding compound does not comprise the pair of peptides VSQDL:MIVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein said GFR-binding compound does not comprise the pair of peptides VPQDL:MVVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein said GFR-binding compound does not comprise the pair of peptides VPTEE:FLQHN when PEP1 is SNIT and PEP2 is IGEMS; wherein said GFR-binding compound does not comprise the pair of peptides VPTGQ:LEEHS when PEP1 is SNIT and PEP2 is LGEMS; wherein said GFR-binding compound does not comprise the pair of peptides SRVHH:RLEEH when PEP1 is RSVK and PEP2 is KEVQV; and wherein said GFR-

binding compound does not comprise the pair of peptides TQVQL:TLEDH when PEP1 is RPVQ and PEP2 is KKATV.

In one particular example, said GFR-binding compound is a peptide, a variant or analog thereof, or a peptidomimetic as defined herein, with between 20 and 60 (in particular between 20 and 50, and more particularly, between 20 and 45) amino acids, comprising a peptide with four amino acids (PEP1) or a peptide with eight amino acids (PEP12), a peptide with five amino acids (PEP2), and optionally a pair of peptides selected form the group consisting of PEP3:PEP4, PEP3:PEP6, PEP3:PEP10, PEP5:PEP4, PEP9:PEP4, PEP5:PEP6, PEP5:PEP10, PEP9:PEP6 and PEP9:PEP10; wherein said GFR-binding compound does not comprise the pair of peptides KIPKAXXVPTEL:DMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ ; wherein said GFR-binding compound does not comprise the pair of peptides GIPEPXXVPEKM:NMTVESXAXR when PEP1 is SSLS and PEP2 is LKVYP; wherein said GFR-binding compound does not comprise the pair of peptides SIPKAXXVPTEL:EMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ; wherein said GFR-binding compound does not comprise the pair of peptides HVTKPTXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides YVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides TVPKPXXAPTQL:NMVVRAXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides AVPKAXXAPTKL:NMVVKAXGXH when PEP1 is SATS and PEP2 is LRKHR; wherein said GFR-binding compound does not comprise the pair of peptides KVGKAXXVPTKL:EGMSVAEXGXR when PEP1 is SPIS and PEP2 is LKYHY; wherein said GFR-binding compound does not comprise the pair of peptides KASKAXXVPTKL:GMAVSEXGXR when PEP1 is EPIS and PEP2 is KFKYE; wherein said GFR-binding compound does not comprise the pair of peptides GSAGPXXTPTKM:GMVVDRXGXS when PEP1 is SPIN and PEP2 is YGKIP; wherein said GFR-binding compound does not comprise the pair of peptides AAPASXXVPARL:DMVVEAXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein said GFR-binding compound does not comprise the pair of peptides STPPTXXVPTRL:DMVVESXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein said GFR-binding compound does not comprise the pair of peptides HVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein said GFR-binding compound does not comprise the pair of peptides RVPSTXXAPVKT:MIVEEXGXL when PEP1 is KPLS and PEP2 is DHHKD; wherein said GFR-binding compound does not comprise the pair of peptides ASAAPXXVPQAL:MIVRSXKXS when PEP1 is EPLP and PEP2 is EQLSN; ASASPXXVSQDL:MIVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein said GFR-binding compound does not comprise the pair of peptides ASASPXXVPQDL:MVVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein said GFR-binding compound does not comprise the pair of peptides NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein said GFR-binding compound does not comprise the pair of peptides NDEGLEXVPTGQ:LEEHSQXEXR when PEP1 is SNIT and PEP2 is LGEMS ; wherein said GFR-binding compound does not comprise the pair of peptides NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein said GFR-binding compound does not comprise the pair of peptides NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein said GFR-binding compound does not comprise the pair of peptides SSVKXQPSRVHH:RLEEHLEXAXA when PEP1 is RSVK and PEP2 is KEVQV; wherein said GFR-binding compound does not comprise the pair of peptides

RNVQXRPTQVQL:TLEDHLAXKXE when PEP1 is RPVQ and PEP2 is KKATV.

In particular, in certain embodiments, the quadruplet PEP3:PEP1:PEP2:PEP4 is selected from the group consisting of VPT:SAIS:LKNYQ:VVE, VPE:SAIS:LKNYQ:TVE, APT:SAIS:LKNYQ:VVR, APT:SAIS:LKNYQ:VVK, VPT:SAIS:LKNYQ:VAE, VPT:SAIS:LKNYQ:AVS, TPT:SAIS:LKNYQ:VVD, VPA:SAIS:LKNYQ:VVE, APV:SAIS:LKNYQ:VEE, VPQ:SAIS:LKNYQ:VRS, VSQ:SAIS:LKNYQ:VKS, VPQ:SAIS:LKNYQ:VKS, VPT:SAIS:LKNYQ:QHN, VPT:SAIS:LKNYQ:EHS, SRV:SAIS:LKNYQ:EEH, TQV:SAIS:LKNYQ:EDH, VPE:SSLS:LKVYP:TVE, VPT:SSLS:LKVYP:VVE, APT:SSLS:LKVYP:VVR, APT:SSLS:LKVYP:VVK, VPT:SSLS:LKVYP:VAE, VPT:SSLS:LKVYP:AVS, TPT:SSLS:LKVYP:VVD, VPA:SSLS:LKVYP:VVE, APV:SSLS:LKVYP:VEE, VPQ:SSLS:LKVYP:VRS, VSQ:SSLS:LKVYP:VKS, VPQ:SSLS:LKVYP:VKS, VPT:SSLS:LKVYP:QHN, VPT:SSLS:LKVYP:EHS, SRV:SSLS:LKVYP:EEH, TQV:SSLS:LKVYP:EDH, APT:NAIS:LKKYR:VVR, VPT:NAIS:LKKYR:VVE, VPE:NAIS:LKKYR:TVE, APT:NAIS:LKKYR:VVK, VPT:NAIS:LKKYR:VAE, VPT:NAIS:LKKYR:AVS, TPT:NAIS:LKKYR:VVD, VPA:NAIS:LKKYR:VVE, APV:NAIS:LKKYR:VEE, VPQ:NAIS:LKKYR:VRS, VSQ:NAIS:LKKYR:VKS, VPQ:NAIS:LKKYR:VKS, VPT:NAIS:LKKYR:QHN, VPT:NAIS:LKKYR:EHS, SRV:NAIS:LKKYR:EEH, TQV:NAIS:LKKYR:EDH, APT:SATS:LRKHR:VVK, VPT:SATS:LRKHR:VVE, VPE:SATS:LRKHR:TVE, APT:SATS:LRKHR:VVR, VPT:SATS:LRKHR:VAE, VPT:SATS:LRKHR:AVS, TPT:SATS:LRKHR:VVD, VPA:SATS:LRKHR:VVE, APV:SATS:LRKHR:VEE, VPQ:SATS:LRKHR:VRS, VSQ:SATS:LRKHR:VKS, VPQ:SATS:LRKHR:VKS, VPT:SATS:LRKHR:QHN, VPT:SATS:LRKHR:EHS, SRV:SATS:LRKHR:EEH, TQV:SATS:LRKHR:EDH, VPT:SPIS:LKYHY:VAE, VPT:SPIS:LKYHY:VVE, VPE:SPIS:LKYHY:TVE, APT:SPIS:LKYHY:VVR, APT:SPIS:LKYHY:VVK, VPT:SPIS:LKYHY:AVS, TPT:SPIS:LKYHY:VVD, VPA:SPIS:LKYHY:VVE, APV:SPIS:LKYHY:VEE, VPQ:SPIS:LKYHY:VRS, VSQ:SPIS:LKYHY:VKS, VPQ:SPIS:LKYHY:VKS, VPT:SPIS:LKYHY:QHN, VPT:SPIS:LKYHY:EHS, SRV:SPIS:LKYHY:EEH, TQV:SPIS:LKYHY:EDH, VPT:EPIS:KFKYE:AVS, VPT:EPIS:KFKYE:VVE, VPE:EPIS:KFKYE:TVE, APT:EPIS:KFKYE:VVR, APT:EPIS:KFKYE:VVK, VPT:EPIS:KFKYE:VAE, TPT:EPIS:KFKYE:VVD, VPA:EPIS:KFKYE:VVE, APV:EPIS:KFKYE:VEE, VPQ:EPIS:KFKYE:VRS, VSQ:EPIS:KFKYE:VKS, VPQ:EPIS:KFKYE:VKS, VPT:EPIS:KFKYE:QHN, VPT:EPIS:KFKYE:EHS, SRV:EPIS:KFKYE:EEH, TQV:EPIS:KFKYE:EDH, TPT:SPIN:YGKIP:VVD, VPT:SPIN:YGKIP:VVE, VPE:SPIN:YGKIP:TVE, APT:SPIN:YGKIP:VVR, APT:SPIN:YGKIP:VVK, VPT:SPIN:YGKIP:VAE, VPT:SPIN:YGKIP:AVS, VPA:SPIN:YGKIP:VVE, APV:SPIN:YGKIP:VEE, VPQ:SPIN:YGKIP:VRS, VSQ:SPIN:YGKIP:VKS, VPQ:SPIN:YGKIP:VKS, VPT:SPIN:YGKIP:QHN, VPT:SPIN:YGKIP:EHS, SRV:SPIN:YGKIP:EEH, TQV:SPIN:YGKIP:EDH, VPA:SPIS:YKQYE:VVE, VPT:SPIS:YKQYE:VVE, VPE:SPIS:YKQYE:TVE, APT:SPIS:YKQYE:VVR, APT:SPIS:YKQYE:VVK, VPT:SPIS:YKQYE:VAE, VPT:SPIS:YKQYE:AVS, TPT:SPIS:YKQYE:VVD, APV:SPIS:YKQYE:VEE, VPQ:SPIS:YKQYE:VRS, VSQ:SPIS:YKQYE:VKS, VPQ:SPIS:YKQYE:VKS, VPT:SPIS:YKQYE:QHN, VPT:SPIS:YKQYE:EHS, SRV:SPIS:YKQYE:EEH, TQV:SPIS:YKQYE:EDH, APV:KPLS:DHHKD:VEE, VPT:KPLS:DHHKD:VVE, VPE:KPLS:DHHKD:TVE, APT:KPLS:DHHKD:VVR, APT:KPLS:DHHKD:VVK, VPT:KPLS:DHHKD:VAE, VPT:KPLS:DHHKD:AVS, TPT:KPLS:DHHKD:VVD, VPA:KPLS:DHHKD:VVE, VPQ:KPLS:DHHKD:VRS, VSQ:KPLS:DHHKD:VKS, VPQ:KPLS:DHHKD:VKS, VPT:KPLS:DHHKD:QHN, VPT:KPLS:DHHKD:EHS, SRV:KPLS:DHHKD:EEH, TQV:KPLS:DHHKD:EDH, VPQ:EPLP:EQLSN:VRS, VPT:EPLP:EQLSN:VVE, VPE:EPLP:EQLSN:TVE, APT:EPLP:EQLSN:VVR, APT:EPLP:EQLSN:VVK, VPT:EPLP:EQLSN:VAE, VPT:EPLP:EQLSN:AVS, TPT:EPLP:EQLSN:VVD, VPA:EPLP:EQLSN:VVE, APV:EPLP:EQLSN:VEE, VSQ:EPLP:EQLSN:VKS,

VPQ:EPLP:EQLSN:VKS, VPT:EPLP:EQLSN:QHN, VPT:EPLP:EQLSN:EHS, SRV:EPLP:EQLSN:EEH, TQV:EPLP:EQLSN:EDH, VSQ:EPLT:EQLSN:VKS, VPT:EPLT:EQLSN:VVE, VPE:EPLT:EQLSN:TVE, APT:EPLT:EQLSN:VVR, APT:EPLT:EQLSN:VVK, VPT:EPLT:EQLSN:VAE, VPT:EPLT:EQLSN:AVS, TPT:EPLT:EQLSN:VVD, VPA:EPLT:EQLSN:VVE, APV:EPLT:EQLSN:VEE, VPQ:EPLT:EQLSN:VRS, VPQ:EPLT:EQLSN:VKS, VPT:EPLT:EQLSN:QHN, VPT:EPLT:EQLSN:EHS, SRV:EPLT:EQLSN:EEH, TQV:EPLT:EQLSN:EDH, VPT:SNIT:IGEMS:QHN, VPT:SNIT:IGEMS:VVE, VPE:SNIT:IGEMS:TVE, APT:SNIT:IGEMS:VVR, APT:SNIT:IGEMS:VVK, VPT:SNIT:IGEMS:VAE, VPT:SNIT:IGEMS:AVS, TPT:SNIT:IGEMS:VVD, VPA:SNIT:IGEMS:VVE, APV:SNIT:IGEMS:VEE, VPQ:SNIT:IGEMS:VRS, VSQ:SNIT:IGEMS:VKS, VPQ:SNIT:IGEMS:VKS, VPT:SNIT:IGEMS:EHS, SRV:SNIT:IGEMS:EEH, TQV:SNIT:IGEMS:EDH, VPT:SNIT:LGEMS:EHS, VPT:SNIT:LGEMS:VVE, VPE:SNIT:LGEMS:TVE, APT:SNIT:LGEMS:VVR, APT:SNIT:LGEMS:VVK, VPT:SNIT:LGEMS:VAE, VPT:SNIT:LGEMS:AVS, TPT:SNIT:LGEMS:VVD, VPA:SNIT:LGEMS:VVE, APV:SNIT:LGEMS:VEE, VPQ:SNIT:LGEMS:VRS, VSQ:SNIT:LGEMS:VKS, VPQ:SNIT:LGEMS:VKS, VPT:SNIT:LGEMS:QHN, SRV:SNIT:LGEMS:EEH, TQV:SNIT:LGEMS:EDH, SRV:RSVK:KEVQV:EEH, VPT:RSVK:KEVQV:VVE, VPE:RSVK:KEVQV:TVE, APT:RSVK:KEVQV:VVR, APT:RSVK:KEVQV:VVK, VPT:RSVK:KEVQV:VAE, VPT:RSVK:KEVQV:AVS, TPT:RSVK:KEVQV:VVD, VPA:RSVK:KEVQV:VVE, APV:RSVK:KEVQV:VEE, VPQ:RSVK:KEVQV:VRS, VSQ:RSVK:KEVQV:VKS, VPQ:RSVK:KEVQV:VKS, VPT:RSVK:KEVQV:QHN, VPT:RSVK:KEVQV:EHS, TQV:RSVK:KEVQV:EDH, TQV:RPVQ:KKATV:EDH, VPT:RPVQ:KKATV:VVE, VPE:RPVQ:KKATV:TVE, APT:RPVQ:KKATV:VVR, APT:RPVQ:KKATV:VVK, VPT:RPVQ:KKATV:VAE, VPT:RPVQ:KKATV:AVS, TPT:RPVQ:KKATV:VVD, VPA:RPVQ:KKATV:VVE, APV:RPVQ:KKATV:VEE, VPQ:RPVQ:KKATV:VRS, VSQ:RPVQ:KKATV:VKS, VPQ:RPVQ:KKATV:VKS, VPT:RPVQ:KKATV:QHN, VPT:RPVQ:KKATV:EHS and SRV:RPVQ:KKATV:EEH.

In particular, in certain embodiments, the quadruplet PEP3:PEP12:PEP2:PEP4 is selected from the group consisting of VPT:SAIS-AA[17]-LYL:LKNYQ:VVE, VPE:SAIS-AA[17]-LYL:LKNYQ:TVE, APT:SAIS-AA[17]-LYL:LKNYQ:VVR, APT:SAIS-AA[17]-LYL:LKNYQ:VVK, VPT:SAIS-AA[17]-LYL:LKNYQ:VAE, VPT:SAIS-AA[17]-LYL:LKNYQ:AVS, TPT:SAIS-AA[17]-LYL:LKNYQ:VVD, VPA:SAIS-AA[17]-LYL:LKNYQ:VVE, APV:SAIS-AA[17]-LYL:LKNYQ:VEE, VPQ:SAIS-AA[17]-LYL:LKNYQ:VRS, VSQ:SAIS-AA[17]-LYL:LKNYQ:VKS, VPQ:SAIS-AA[17]-LYL:LKNYQ:VKS, VPT:SAIS-AA[17]-LYL:LKNYQ:QHN, VPT:SAIS-AA[17]-LYL:LKNYQ:EHS, SRV:SAIS-AA[17]-LYL:LKNYQ:EEH, TQV:SAIS-AA[17]-LYL:LKNYQ:EDH, VPE:SSLS-AA[17]-LFF:LKVYP:TVE, VPT:SSLS-AA[17]-LFF:LKVYP:VVE, APT:SSLS-AA[17]-LFF:LKVYP:VVR, APT:SSLS-AA[17]-LFF:LKVYP:VVK, VPT:SSLS-AA[17]-LFF:LKVYP:VAE, VPT:SSLS-AA[17]-LFF:LKVYP:AVS, TPT:SSLS-AA[17]-LFF:LKVYP:VVD, VPA:SSLS-AA[17]-LFF:LKVYP:VVE, APV:SSLS-AA[17]-LFF:LKVYP:VEE, VPQ:SSLS-AA[17]-LFF:LKVYP:VRS, VSQ:SSLS-AA[17]-LFF:LKVYP:VKS, VPQ:SSLS-AA[17]-LFF:LKVYP:VKS, VPT:SSLS-AA[17]-LFF:LKVYP:QHN, VPT:SSLS-AA[17]-LFF:LKVYP:EHS, SRV:SSLS-AA[17]-LFF:LKVYP:EEH, TQV:SSLS-AA[17]-LFF:LKVYP:EDH, APT:NAIS-AA[17]-LYF:LKKYR:VVR, VPT:NAIS-AA[17]-LYF:LKKYR:VVE, VPE:NAIS-AA[17]-LYF:LKKYR:TVE, APT:NAIS-AA[17]-LYF:LKKYR:VVK, VPT:NAIS-AA[17]-LYF:LKKYR:VAE, VPT:NAIS-AA[17]-LYF:LKKYR:AVS, TPT:NAIS-AA[17]-LYF:LKKYR:VVD, VPA:NAIS-AA[17]-LYF:LKKYR:VVE, APV:NAIS-AA[17]-LYF:LKKYR:VEE, VPQ:NAIS-AA[17]-LYF:LKKYR:VRS, VSQ:NAIS-AA[17]-LYF:LKKYR:VKS, VPQ:NAIS-AA[17]-LYF:LKKYR:VKS, VPT:NAIS-AA[17]-LYF:LKKYR:QHN, VPT:NAIS-AA[17]-LYF:LKKYR:EHS, SRV:NAIS-AA[17]-LYF:LKKYR:EEH, TQV:NAIS-AA[17]-LYF:LKKYR:EDH, APT:SATS-AA[17]-LYY:LRKHR:VVK, VPT:SATS-AA[17]-LYY:LRKHR:VVE, VPE:SATS-AA[17]-LYY:LRKHR:TVE, APT:SATS-

AA[17]-LYY:LRKHR:VVR, VPT:SATS-AA[17]-LYY:LRKHR:VAE, VPT:SATS-AA[17]-LYY:LRKHR:AVS, TPT:SATS-AA[17]-LYY:LRKHR:VVD, VPA:SATS-AA[17]-LYY:LRKHR:VVE, APV:SATS-AA[17]-LYY:LRKHR:VEE, VPQ:SATS-AA[17]-LYY:LRKHR:VRS, VSQ:SATS-AA[17]-LYY:LRKHR:VKS, VPQ:SATS-AA[17]-LYY:LRKHR:VKS, VPT:SATS-AA[17]-LYY:LRKHR:QHN, VPT:SATS-AA[17]-LYY:LRKHR:EHS, SRV:SATS-AA[17]-LYY:LRKHR:EEH, TQV:SATS-AA[17]-LYY:LRKHR:EDH, VPT:SPIS-AA[17]-LYK:LKYHY:VAE, VPT:SPIS-AA[17]-LYK:LKYHY:VVE, VPE:SPIS-AA[17]-LYK:LKYHY:TVE, APT:SPIS-AA[17]-LYK:LKYHY:VVR, APT:SPIS-AA[17]-LYK:LKYHY:VVK, VPT:SPIS-AA[17]-LYK:LKYHY:AVS, TPT:SPIS-AA[17]-LYK:LKYHY:VVD, VPA:SPIS-AA[17]-LYK:LKYHY:VVE, APV:SPIS-AA[17]-LYK:LKYHY:VEE, VPQ:SPIS-AA[17]-LYK:LKYHY:VRS, VSQ:SPIS-AA[17]-LYK:LKYHY:VKS, VPQ:SPIS-AA[17]-LYK:LKYHY:VKS, VPT:SPIS-AA[17]-LYK:LKYHY:QHN, VPT:SPIS-AA[17]-LYK:LKYHY:EHS, SRV:SPIS-AA[17]-LYK:LKYHY:EEH, TQV:SPIS-AA[17]-LYK:LKYHY:EDH, VPT:EPIS-AA[17]-LYL:KFKYE:AVS, VPT:EPIS-AA[17]-LYL:KFKYE:VVE, VPE:EPIS-AA[17]-LYL:KFKYE:TVE, APT:EPIS-AA[17]-LYL:KFKYE:VVR, APT:EPIS-AA[17]-LYL:KFKYE:VVK, VPT:EPIS-AA[17]-LYL:KFKYE:VAE, TPT:EPIS-AA[17]-LYL:KFKYE:VVD, VPA:EPIS-AA[17]-LYL:KFKYE:VVE, APV:EPIS-AA[17]-LYL:KFKYE:VEE, VPQ:EPIS-AA[17]-LYL:KFKYE:VRS, VSQ:EPIS-AA[17]-LYL:KFKYE:VKS, VPQ:EPIS-AA[17]-LYL:KFKYE:VKS, VPT:EPIS-AA[17]-LYL:KFKYE:QHN, VPT:EPIS-AA[17]-LYL:KFKYE:EHS, SRV:EPIS-AA[17]-LYL:KFKYE:EEH, TQV:EPIS-AA[17]-LYL:KFKYE:EDH, TPT:SPIN-AA[17]-LYF:YGKIP:VVD, VPT:SPIN-AA[17]-LYF:YGKIP:VVE, VPE:SPIN-AA[17]-LYF:YGKIP:TVE, APT:SPIN-AA[17]-LYF:YGKIP:VVR, APT:SPIN-AA[17]-LYF:YGKIP:VVK, VPT:SPIN-AA[17]-LYF:YGKIP:VAE, VPT:SPIN-AA[17]-LYF:YGKIP:AVS, VPA:SPIN-AA[17]-LYF:YGKIP:VVE, APV:SPIN-AA[17]-LYF:YGKIP:VEE, VPQ:SPIN-AA[17]-LYF:YGKIP:VRS, VSQ:SPIN-AA[17]-LYF:YGKIP:VKS, VPQ:SPIN-AA[17]-LYF:YGKIP:VKS, VPT:SPIN-AA[17]-LYF:YGKIP:QHN, VPT:SPIN-AA[17]-LYF:YGKIP:EHS, SRV:SPIN-AA[17]-LYF:YGKIP:EEH, TQV:SPIN-AA[17]-LYF:YGKIP:EDH, VPA:SPIS-AA[17]-LYI:YKQYE:VVE, VPT:SPIS-AA[17]-LYI:YKQYE:VVE, VPE:SPIS-AA[17]-LYI:YKQYE:TVE, APT:SPIS-AA[17]-LYI:YKQYE:VVR, APT:SPIS-AA[17]-LYI:YKQYE:VVK, VPT:SPIS-AA[17]-LYI:YKQYE:VAE, VPT:SPIS-AA[17]-LYI:YKQYE:AVS, TPT:SPIS-AA[17]-LYI:YKQYE:VVD, APV:SPIS-AA[17]-LYI:YKQYE:VEE, VPQ:SPIS-AA[17]-LYI:YKQYE:VRS, VSQ:SPIS-AA[17]-LYI:YKQYE:VKS, VPQ:SPIS-AA[17]-LYI:YKQYE:VKS, VPT:SPIS-AA[17]-LYI:YKQYE:QHN, VPT:SPIS-AA[17]-LYI:YKQYE:EHS, SRV:SPIS-AA[17]-LYI:YKQYE:EEH, TQV:SPIS-AA[17]-LYI:YKQYE:EDH, VPT:SPIS-AA[17]-LFI:YKQYE:VVE, VPE:SPIS-AA[17]-LFI:YKQYE:TVE, APT:SPIS-AA[17]-LFI:YKQYE:VVR, APT:SPIS-AA[17]-LFI:YKQYE:VVK, VPT:SPIS-AA[17]-LFI:YKQYE:VAE, VPT:SPIS-AA[17]-LFI:YKQYE:AVS, TPT:SPIS-AA[17]-LFI:YKQYE:VVD, VPA:SPIS-AA[17]-LFI:YKQYE:VVE, APV:SPIS-AA[17]-LFI:YKQYE:VEE, VPQ:SPIS-AA[17]-LFI:YKQYE:VRS, VSQ:SPIS-AA[17]-LFI:YKQYE:VKS, VPQ:SPIS-AA[17]-LFI:YKQYE:VKS, VPT:SPIS-AA[17]-LFI:YKQYE:QHN, VPT:SPIS-AA[17]-LFI:YKQYE:EHS, SRV:SPIS-AA[17]-LFI:YKQYE:EEH, TQV:SPIS-AA[17]-LFI:YKQYE:EDH, APV:KPLS-AA[17]-LYV:DHHKD:VEE, VPT:KPLS-AA[17]-LYV:DHHKD:VVE, VPE:KPLS-AA[17]-LYV:DHHKD:TVE, APT:KPLS-AA[17]-LYV:DHHKD:VVR, APT:KPLS-AA[17]-LYV:DHHKD:VVK, VPT:KPLS-AA[17]-LYV:DHHKD:VAE, VPT:KPLS-AA[17]-LYV:DHHKD:AVS, TPT:KPLS-AA[17]-LYV:DHHKD:VVD, VPA:KPLS-AA[17]-LYV:DHHKD:VVE, VPQ:KPLS-AA[17]-LYV:DHHKD:VRS, VSQ:KPLS-AA[17]-LYV:DHHKD:VKS, VPQ:KPLS-AA[17]-LYV:DHHKD:VKS, VPT:KPLS-AA[17]-LYV:DHHKD:QHN, VPT:KPLS-AA[17]-LYV:DHHKD:EHS, SRV:KPLS-AA[17]-LYV:DHHKD:EEH, TQV:KPLS-AA[17]-LYV:DHHKD:EDH, VPQ:EPLP-AA[17]-VYY:EQLSN:VRS, VPT:EPLP-AA[17]-VYY:EQLSN:VVE, VPE:EPLP-AA[17]-VYY:EQLSN:TVE, APT:EPLP-AA[17]-VYY:EQLSN:VVR, APT:EPLP-AA[17]-VYY:EQLSN:VVK, VPT:EPLP-AA[17]-VYY:EQLSN:VAE, VPT:EPLP-AA[17]-VYY:EQLSN:AVS, TPT:EPLP-AA[17]-VYY:EQLSN:VVD, VPA:EPLP-AA[17]-VYY:EQLSN:VVE, APV:EPLP-AA[17]-VYY:EQLSN:VEE, VSQ:EPLP-AA[17]-VYY:EQLSN:VKS, VPQ:EPLP-AA[17]-

VYY:EQLSN:VKS, VPT:EPLP-AA[17]-VYY:EQLSN:QHN, VPT:EPLP-AA[17]-VYY:EQLSN:EHS, SRV:EPLP-AA[17]-VYY:EQLSN:EEH, TQV:EPLP-AA[17]-VYY:EQLSN:EDH, VSQ:EPLT-AA[17]-LYY:EQLSN:VKS, VPT:EPLT-AA[17]-LYY:EQLSN:VVE, VPE:EPLT-AA[17]-LYY:EQLSN:TVE, APT:EPLT-AA[17]-LYY:EQLSN:VVR, APT:EPLT-AA[17]-LYY:EQLSN:VVK, VPT:EPLT-AA[17]-LYY:EQLSN:VAE, VPT:EPLT-AA[17]-LYY:EQLSN:AVS, TPT:EPLT-AA[17]-LYY:EQLSN:VVD, VPA:EPLT-AA[17]-LYY:EQLSN:VVE, APV:EPLT-AA[17]-LYY:EQLSN:VEE, VPQ:EPLT-AA[17]-LYY:EQLSN:VRS, VPQ:EPLT-AA[17]-LYY:EQLSN:VKS, VPT:EPLT-AA[17]-LYY:EQLSN:QHN, VPT:EPLT-AA[17]-LYY:EQLSN:EHS, SRV:EPLT-AA[17]-LYY:EQLSN:EEH, TQV:EPLT-AA[17]-LYY:EQLSN:EDH, VPT:SNIT-AA[17]-QIM:IGEMS:QHN, VPT:SNIT-AA[17]-QIM:IGEMS:VVE, VPE:SNIT-AA[17]-QIM:IGEMS:TVE, APT:SNIT-AA[17]-QIM:IGEMS:VVR, APT:SNIT-AA[17]-QIM:IGEMS:VVK, VPT:SNIT-AA[17]-QIM:IGEMS:VAE, VPT:SNIT-AA[17]-QIM:IGEMS:AVS, TPT:SNIT-AA[17]-QIM:IGEMS:VVD, VPA:SNIT-AA[17]-QIM:IGEMS:VVE, APV:SNIT-AA[17]-QIM:IGEMS:VEE, VPQ:SNIT-AA[17]-QIM:IGEMS:VRS, VSQ:SNIT-AA[17]-QIM:IGEMS:VKS, VPQ:SNIT-AA[17]-QIM:IGEMS:VKS, VPT:SNIT-AA[17]-QIM:IGEMS:EHS, SRV:SNIT-AA[17]-QIM:IGEMS:EEH, TQV:SNIT-AA[17]-QIM:IGEMS:EDH, VPT:SNIT-AA[17]-QIM:LGEMS:EHS, VPT:SNIT-AA[17]-QIM:LGEMS:VVE, VPE:SNIT-AA[17]-QIM:LGEMS:TVE, APT:SNIT-AA[17]-QIM:LGEMS:VVR, APT:SNIT-AA[17]-QIM:LGEMS:VVK, VPT:SNIT-AA[17]-QIM:LGEMS:VAE, VPT:SNIT-AA[17]-QIM:LGEMS:AVS, TPT:SNIT-AA[17]-QIM:LGEMS:VVD, VPA:SNIT-AA[17]-QIM:LGEMS:VVE, APV:SNIT-AA[17]-QIM:LGEMS:VEE, VPQ:SNIT-AA[17]-QIM:LGEMS:VRS, VSQ:SNIT-AA[17]-QIM:LGEMS:VKS, VPQ:SNIT-AA[17]-QIM:LGEMS:VKS, VPT:SNIT-AA[17]-QIM:LGEMS:QHN, SRV:SNIT-AA[17]-QIM:LGEMS:EEH, TQV:SNIT-AA[17]-QIM:LGEMS:EDH, SRV:RSVK-AA[17]-AKV:KEVQV:EEH, VPT:RSVK-AA[17]-AKV:KEVQV:VVE, VPE:RSVK-AA[17]-AKV:KEVQV:TVE, APT:RSVK-AA[17]-AKV:KEVQV:VVR, APT:RSVK-AA[17]-AKV:KEVQV:VVK, VPT:RSVK-AA[17]-AKV:KEVQV:VAE, VPT:RSVK-AA[17]-AKV:KEVQV:AVS, TPT:RSVK-AA[17]-AKV:KEVQV:VVD, VPA:RSVK-AA[17]-AKV:KEVQV:VVE, APV:RSVK-AA[17]-AKV:KEVQV:VEE, VPQ:RSVK-AA[17]-AKV:KEVQV:VRS, VSQ:RSVK-AA[17]-AKV:KEVQV:VKS, VPQ:RSVK-AA[17]-AKV:KEVQV:VKS, VPT:RSVK-AA[17]-AKV:KEVQV:QHN, VPT:RSVK-AA[17]-AKV:KEVQV:EHS, TQV:RSVK-AA[17]-AKV:KEVQV:EDH, TQV:RPVQ-AA[17]-RKI:KKATV:EDH, VPT:RPVQ-AA[17]-RKI:KKATV:VVE, VPE:RPVQ-AA[17]-RKI:KKATV:TVE, APT:RPVQ-AA[17]-RKI:KKATV:VVR, APT:RPVQ-AA[17]-RKI:KKATV:VVK, VPT:RPVQ-AA[17]-RKI:KKATV:VAE, VPT:RPVQ-AA[17]-RKI:KKATV:AVS, TPT:RPVQ-AA[17]-RKI:KKATV:VVD, VPA:RPVQ-AA[17]-RKI:KKATV:VVE, APV:RPVQ-AA[17]-RKI:KKATV:VEE, VPQ:RPVQ-AA[17]-RKI:KKATV:VRS, VSQ:RPVQ-AA[17]-RKI:KKATV:VKS, VPQ:RPVQ-AA[17]-RKI:KKATV:VKS, VPT:RPVQ-AA[17]-RKI:KKATV:QHN, VPT:RPVQ-AA[17]-RKI:KKATV:EHS and SRV:RPVQ-AA17-RKI:KKATV:EEH; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the quadruplet PEP5:PEP1:PEP2:PEP6 is selected from the group consisting of VPTKM:SAIS:LKNYQ:NMVVE, VPTEL:SAIS:LKNYQ:EMVVE, VPTKL:SAIS:LKNYQ:NMVVE, VPTQL:SAIS:LKNYQ:NMVVE, VPTKL:SAIS:LKNYQ:EGMSVVE, VPTKL:SAIS:LKNYQ:GMVVE, VPTKM:SAIS:LKNYQ:GMVVE, VPTRL:SAIS:LKNYQ:DMVVE, VPTKT:SAIS:LKNYQ:MIVVE, VPTAL:SAIS:LKNYQ:MIVVE, VPTDL:SAIS:LKNYQ:MIVVE, VPTDL:SAIS:LKNYQ:MVVVE, VPTEE:SAIS:LKNYQ:FLVVE, VPTGQ:SAIS:LKNYQ:LEVVE, VPTHH:SAIS:LKNYQ:RLVVE, VPTQL:SAIS:LKNYQ:TLVVE, VPEKM:SAIS:LKNYQ:NMTVE, APTKL:SAIS:LKNYQ:NMVVR, APTQL:SAIS:LKNYQ:NMVVR, APTKL:SAIS:LKNYQ:NMVVK,

VPTKL:SAIS:LKNYQ:EGMSVAE, VPTKL:SAIS:LKNYQ:GMAVS, TPTKM:SAIS:LKNYQ:GMVVD,
VPARL:SAIS:LKNYQ:DMVVE, APVKT:SAIS:LKNYQ:MIVEE, VPQAL:SAIS:LKNYQ:MIVRS,
VSQDL:SAIS:LKNYQ:MIVKS, VPQDL:SAIS:LKNYQ:MVVKS, VPTEE:SAIS:LKNYQ:FLQHN,
VPTGQ:SAIS:LKNYQ:LEEHS, SRVHH:SAIS:LKNYQ:RLEEH, TQVQL:SAIS:LKNYQ:TLEDH,
VPEEL:SSLS:LKVYP:DMTVE, VPEEL:SSLS:LKVYP:EMTVE, VPEKL:SSLS:LKVYP:NMTVE,
VPEQL:SSLS:LKVYP:NMTVE, VPEKL:SSLS:LKVYP:EGMSTVE, VPEKL:SSLS:LKVYP:GMTVE,
VPEKM:SSLS:LKVYP:GMTVE, VPERL:SSLS:LKVYP:DMTVE, VPEKT:SSLS:LKVYP:MITVE,
VPEAL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MVTVE,
VPEEE:SSLS:LKVYP:FLTVE, VPEGQ:SSLS:LKVYP:LETVE, VPEHH:SSLS:LKVYP:RLTVE,
VPEQL:SSLS:LKVYP:TLTVE, VPTEL:SSLS:LKVYP:DMVVE, VPTEL:SSLS:LKVYP:EMVVE,
APTKL:SSLS:LKVYP:NMVVR, APTQL:SSLS:LKVYP:NMVVR, APTKL:SSLS:LKVYP:NMVVK,
VPTKL:SSLS:LKVYP:EGMSVAE, VPTKL:SSLS:LKVYP:GMAVS, TPTKM:SSLS:LKVYP:GMVVD,
VPARL:SSLS:LKVYP:DMVVE, VPTRL:SSLS:LKVYP:DMVVE, APVKT:SSLS:LKVYP:MIVEE,
VPQAL:SSLS:LKVYP:MIVRS, VSQDL:SSLS:LKVYP:MIVKS, VPQDL:SSLS:LKVYP:MVVKS,
VPTEE:SSLS:LKVYP:FLQHN, VPTGQ:SSLS:LKVYP:LEEHS, SRVHH:SSLS:LKVYP:RLEEH,
TQVQL:SSLS:LKVYP:TLEDH, VPTEL:SAIS:LKNYQ:DMVVE, APTEL:NAIS:LKKYR:DMVVR,
APTKM:NAIS:LKKYR:NMVVR, APTEL:NAIS:LKKYR:EMVVR, APTKL:NAIS:LKKYR:NMVVR,
APTQL:NAIS:LKKYR:NMVVR, APTKL:NAIS:LKKYR:EGMSVVR, APTKL:NAIS:LKKYR:GMVVR,
APTKM:NAIS:LKKYR:GMVVR, APTRL:NAIS:LKKYR:DMVVR, APTKT:NAIS:LKKYR:MIVVR,
APTAL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MVVVR,
APTEE:NAIS:LKKYR:FLVVR, APTGQ:NAIS:LKKYR:LEVVR, APTHH:NAIS:LKKYR:RLVVR,
APTQL:NAIS:LKKYR:TLVVR, VPTEL:NAIS:LKKYR:DMVVE, VPEKM:NAIS:LKKYR:NMTVE,
VPTEL:NAIS:LKKYR:EMVVE, APTKL:NAIS:LKKYR:NMVVK, VPTKL:NAIS:LKKYR:EGMSVAE,
VPTKL:NAIS:LKKYR:GMAVS, TPTKM:NAIS:LKKYR:GMVVD, VPARL:NAIS:LKKYR:DMVVE,
VPTRL:NAIS:LKKYR:DMVVE, APVKT:NAIS:LKKYR:MIVEE, VPQAL:NAIS:LKKYR:MIVRS,
VSQDL:NAIS:LKKYR:MIVKS, VPQDL:NAIS:LKKYR:MVVKS, VPTEE:NAIS:LKKYR:FLQHN,
VPTGQ:NAIS:LKKYR:LEEHS, SRVHH:NAIS:LKKYR:RLEEH, TQVQL:NAIS:LKKYR:TLEDH,
APTEL:SATS:LRKHR:DMVVK, APTKM:SATS:LRKHR:NMVVK, APTEL:SATS:LRKHR:EMVVK,
APTKL:SATS:LRKHR:NMVVK, APTQL:SATS:LRKHR:NMVVK, APTKL:SATS:LRKHR:EGMSVVK,
APTKL:SATS:LRKHR:GMVVK, APTKM:SATS:LRKHR:GMVVK, APTRL:SATS:LRKHR:DMVVK,
APTKT:SATS:LRKHR:MIVVK, APTAL:SATS:LRKHR:MIVVK, APTDL:SATS:LRKHR:MIVVK,
APTDL:SATS:LRKHR:MVVVK, APTEE:SATS:LRKHR:FLVVK, APTGQ:SATS:LRKHR:LEVVK,
APTHH:SATS:LRKHR:RLVVK, APTQL:SATS:LRKHR:TLVVK, VPTEL:SATS:LRKHR:DMVVE,
VPEKM:SATS:LRKHR:NMTVE, VPTEL:SATS:LRKHR:EMVVE, APTKL:SATS:LRKHR:NMVVR,
APTQL:SATS:LRKHR:NMVVR, VPTKL:SATS:LRKHR:EGMSVAE, VPTKL:SATS:LRKHR:GMAVS,
TPTKM:SATS:LRKHR:GMVVD, VPARL:SATS:LRKHR:DMVVE, VPTRL:SATS:LRKHR:DMVVE,
APVKT:SATS:LRKHR:MIVEE, VPQAL:SATS:LRKHR:MIVRS, VSQDL:SATS:LRKHR:MIVKS,
VPQDL:SATS:LRKHR:MVVKS, VPTEE:SATS:LRKHR:FLQHN, VPTGQ:SATS:LRKHR:LEEHS,
SRVHH:SATS:LRKHR:RLEEH, TQVQL:SATS:LRKHR:TLEDH, VPTEL:SPIS:LKYHY:DMVAE,
VPTKM:SPIS:LKYHY:NMVAE, VPTEL:SPIS:LKYHY:EMVAE, VPTKL:SPIS:LKYHY:NMVAE,
VPTQL:SPIS:LKYHY:NMVAE, VPTKL:SPIS:LKYHY:GMVAE, VPTKM:SPIS:LKYHY:GMVAE,
VPTRL:SPIS:LKYHY:DMVAE, VPTKT:SPIS:LKYHY:MIVAE, VPTAL:SPIS:LKYHY:MIVAE,

VPTDL:SPIS:LKYHY:MIVAE, VPTDL:SPIS:LKYHY:MVVAE, VPTEE:SPIS:LKYHY:FLVAE,
VPTGQ:SPIS:LKYHY:LEVAE, VPTHH:SPIS:LKYHY:RLVAE, VPTQL:SPIS:LKYHY:TLVAE,
VPTEL:SPIS:LKYHY:DMVVE, VPEKM:SPIS:LKYHY:NMTVE, VPTEL:SPIS:LKYHY:EMVVE,
APTKL:SPIS:LKYHY:NMVVR, APTQL:SPIS:LKYHY:NMVVR, APTKL:SPIS:LKYHY:NMVVK,
VPTKL:SPIS:LKYHY:GMAVS, TPTKM:SPIS:LKYHY:GMVVD, VPARL:SPIS:LKYHY:DMVVE,
VPTRL:SPIS:LKYHY:DMVVE, APVKT:SPIS:LKYHY:MIVEE, VPQAL:SPIS:LKYHY:MIVRS,
VSQDL:SPIS:LKYHY:MIVKS, VPQDL:SPIS:LKYHY:MVVKS, VPTEE:SPIS:LKYHY:FLQHN,
VPTGQ:SPIS:LKYHY:LEEHS, SRVHH:SPIS:LKYHY:RLEEH, TQVQL:SPIS:LKYHY:TLEDH,
VPTEL:EPIS:KFKYE:DMAVS, VPTKM:EPIS:KFKYE:NMAVS, VPTEL:EPIS:KFKYE:EMAVS,
VPTKL:EPIS:KFKYE:NMAVS, VPTQL:EPIS:KFKYE:NMAVS, VPTKL:EPIS:KFKYE:EGMSAVS,
VPTKM:EPIS:KFKYE:GMAVS, VPTRL:EPIS:KFKYE:DMAVS, VPTKT:EPIS:KFKYE:MIAVS,
VPTAL:EPIS:KFKYE:MIAVS, VPTDL:EPIS:KFKYE:MIAVS, VPTDL:EPIS:KFKYE:MVAVS,
VPTEE:EPIS:KFKYE:FLAVS, VPTGQ:EPIS:KFKYE:LEAVS, VPTHH:EPIS:KFKYE:RLAVS,
VPTQL:EPIS:KFKYE:TLAVS, VPTEL:EPIS:KFKYE:DMVVE, VPEKM:EPIS:KFKYE:NMTVE,
VPTEL:EPIS:KFKYE:EMVVE, APTKL:EPIS:KFKYE:NMVVR, APTQL:EPIS:KFKYE:NMVVR,
APTKL:EPIS:KFKYE:NMVVK, VPTKL:EPIS:KFKYE:EGMSVAE, TPTKM:EPIS:KFKYE:GMVVD,
VPARL:EPIS:KFKYE:DMVVE, VPTRL:EPIS:KFKYE:DMVVE, APVKT:EPIS:KFKYE:MIVEE,
VPQAL:EPIS:KFKYE:MIVRS, VSQDL:EPIS:KFKYE:MIVKS, VPQDL:EPIS:KFKYE:MVVKS,
VPTEE:EPIS:KFKYE:FLQHN, VPTGQ:EPIS:KFKYE:LEEHS, SRVHH:EPIS:KFKYE:RLEEH,
TQVQL:EPIS:KFKYE:TLEDH, TPTEL:SPIN:YGKIP:DMVVD, TPTKM:SPIN:YGKIP:NMVVD,
TPTEL:SPIN:YGKIP:EMVVD, TPTKL:SPIN:YGKIP:NMVVD, TPTQL:SPIN:YGKIP:NMVVD,
TPTKL:SPIN:YGKIP:EGMSVVD, TPTKL:SPIN:YGKIP:GMVVD, TPTRL:SPIN:YGKIP:DMVVD,
TPTKT:SPIN:YGKIP:MIVVD, TPTAL:SPIN:YGKIP:MIVVD, TPTDL:SPIN:YGKIP:MIVVD,
TPTDL:SPIN:YGKIP:MVVVD, TPTEE:SPIN:YGKIP:FLVVD, TPTGQ:SPIN:YGKIP:LEVVD,
TPTHH:SPIN:YGKIP:RLVVD, TPTQL:SPIN:YGKIP:TLVVD, VPTEL:SPIN:YGKIP:DMVVE,
VPEKM:SPIN:YGKIP:NMTVE, VPTEL:SPIN:YGKIP:EMVVE, APTKL:SPIN:YGKIP:NMVVR,
APTQL:SPIN:YGKIP:NMVVR, APTKL:SPIN:YGKIP:NMVVK, VPTKL:SPIN:YGKIP:EGMSVAE,
VPTKL:SPIN:YGKIP:GMAVS, VPARL:SPIN:YGKIP:DMVVE, VPTRL:SPIN:YGKIP:DMVVE,
APVKT:SPIN:YGKIP:MIVEE, VPQAL:SPIN:YGKIP:MIVRS, VSQDL:SPIN:YGKIP:MIVKS,
VPQDL:SPIN:YGKIP:MVVKS, VPTEE:SPIN:YGKIP:FLQHN, VPTGQ:SPIN:YGKIP:LEEHS,
SRVHH:SPIN:YGKIP:RLEEH, TQVQL:SPIN:YGKIP:TLEDH, VPAEL:SPIS:YKQYE:DMVVE,
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VPQEE:EPLT:EQLSN:FLVKS, VPQGQ:EPLT:EQLSN:LEVKS, VPQHH:EPLT:EQLSN:RLVKS,
VPQQL:EPLT:EQLSN:TLVKS, VSQDL:EPLT:EQLSN:MIVKS, VPTEL:SNIT:IGEMS:DMQHN,
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TPTKM:SNIT:IGEMS:GMVVD, VPARL:SNIT:IGEMS:DMVVE, VPTRL:SNIT:IGEMS:DMVVE,
APVKT:SNIT:IGEMS:MIVEE, VPQAL:SNIT:IGEMS:MIVRS, VSQDL:SNIT:IGEMS:MIVKS,
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VPTEL:SNIT:LGEMS:EMEHS, VPTKL:SNIT:LGEMS:NMEHS, VPTQL:SNIT:LGEMS:NMEHS,
VPTKL:SNIT:LGEMS:EGMSEHS, VPTKL:SNIT:LGEMS:GMEHS, VPTKM:SNIT:LGEMS:GMEHS,
VPTRL:SNIT:LGEMS:DMEHS, VPTKT:SNIT:LGEMS:MIEHS, VPTAL:SNIT:LGEMS:MIEHS,
VPTDL:SNIT:LGEMS:MIEHS, VPTDL:SNIT:LGEMS:MVEHS, VPTEE:SNIT:LGEMS:FLEHS,
VPTHH:SNIT:LGEMS:RLEHS, VPTQL:SNIT:LGEMS:TLEHS, VPTEL:SNIT:LGEMS:DMVVE,
VPEKM:SNIT:LGEMS:NMTVE, VPTEL:SNIT:LGEMS:EMVVE, APTKL:SNIT:LGEMS:NMVVR,
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VPTKL:SNIT:LGEMS:GMAVS, TPTKM:SNIT:LGEMS:GMVVD, VPARL:SNIT:LGEMS:DMVVE,
VPTRL:SNIT:LGEMS:DMVVE, APVKT:SNIT:LGEMS:MIVEE, VPQAL:SNIT:LGEMS:MIVRS,
VSQDL:SNIT:LGEMS:MIVKS, VPQDL:SNIT:LGEMS:MVVKS, VPTEE:SNIT:LGEMS:FLQHN,
SRVHH:SNIT:LGEMS:RLEEH, TQVQL:SNIT:LGEMS:TLEDH, SRVEL:RSVK:KEVQV:DMEEH,
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SRVAL:RSVK:KEVQV:MIEEH, SRVDL:RSVK:KEVQV:MIEEH, SRVDL:RSVK:KEVQV:MVEEH,
SRVEE:RSVK:KEVQV:FLEEH, SRVGQ:RSVK:KEVQV:LEEEH, SRVQL:RSVK:KEVQV:TLEEH,
VPTEL:RSVK:KEVQV:DMVVE, VPEKM:RSVK:KEVQV:NMTVE, VPTEL:RSVK:KEVQV:EMVVE,
APTKL:RSVK:KEVQV:NMVVR, APTQL:RSVK:KEVQV:NMVVR, APTKL:RSVK:KEVQV:NMVVK,
VPTKL:RSVK:KEVQV:EGMSVAE, VPTKL:RSVK:KEVQV:GMAVS, TPTKM:RSVK:KEVQV:GMVVD,
VPARL:RSVK:KEVQV:DMVVE, VPTRL:RSVK:KEVQV:DMVVE, APVKT:RSVK:KEVQV:MIVEE,
VPQAL:RSVK:KEVQV:MIVRS, VSQDL:RSVK:KEVQV:MIVKS, VPQDL:RSVK:KEVQV:MVVKS,
VPTEE:RSVK:KEVQV:FLQHN, VPTGQ:RSVK:KEVQV:LEEHS, TQVQL:RSVK:KEVQV:TLEDH,
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TQVKT:RPVQ:KKATV:MIEDH, TQVAL:RPVQ:KKATV:MIEDH, TQVDL:RPVQ:KKATV:MIEDH,
TQVDL:RPVQ:KKATV:MVEDH, TQVEE:RPVQ:KKATV:FLEDH, TQVGQ:RPVQ:KKATV:LEEDH,

TQVHH:RPVQ:KKATV:RLEDH, VPTEL:RPVQ:KKATV:DMVVE, VPEKM:RPVQ:KKATV:NMTVE, VPTEL:RPVQ:KKATV:EMVVE, APTKL:RPVQ:KKATV:NMVVR, APTQL:RPVQ:KKATV:NMVVR, APTKL:RPVQ:KKATV:NMVVK, VPTKL:RPVQ:KKATV:EGMSVAE, VPTKL:RPVQ:KKATV:GMAVS, TPTKM:RPVQ:KKATV:GMVVD, VPARL:RPVQ:KKATV:DMVVE, VPTRL:RPVQ:KKATV:DMVVE, APVKT:RPVQ:KKATV:MIVEE, VPQAL:RPVQ:KKATV:MIVRS, VSQDL:RPVQ:KKATV:MIVKS, VPQDL:RPVQ:KKATV:MVVKS, VPTEE:RPVQ:KKATV:FLQHN, VPTGQ:RPVQ:KKATV:LEEHS and SRVHH:RPVQ:KKATV:RLEEH. More particularly, the quadruplet PEP5:PEP1:PEP2:PEP6 is selected from the group consisting of VPTKM:SAIS:LKNYQ:NMVVE, VPTKL:SAIS:LKNYQ:NMVVE, VPTQL:SAIS:LKNYQ:NMVVE, VPTKL:SAIS:LKNYQ:EGMSVVE, VPTKL:SAIS:LKNYQ:GMVVE, VPTKM:SAIS:LKNYQ:GMVVE, VPTRL:SAIS:LKNYQ:DMVVE, VPTKT:SAIS:LKNYQ:MIVVE, VPTAL:SAIS:LKNYQ:MIVVE, VPTDL:SAIS:LKNYQ:MIVVE, VPTDL:SAIS:LKNYQ:MVVVE, VPEKM:SAIS:LKNYQ:NMTVE, APTKL:SAIS:LKNYQ:NMVVR, APTQL:SAIS:LKNYQ:NMVVR, APTKL:SAIS:LKNYQ:NMVVK, VPTKL:SAIS:LKNYQ:EGMSVAE, VPTKL:SAIS:LKNYQ:GMAVS, TPTKM:SAIS:LKNYQ:GMVVD, VPARL:SAIS:LKNYQ:DMVVE, APVKT:SAIS:LKNYQ:MIVEE, VPQAL:SAIS:LKNYQ:MIVRS, VSQDL:SAIS:LKNYQ:MIVKS, VPQDL:SAIS:LKNYQ:MVVKS, VPTEE:SAIS:LKNYQ:FLQHN, VPTGQ:SAIS:LKNYQ:LEEHS, SRVHH:SAIS:LKNYQ:RLEEH, TQVQL:SAIS:LKNYQ:TLEDH, VPEEL:SSLS:LKVYP:DMTVE, VPEEL:SSLS:LKVYP:EMTVE, VPEKL:SSLS:LKVYP:NMTVE, VPEQL:SSLS:LKVYP:NMTVE, VPEKL:SSLS:LKVYP:EGMSTVE, VPEKL:SSLS:LKVYP:GMTVE, VPEKM:SSLS:LKVYP:GMTVE, VPERL:SSLS:LKVYP:DMTVE, VPEKT:SSLS:LKVYP:MITVE, VPEAL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MVTVE, VPTEL:SSLS:LKVYP:DMVVE, VPTEL:SSLS:LKVYP:EMVVE, APTKL:SSLS:LKVYP:NMVVR, APTQL:SSLS:LKVYP:NMVVR, APTKL:SSLS:LKVYP:NMVVK, VPTKL:SSLS:LKVYP:EGMSVAE, VPTKL:SSLS:LKVYP:GMAVS, TPTKM:SSLS:LKVYP:GMVVD, VPARL:SSLS:LKVYP:DMVVE, VPTRL:SSLS:LKVYP:DMVVE, APVKT:SSLS:LKVYP:MIVEE, VPQAL:SSLS:LKVYP:MIVRS, VSQDL:SSLS:LKVYP:MIVKS, VPQDL:SSLS:LKVYP:MVVKS, VPTEE:SSLS:LKVYP:FLQHN, VPTGQ:SSLS:LKVYP:LEEHS, SRVHH:SSLS:LKVYP:RLEEH, TQVQL:SSLS:LKVYP:TLEDH, APTEL:NAIS:LKKYR:DMVVR, APTKM:NAIS:LKKYR:NMVVR, APTEL:NAIS:LKKYR:EMVVR, APTKL:NAIS:LKKYR:NMVVR, APTKL:NAIS:LKKYR:EGMSVVR, APTKL:NAIS:LKKYR:GMVVR, APTKM:NAIS:LKKYR:GMVVR, APTRL:NAIS:LKKYR:DMVVR, APTKT:NAIS:LKKYR:MIVVR, APTAL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MVVVR, VPTEL:NAIS:LKKYR:DMVVE, VPEKM:NAIS:LKKYR:NMTVE, VPTEL:NAIS:LKKYR:EMVVE, APTKL:NAIS:LKKYR:NMVVK, VPTKL:NAIS:LKKYR:EGMSVAE, VPTKL:NAIS:LKKYR:GMAVS, TPTKM:NAIS:LKKYR:GMVVD, VPARL:NAIS:LKKYR:DMVVE, VPTRL:NAIS:LKKYR:DMVVE, APVKT:NAIS:LKKYR:MIVEE, VPQAL:NAIS:LKKYR:MIVRS, VSQDL:NAIS:LKKYR:MIVKS, VPQDL:NAIS:LKKYR:MVVKS, VPTEE:NAIS:LKKYR:FLQHN, VPTGQ:NAIS:LKKYR:LEEHS, SRVHH:NAIS:LKKYR:RLEEH, TQVQL:NAIS:LKKYR:TLEDH, APTEL:SATS:LRKHR:DMVVK, APTKM:SATS:LRKHR:NMVVK, APTEL:SATS:LRKHR:EMVVK, APTKL:SATS:LRKHR:NMVVK, APTQL:SATS:LRKHR:NMVVK, APTKL:SATS:LRKHR:EGMSVVK, APTKL:SATS:LRKHR:GMVVK, APTKM:SATS:LRKHR:GMVVK, APTRL:SATS:LRKHR:DMVVK, APTKT:SATS:LRKHR:MIVVK, APTAL:SATS:LRKHR:MIVVK, APTDL:SATS:LRKHR:MIVVK, APTDL:SATS:LRKHR:MVVVK, VPTEL:SATS:LRKHR:DMVVE, VPEKM:SATS:LRKHR:NMTVE, VPTEL:SATS:LRKHR:EMVVE, APTKL:SATS:LRKHR:NMVVR, APTQL:SATS:LRKHR:NMVVR,

VPTKL:SATS:LRKHR:EGMSVAE, VPTKL:SATS:LRKHR:GMAVS, TPTKM:SATS:LRKHR:GMVVD,
VPARL:SATS:LRKHR:DMVVE, VPTRL:SATS:LRKHR:DMVVE, APVKT:SATS:LRKHR:MIVEE,
VPQAL:SATS:LRKHR:MIVRS, VSQDL:SATS:LRKHR:MIVKS, VPQDL:SATS:LRKHR:MVVKS,
VPTEE:SATS:LRKHR:FLQHN, VPTGQ:SATS:LRKHR:LEEHS, SRVHH:SATS:LRKHR:RLEEH,
TQVQL:SATS:LRKHR:TLEDH, VPTEL:SPIS:LKYHY:DMVAE, VPTKM:SPIS:LKYHY:NMVAE,
VPTEL:SPIS:LKYHY:EMVAE, VPTKL:SPIS:LKYHY:NMVAE, VPTQL:SPIS:LKYHY:NMVAE,
VPTKL:SPIS:LKYHY:GMVAE, VPTKM:SPIS:LKYHY:GMVAE, VPTRL:SPIS:LKYHY:DMVAE,
VPTKT:SPIS:LKYHY:MIVAE, VPTAL:SPIS:LKYHY:MIVAE, VPTDL:SPIS:LKYHY:MIVAE,
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VPTEL:SPIS:LKYHY:EMVVE, APTKL:SPIS:LKYHY:NMVVR, APTQL:SPIS:LKYHY:NMVVR,
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VPARL:SPIS:LKYHY:DMVVE, VPTRL:SPIS:LKYHY:DMVVE, APVKT:SPIS:LKYHY:MIVEE,
VPQAL:SPIS:LKYHY:MIVRS, VSQDL:SPIS:LKYHY:MIVKS, VPQDL:SPIS:LKYHY:MVVKS,
VPTEE:SPIS:LKYHY:FLQHN, VPTGQ:SPIS:LKYHY:LEEHS, SRVHH:SPIS:LKYHY:RLEEH,
TQVQL:SPIS:LKYHY:TLEDH, VPTEL:EPIS:KFKYE:DMAVS, VPTKM:EPIS:KFKYE:NMAVS,
VPTEL:EPIS:KFKYE:EMAVS, VPTKL:EPIS:KFKYE:NMAVS, VPTQL:EPIS:KFKYE:NMAVS,
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VPTEE:SPIN:YGKIP:FLQHN, VPTGQ:SPIN:YGKIP:LEEHS, SRVHH:SPIN:YGKIP:RLEEH,
TQVQL:SPIN:YGKIP:TLEDH, VPAEL:SPIS:YKQYE:DMVVE, VPAKM:SPIS:YKQYE:NMVVE,
VPAEL:SPIS:YKQYE:EMVVE, VPAKL:SPIS:YKQYE:NMVVE, VPAQL:SPIS:YKQYE:NMVVE,
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VPTKL:SPIS:YKQYE:GMAVS, TPTKM:SPIS:YKQYE:GMVVD, VPTRL:SPIS:YKQYE:DMVVE,

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VPQDL:SPIS:YKQYE:MVVKS, VPTEE:SPIS:YKQYE:FLQHN, VPTGQ:SPIS:YKQYE:LEEHS,
SRVHH:SPIS:YKQYE:RLEEH, TQVQL:SPIS:YKQYE:TLEDH, VPTKM:SPIS:YKQYE:NMVVE,
VPTKL:SPIS:YKQYE:NMVVE, VPTQL:SPIS:YKQYE:NMVVE, VPTKL:SPIS:YKQYE:EGMSVVE,
VPTKL:SPIS:YKQYE:GMVVE, VPTKM:SPIS:YKQYE:GMVVE, VPTKT:SPIS:YKQYE:MIVVE,
VPTAL:SPIS:YKQYE:MIVVE, VPTDL:SPIS:YKQYE:MIVVE, VPTDL:SPIS:YKQYE:MVVVE,
APVEL:KPLS:DHHKD:DMVEE, APVKM:KPLS:DHHKD:NMVEE, APVEL:KPLS:DHHKD:EMVEE,
APVKL:KPLS:DHHKD:NMVEE, APVQL:KPLS:DHHKD:NMVEE, APVKL:KPLS:DHHKD:EGMSVEE,
APVKL:KPLS:DHHKD:GMVEE, APVKM:KPLS:DHHKD:GMVEE, APVRL:KPLS:DHHKD:DMVEE,
APVAL:KPLS:DHHKD:MIVEE, APVDL:KPLS:DHHKD:MIVEE, APVDL:KPLS:DHHKD:MVVEE,
VPTEL:KPLS:DHHKD:DMVVE, VPEKM:KPLS:DHHKD:NMTVE, VPTEL:KPLS:DHHKD:EMVVE,
APTKL:KPLS:DHHKD:NMVVR, APTQL:KPLS:DHHKD:NMVVR, APTKL:KPLS:DHHKD:NMVVK,
VPTKL:KPLS:DHHKD:EGMSVAE, VPTKL:KPLS:DHHKD:GMAVS, TPTKM:KPLS:DHHKD:GMVVD,
VPARL:KPLS:DHHKD:DMVVE, VPTRL:KPLS:DHHKD:DMVVE, VPQAL:KPLS:DHHKD:MIVRS,
VSQDL:KPLS:DHHKD:MIVKS, VPQDL:KPLS:DHHKD:MVVKS, VPTEE:KPLS:DHHKD:FLQHN,
VPTGQ:KPLS:DHHKD:LEEHS, SRVHH:KPLS:DHHKD:RLEEH, TQVQL:KPLS:DHHKD:TLEDH,
VPQEL:EPLP:EQLSN:DMVRS, VPQKM:EPLP:EQLSN:NMVRS, VPQEL:EPLP:EQLSN:EMVRS,
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APTKL:EPLP:EQLSN:NMVVR, APTQL:EPLP:EQLSN:NMVVR, APTKL:EPLP:EQLSN:NMVVK,
VPTKL:EPLP:EQLSN:EGMSVAE, VPTKL:EPLP:EQLSN:GMAVS, TPTKM:EPLP:EQLSN:GMVVD,
VPARL:EPLP:EQLSN:DMVVE, VPTRL:EPLP:EQLSN:DMVVE, APVKT:EPLP:EQLSN:MIVEE,
VSQDL:EPLP:EQLSN:MIVKS, VPQDL:EPLP:EQLSN:MVVKS, VPTEE:EPLP:EQLSN:FLQHN,
VPTGQ:EPLP:EQLSN:LEEHS, SRVHH:EPLP:EQLSN:RLEEH, TQVQL:EPLP:EQLSN:TLEDH,
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APTKL:EPLT:EQLSN:NMVVR, APTQL:EPLT:EQLSN:NMVVR, APTKL:EPLT:EQLSN:NMVVK,
VPTKL:EPLT:EQLSN:EGMSVAE, VPTKL:EPLT:EQLSN:GMAVS, TPTKM:EPLT:EQLSN:GMVVD,
VPARL:EPLT:EQLSN:DMVVE, VPTRL:EPLT:EQLSN:DMVVE, APVKT:EPLT:EQLSN:MIVEE,
VPQAL:EPLT:EQLSN:MIVRS, VPTEE:EPLT:EQLSN:FLQHN, VPTGQ:EPLT:EQLSN:LEEHS,
SRVHH:EPLT:EQLSN:RLEEH, TQVQL:EPLT:EQLSN:TLEDH, VPQEL:EPLT:EQLSN:DMVKS,
VPQKM:EPLT:EQLSN:NMVKS, VPQEL:EPLT:EQLSN:EMVKS, VPQKL:EPLT:EQLSN:NMVKS,
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VPQKM:EPLT:EQLSN:GMVKS, VPQRL:EPLT:EQLSN:DMVKS, VPQKT:EPLT:EQLSN:MIVKS,
VPQAL:EPLT:EQLSN:MIVKS, VPQDL:EPLT:EQLSN:MIVKS, VPTGQ:SNIT:IGEMS:LEQHN,
VPTEL:SNIT:IGEMS:DMVVE, VPEKM:SNIT:IGEMS:NMTVE, VPTEL:SNIT:IGEMS:EMVVE,
APTKL:SNIT:IGEMS:NMVVR, APTQL:SNIT:IGEMS:NMVVR, APTKL:SNIT:IGEMS:NMVVK,

VPTKL:SNIT:IGEMS:EGMSVAE, VPTKL:SNIT:IGEMS:GMAVS, TPTKM:SNIT:IGEMS:GMVVD, VPARL:SNIT:IGEMS:DMVVE, VPTRL:SNIT:IGEMS:DMVVE, APVKT:SNIT:IGEMS:MIVEE, VPQAL:SNIT:IGEMS:MIVRS, VSQDL:SNIT:IGEMS:MIVKS, VPQDL:SNIT:IGEMS:MVVKS, VPTGQ:SNIT:IGEMS:LEEHS, SRVHH:SNIT:IGEMS:RLEEH, TQVQL:SNIT:IGEMS:TLEDH, VPTEE:SNIT:LGEMS:FLEHS, VPTEL:SNIT:LGEMS:DMVVE, VPEKM:SNIT:LGEMS:NMTVE, VPTEL:SNIT:LGEMS:EMVVE, APTKL:SNIT:LGEMS:NMVVR, APTQL:SNIT:LGEMS:NMVVR, APTKL:SNIT:LGEMS:NMVVK, VPTKL:SNIT:LGEMS:EGMSVAE, VPTKL:SNIT:LGEMS:GMAVS, TPTKM:SNIT:LGEMS:GMVVD, VPARL:SNIT:LGEMS:DMVVE, VPTRL:SNIT:LGEMS:DMVVE, APVKT:SNIT:LGEMS:MIVEE, VPQAL:SNIT:LGEMS:MIVRS, VSQDL:SNIT:LGEMS:MIVKS, VPQDL:SNIT:LGEMS:MVVKS, VPTEE:SNIT:LGEMS:FLQHN, SRVHH:SNIT:LGEMS:RLEEH, TQVQL:SNIT:LGEMS:TLEDH, SRVQL:RSVK:KEVQV:TLEEH, VPTEL:RSVK:KEVQV:DMVVE, VPEKM:RSVK:KEVQV:NMTVE, VPTEL:RSVK:KEVQV:EMVVE, APTKL:RSVK:KEVQV:NMVVR, APTQL:RSVK:KEVQV:NMVVR, APTKL:RSVK:KEVQV:NMVVK, VPTKL:RSVK:KEVQV:EGMSVAE, VPTKL:RSVK:KEVQV:GMAVS, TPTKM:RSVK:KEVQV:GMVVD, VPARL:RSVK:KEVQV:DMVVE, VPTRL:RSVK:KEVQV:DMVVE, APVKT:RSVK:KEVQV:MIVEE, VPQAL:RSVK:KEVQV:MIVRS, VSQDL:RSVK:KEVQV:MIVKS, VPQDL:RSVK:KEVQV:MVVKS, VPTEE:RSVK:KEVQV:FLQHN, VPTGQ:RSVK:KEVQV:LEEHS, TQVQL:RSVK:KEVQV:TLEDH, TQVHH:RPVQ:KKATV:RLEDH, VPTEL:RPVQ:KKATV:DMVVE, VPEKM:RPVQ:KKATV:NMTVE, VPTEL:RPVQ:KKATV:EMVVE, APTKL:RPVQ:KKATV:NMVVR, APTQL:RPVQ:KKATV:NMVVR, APTKL:RPVQ:KKATV:NMVVK, VPTKL:RPVQ:KKATV:EGMSVAE, VPTKL:RPVQ:KKATV:GMAVS, TPTKM:RPVQ:KKATV:GMVVD, VPARL:RPVQ:KKATV:DMVVE, VPTRL:RPVQ:KKATV:DMVVE, APVKT:RPVQ:KKATV:MIVEE, VPQAL:RPVQ:KKATV:MIVRS, VSQDL:RPVQ:KKATV:MIVKS, VPQDL:RPVQ:KKATV:MVVKS, VPTEE:RPVQ:KKATV:FLQHN, VPTGQ:RPVQ:KKATV:LEEHS and SRVHH:RPVQ:KKATV:RLEEH.

In particular, in certain embodiments, the quadruplet PEP5:PEP12:PEP2:PEP6 is selected from the group consisting of VPTKM:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTEL:SAIS-AA[17]-LYL:LKNYQ:EMVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:GMVVE, VPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVE, VPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVE, VPTKT:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTAL:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTDL:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTDL:SAIS-AA[17]-LYL:LKNYQ:MVVVE, VPTEE:SAIS-AA[17]-LYL:LKNYQ:FLVVE, VPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEVVE, VPTHH:SAIS-AA[17]-LYL:LKNYQ:RLVVE, VPTQL:SAIS-AA[17]-LYL:LKNYQ:TLVVE, VPEKM:SAIS-AA[17]-LYL:LKNYQ:NMTVE, APTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVR, APTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVR, APTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVK, VPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVAE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:GMAVS, TPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVD, VPARL:SAIS-AA[17]-LYL:LKNYQ:DMVVE, APVKT:SAIS-AA[17]-LYL:LKNYQ:MIVEE, VPQAL:SAIS-AA[17]-LYL:LKNYQ:MIVRS, VSQDL:SAIS-AA[17]-LYL:LKNYQ:MIVKS, VPQDL:SAIS-AA[17]-LYL:LKNYQ:MVVKS, VPTEE:SAIS-AA[17]-LYL:LKNYQ:FLQHN, VPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEEHS, SRVHH:SAIS-AA[17]-LYL:LKNYQ:RLEEH, TQVQL:SAIS-AA[17]-LYL:LKNYQ:TLEDH, VPEEL:SSLS-AA[17]-LFF:LKVYP:DMTVE, VPEEL:SSLS-AA[17]-LFF:LKVYP:EMTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE, VPEQL:SSLS-AA[17]-LFF:LKVYP:NMTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:EGMSTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:GMTVE, VPEKM:SSLS-AA[17]-LFF:LKVYP:GMTVE, VPERL:SSLS-AA[17]-LFF:LKVYP:DMTVE, VPEKT:SSLS-AA[17]-LFF:LKVYP:MITVE,

VPEAL:SSLS-AA[17]-LFF:LKVYP:MITVE, VPEDL:SSLS-AA[17]-LFF:LKVYP:MITVE, VPEDL:SSLS-AA[17]-LFF:LKVYP:MVTVE, VPEEE:SSLS-AA[17]-LFF:LKVYP:FLTVE, VPEGQ:SSLS-AA[17]-LFF:LKVYP:LETVE, VPEHH:SSLS-AA[17]-LFF:LKVYP:RLTVE, VPEQL:SSLS-AA[17]-LFF:LKVYP:TLTVE, VPTEL:SSLS-AA[17]-LFF:LKVYP:DMVVE, VPTEL:SSLS-AA[17]-LFF:LKVYP:EMVVE, APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVR, APTQL:SSLS-AA[17]-LFF:LKVYP:NMVVR, APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVK, VPTKL:SSLS-AA[17]-LFF:LKVYP:EGMSVAE, VPTKL:SSLS-AA[17]-LFF:LKVYP:GMAVS, TPTKM:SSLS-AA[17]-LFF:LKVYP:GMVVD, VPARL:SSLS-AA[17]-LFF:LKVYP:DMVVE, VPTRL:SSLS-AA[17]-LFF:LKVYP:DMVVE, APVKT:SSLS-AA[17]-LFF:LKVYP:MIVEE, VPQAL:SSLS-AA[17]-LFF:LKVYP:MIVRS, VSQDL:SSLS-AA[17]-LFF:LKVYP:MIVKS, VPQDL:SSLS-AA[17]-LFF:LKVYP:MVVKS, VPTEE:SSLS-AA[17]-LFF:LKVYP:FLQHN, VPTGQ:SSLS-AA[17]-LFF:LKVYP:LEEHS, SRVHH:SSLS-AA[17]-LFF:LKVYP:RLEEH, TQVQL:SSLS-AA[17]-LFF:LKVYP:TLEDH, VPTEL:SAIS-AA[17]-LYL:LKNYQ:DMVVE, APTEL:NAIS-AA[17]-LYF:LKKYR:DMVVR, APTKM:NAIS-AA[17]-LYF:LKKYR:NMVVR, APTEL:NAIS-AA[17]-LYF:LKKYR:EMVVR, APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR, APTQL:NAIS-AA[17]-LYF:LKKYR:NMVVR, APTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVVR, APTKL:NAIS-AA[17]-LYF:LKKYR:GMVVR, APTKM:NAIS-AA[17]-LYF:LKKYR:GMVVR, APTRL:NAIS-AA[17]-LYF:LKKYR:DMVVR, APTKT:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTAL:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTDL:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTDL:NAIS-AA[17]-LYF:LKKYR:MVVVR, APTEE:NAIS-AA[17]-LYF:LKKYR:FLVVR, APTGQ:NAIS-AA[17]-LYF:LKKYR:LEVVR, APTHH:NAIS-AA[17]-LYF:LKKYR:RLVVR, APTQL:NAIS-AA[17]-LYF:LKKYR:TLVVR, VPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVE, VPEKM:NAIS-AA[17]-LYF:LKKYR:NMTVE, VPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVE, APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVK, VPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVAE, VPTKL:NAIS-AA[17]-LYF:LKKYR:GMAVS, TPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVD, VPARL:NAIS-AA[17]-LYF:LKKYR:DMVVE, VPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVE, APVKT:NAIS-AA[17]-LYF:LKKYR:MIVEE, VPQAL:NAIS-AA[17]-LYF:LKKYR:MIVRS, VSQDL:NAIS-AA[17]-LYF:LKKYR:MIVKS, VPQDL:NAIS-AA[17]-LYF:LKKYR:MVVKS, VPTEE:NAIS-AA[17]-LYF:LKKYR:FLQHN, VPTGQ:NAIS-AA[17]-LYF:LKKYR:LEEHS, SRVHH:NAIS-AA[17]-LYF:LKKYR:RLEEH, TQVQL:NAIS-AA[17]-LYF:LKKYR:TLEDH, APTEL:SATS-AA[17]-LYY:LRKHR:DMVVK, APTKM:SATS-AA[17]-LYY:LRKHR:NMVVK, APTEL:SATS-AA[17]-LYY:LRKHR:EMVVK, APTKL:SATS-AA[17]-LYY:LRKHR:NMVVK, APTQL:SATS-AA[17]-LYY:LRKHR:NMVVK, APTKL:SATS-AA[17]-LYY:LRKHR:EGMSVVK, APTKL:SATS-AA[17]-LYY:LRKHR:GMVVK, APTKM:SATS-AA[17]-LYY:LRKHR:GMVVK, APTRL:SATS-AA[17]-LYY:LRKHR:DMVVK, APTKT:SATS-AA[17]-LYY:LRKHR:MIVVK, APTAL:SATS-AA[17]-LYY:LRKHR:MIVVK, APTDL:SATS-AA[17]-LYY:LRKHR:MIVVK, APTDL:SATS-AA[17]-LYY:LRKHR:MVVVK, APTEE:SATS-AA[17]-LYY:LRKHR:FLVVK, APTGQ:SATS-AA[17]-LYY:LRKHR:LEVVK, APTHH:SATS-AA[17]-LYY:LRKHR:RLVVK, APTQL:SATS-AA[17]-LYY:LRKHR:TLVVK, VPTEL:SATS-AA[17]-LYY:LRKHR:DMVVE, VPEKM:SATS-AA[17]-LYY:LRKHR:NMTVE, VPTEL:SATS-AA[17]-LYY:LRKHR:EMVVE, APTKL:SATS-AA[17]-LYY:LRKHR:NMVVR, APTQL:SATS-AA[17]-LYY:LRKHR:NMVVR, VPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVAE, VPTKL:SATS-AA[17]-LYY:LRKHR:GMAVS, TPTKM:SATS-AA[17]-LYY:LRKHR:GMVVD, VPARL:SATS-AA[17]-LYY:LRKHR:DMVVE, VPTRL:SATS-AA[17]-LYY:LRKHR:DMVVE, APVKT:SATS-AA[17]-LYY:LRKHR:MIVEE, VPQAL:SATS-AA[17]-LYY:LRKHR:MIVRS, VSQDL:SATS-AA[17]-LYY:LRKHR:MIVKS, VPQDL:SATS-AA[17]-LYY:LRKHR:MVVKS, VPTEE:SATS-AA[17]-LYY:LRKHR:FLQHN, VPTGQ:SATS-AA[17]-LYY:LRKHR:LEEHS, SRVHH:SATS-AA[17]-LYY:LRKHR:RLEEH, TQVQL:SATS-AA[17]-LYY:LRKHR:TLEDH, VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVAE, VPTKM:SPIS-AA[17]-LYK:LKYHY:NMVAE, VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVAE, VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE, VPTQL:SPIS-AA[17]-LYK:LKYHY:NMVAE,

VPTKL:SPIS-AA[17]-LYK:LKYHY:GMVAE, VPTKM:SPIS-AA[17]-LYK:LKYHY:GMVAE, VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAE, VPTKT:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTAL:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTDL:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTDL:SPIS-AA[17]-LYK:LKYHY:MVVAE, VPTEE:SPIS-AA[17]-LYK:LKYHY:FLVAE, VPTGQ:SPIS-AA[17]-LYK:LKYHY:LEVAE, VPTHH:SPIS-AA[17]-LYK:LKYHY:RLVAE, VPTQL:SPIS-AA[17]-LYK:LKYHY:TLVAE, VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVVE, VPEKM:SPIS-AA[17]-LYK:LKYHY:NMTVE, VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVVE, APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVR, APTQL:SPIS-AA[17]-LYK:LKYHY:NMVVR, APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVK, VPTKL:SPIS-AA[17]-LYK:LKYHY:GMAVS, TPTKM:SPIS-AA[17]-LYK:LKYHY:GMVVD, VPARL:SPIS-AA[17]-LYK:LKYHY:DMVVE, VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVVE, APVKT:SPIS-AA[17]-LYK:LKYHY:MIVEE, VPQAL:SPIS-AA[17]-LYK:LKYHY:MIVRS, VSQDL:SPIS-AA[17]-LYK:LKYHY:MIVKS, VPQDL:SPIS-AA[17]-LYK:LKYHY:MVVKS, VPTEE:SPIS-AA[17]-LYK:LKYHY:FLQHN, VPTGQ:SPIS-AA[17]-LYK:LKYHY:LEEHS, SRVHH:SPIS-AA[17]-LYK:LKYHY:RLEEH, TQVQL:SPIS-AA[17]-LYK:LKYHY:TLEDH, VPTEL:EPIS-AA[17]-LYL:KFKYE:DMAVS, VPTKM:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTEL:EPIS-AA[17]-LYL:KFKYE:EMAVS, VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTQL:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSAVS, VPTKM:EPIS-AA[17]-LYL:KFKYE:GMAVS, VPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVS, VPTKT:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTAL:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTDL:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTDL:EPIS-AA[17]-LYL:KFKYE:MVAVS, VPTEE:EPIS-AA[17]-LYL:KFKYE:FLAVS, VPTGQ:EPIS-AA[17]-LYL:KFKYE:LEAVS, VPTHH:EPIS-AA[17]-LYL:KFKYE:RLAVS, VPTQL:EPIS-AA[17]-LYL:KFKYE:TLAVS, VPTEL:EPIS-AA[17]-LYL:KFKYE:DMVVE, VPEKM:EPIS-AA[17]-LYL:KFKYE:NMTVE, VPTEL:EPIS-AA[17]-LYL:KFKYE:EMVVE, APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVR, APTQL:EPIS-AA[17]-LYL:KFKYE:NMVVR, APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVK, VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSVAE, TPTKM:EPIS-AA[17]-LYL:KFKYE:GMVVD, VPARL:EPIS-AA[17]-LYL:KFKYE:DMVVE, VPTRL:EPIS-AA[17]-LYL:KFKYE:DMVVE, APVKT:EPIS-AA[17]-LYL:KFKYE:MIVEE, VPQAL:EPIS-AA[17]-LYL:KFKYE:MIVRS, VSQDL:EPIS-AA[17]-LYL:KFKYE:MIVKS, VPQDL:EPIS-AA[17]-LYL:KFKYE:MVVKS, VPTEE:EPIS-AA[17]-LYL:KFKYE:FLQHN, VPTGQ:EPIS-AA[17]-LYL:KFKYE:LEEHS, SRVHH:EPIS-AA[17]-LYL:KFKYE:RLEEH, TQVQL:EPIS-AA[17]-LYL:KFKYE:TLEDH, TPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVD, TPTKM:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:GMVVD, TPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVD, TPTKT:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTAL:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTDL:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTDL:SPIN-AA[17]-LYF:YGKIP:MVVVD, TPTEE:SPIN-AA[17]-LYF:YGKIP:FLVVD, TPTGQ:SPIN-AA[17]-LYF:YGKIP:LEVVD, TPTHH:SPIN-AA[17]-LYF:YGKIP:RLVVD, TPTQL:SPIN-AA[17]-LYF:YGKIP:TLVVD, VPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVE, VPEKM:SPIN-AA[17]-LYF:YGKIP:NMTVE, VPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVE, APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVR, APTQL:SPIN-AA[17]-LYF:YGKIP:NMVVR, APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVK, VPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVAE, VPTKL:SPIN-AA[17]-LYF:YGKIP:GMAVS, VPARL:SPIN-AA[17]-LYF:YGKIP:DMVVE, VPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVE, APVKT:SPIN-AA[17]-LYF:YGKIP:MIVEE, VPQAL:SPIN-AA[17]-LYF:YGKIP:MIVRS, VSQDL:SPIN-AA[17]-LYF:YGKIP:MIVKS, VPQDL:SPIN-AA[17]-LYF:YGKIP:MVVKS, VPTEE:SPIN-AA[17]-LYF:YGKIP:FLQHN, VPTGQ:SPIN-AA[17]-LYF:YGKIP:LEEHS, SRVHH:SPIN-AA[17]-LYF:YGKIP:RLEEH, TQVQL:SPIN-AA[17]-LYF:YGKIP:TLEDH, VPAEL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPAKM:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAEL:SPIS-AA[17]-LYI:YKQYE:EMVVE, VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAQL:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAKL:SPIS-AA[17]-LYI:YKQYE:EGMSVVE, VPAKL:SPIS-AA[17]-

LYI:YKQYE:GMVVE, VPAKM:SPIS-AA[17]-LYI:YKQYE:GMVVE, VPARL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPAKT:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPAAL:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPADL:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPADL:SPIS-AA[17]-LYI:YKQYE:MVVVE, VPAEE:SPIS-AA[17]-LYI:YKQYE:FLVVE, VPAGQ:SPIS-AA[17]-LYI:YKQYE:LEVVE, VPAHH:SPIS-AA[17]-LYI:YKQYE:RLVVE, VPAQL:SPIS-AA[17]-LYI:YKQYE:TLVVE, VPTEL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPEKM:SPIS-AA[17]-LYI:YKQYE:NMTVE, VPTEL:SPIS-AA[17]-LYI:YKQYE:EMVVE, APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVR, APTQL:SPIS-AA[17]-LYI:YKQYE:NMVVR, APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVK, VPTKL:SPIS-AA[17]-LYI:YKQYE:EGMSVAE, VPTKL:SPIS-AA[17]-LYI:YKQYE:GMAVS, TPTKM:SPIS-AA[17]-LYI:YKQYE:GMVVD, VPTRL:SPIS-AA[17]-LYI:YKQYE:DMVVE, APVKT:SPIS-AA[17]-LYI:YKQYE:MIVEE, VPQAL:SPIS-AA[17]-LYI:YKQYE:MIVRS, VSQDL:SPIS-AA[17]-LYI:YKQYE:MIVKS, VPQDL:SPIS-AA[17]-LYI:YKQYE:MVVKS, VPTEE:SPIS-AA[17]-LYI:YKQYE:FLQHN, VPTGQ:SPIS-AA[17]-LYI:YKQYE:LEEHS, SRVHH:SPIS-AA[17]-LYI:YKQYE:RLEEH, TQVQL:SPIS-AA[17]-LYI:YKQYE:TLEDH, VPTEL:SPIS-AA[17]-LFI:YKQYE:DMVVE, VPTKM:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTEL:SPIS-AA[17]-LFI:YKQYE:EMVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:GMVVE, VPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVE, VPTRL:SPIS-AA[17]-LFI:YKQYE:DMVVE, VPTKT:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTAL:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTDL:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTDL:SPIS-AA[17]-LFI:YKQYE:MVVVE, VPTEE:SPIS-AA[17]-LFI:YKQYE:FLVVE, VPTGQ:SPIS-AA[17]-LFI:YKQYE:LEVVE, VPTHH:SPIS-AA[17]-LFI:YKQYE:RLVVE, VPTQL:SPIS-AA[17]-LFI:YKQYE:TLVVE, VPEKM:SPIS-AA[17]-LFI:YKQYE:NMTVE, APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVR, APTQL:SPIS-AA[17]-LFI:YKQYE:NMVVR, APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVK, VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVAE, VPTKL:SPIS-AA[17]-LFI:YKQYE:GMAVS, TPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVD, VPARL:SPIS-AA[17]-LFI:YKQYE:DMVVE, APVKT:SPIS-AA[17]-LFI:YKQYE:MIVEE, VPQAL:SPIS-AA[17]-LFI:YKQYE:MIVRS, VSQDL:SPIS-AA[17]-LFI:YKQYE:MIVKS, VPQDL:SPIS-AA[17]-LFI:YKQYE:MVVKS, VPTEE:SPIS-AA[17]-LFI:YKQYE:FLQHN, VPTGQ:SPIS-AA[17]-LFI:YKQYE:LEEHS, SRVHH:SPIS-AA[17]-LFI:YKQYE:RLEEH, TQVQL:SPIS-AA[17]-LFI:YKQYE:TLEDH, APVEL:KPLS-AA[17]-LYV:DHHKD:DMVEE, APVKM:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVEL:KPLS-AA[17]-LYV:DHHKD:EMVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVQL:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:EGMSVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:GMVEE, APVKM:KPLS-AA[17]-LYV:DHHKD:GMVEE, APVRL:KPLS-AA[17]-LYV:DHHKD:DMVEE, APVAL:KPLS-AA[17]-LYV:DHHKD:MIVEE, APVDL:KPLS-AA[17]-LYV:DHHKD:MIVEE, APVDL:KPLS-AA[17]-LYV:DHHKD:MVVEE, APVEE:KPLS-AA[17]-LYV:DHHKD:FLVEE, APVGQ:KPLS-AA[17]-LYV:DHHKD:LEVEE, APVHH:KPLS-AA[17]-LYV:DHHKD:RLVEE, APVQL:KPLS-AA[17]-LYV:DHHKD:TLVEE, VPTEL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPEKM:KPLS-AA[17]-LYV:DHHKD:NMTVE, VPTEL:KPLS-AA[17]-LYV:DHHKD:EMVVE, APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVR, APTQL:KPLS-AA[17]-LYV:DHHKD:NMVVR, APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVK, VPTKL:KPLS-AA[17]-LYV:DHHKD:EGMSVAE, VPTKL:KPLS-AA[17]-LYV:DHHKD:GMAVS, TPTKM:KPLS-AA[17]-LYV:DHHKD:GMVVD, VPARL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPTRL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPQAL:KPLS-AA[17]-LYV:DHHKD:MIVRS, VSQDL:KPLS-AA[17]-LYV:DHHKD:MIVKS, VPQDL:KPLS-AA[17]-LYV:DHHKD:MVVKS, VPTEE:KPLS-AA[17]-LYV:DHHKD:FLQHN, VPTGQ:KPLS-AA[17]-LYV:DHHKD:LEEHS, SRVHH:KPLS-AA[17]-LYV:DHHKD:RLEEH, TQVQL:KPLS-AA[17]-LYV:DHHKD:TLEDH, VPQEL:EPLP-AA[17]-VYY:EQLSN:DMVRS, VPQKM:EPLP-AA[17]-VYY:EQLSN:NMVRS, VPQEL:EPLP-AA[17]-

VYY:EQLSN:EMVRS, VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS, VPQQL:EPLP-AA[17]-
VYY:EQLSN:NMVRS, VPQKL:EPLP-AA[17]-VYY:EQLSN:EGMSVRS, VPQKL:EPLP-AA[17]-
VYY:EQLSN:GMVRS, VPQKM:EPLP-AA[17]-VYY:EQLSN:GMVRS, VPQRL:EPLP-AA[17]-
VYY:EQLSN:DMVRS, VPQKT:EPLP-AA[17]-VYY:EQLSN:MIVRS, VPQDL:EPLP-AA[17]-
VYY:EQLSN:MIVRS, VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVRS, VPQEE:EPLP-AA[17]-
VYY:EQLSN:FLVRS, VPQGQ:EPLP-AA[17]-VYY:EQLSN:LEVRS, VPQHH:EPLP-AA[17]-
VYY:EQLSN:RLVRS, VPQQL:EPLP-AA[17]-VYY:EQLSN:TLVRS, VPTEL:EPLP-AA[17]-
VYY:EQLSN:DMVVE, VPEKM:EPLP-AA[17]-VYY:EQLSN:NMTVE, VPTEL:EPLP-AA[17]-
VYY:EQLSN:EMVVE, APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVR, APTQL:EPLP-AA[17]-
VYY:EQLSN:NMVVR, APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVK, VPTKL:EPLP-AA[17]-
VYY:EQLSN:EGMSVAE, VPTKL:EPLP-AA[17]-VYY:EQLSN:GMAVS, TPTKM:EPLP-AA[17]-
VYY:EQLSN:GMVVD, VPARL:EPLP-AA[17]-VYY:EQLSN:DMVVE, VPTRL:EPLP-AA[17]-
VYY:EQLSN:DMVVE, APVKT:EPLP-AA[17]-VYY:EQLSN:MIVEE, VSQDL:EPLP-AA[17]-VYY:EQLSN:MIVKS,
VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVKS, VPTEE:EPLP-AA[17]-VYY:EQLSN:FLQHN, VPTGQ:EPLP-AA[17]-
VYY:EQLSN:LEEHS, SRVHH:EPLP-AA[17]-VYY:EQLSN:RLEEH, TQVQL:EPLP-AA[17]-
VYY:EQLSN:TLEDH, VSQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VSQKM:EPLT-AA[17]-
LYY:EQLSN:NMVKS, VSQEL:EPLT-AA[17]-LYY:EQLSN:EMVKS, VSQKL:EPLT-AA[17]-
LYY:EQLSN:NMVKS, VSQQL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VSQKL:EPLT-AA[17]-
LYY:EQLSN:EGMSVKS, VSQKL:EPLT-AA[17]-LYY:EQLSN:GMVKS, VSQKM:EPLT-AA[17]-
LYY:EQLSN:GMVKS, VSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VSQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS,
VSQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VSQDL:EPLT-AA[17]-LYY:EQLSN:MVVKS, VSQEE:EPLT-AA[17]-
LYY:EQLSN:FLVKS, VSQGQ:EPLT-AA[17]-LYY:EQLSN:LEVKS, VSQHH:EPLT-AA[17]-LYY:EQLSN:RLVKS,
VSQQL:EPLT-AA[17]-LYY:EQLSN:TLVKS, VPTEL:EPLT-AA[17]-LYY:EQLSN:DMVVE, VPEKM:EPLT-AA[17]-
LYY:EQLSN:NMTVE, VPTEL:EPLT-AA[17]-LYY:EQLSN:EMVVE, APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVR,
APTQL:EPLT-AA[17]-LYY:EQLSN:NMVVR, APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVK, VPTKL:EPLT-AA[17]-
LYY:EQLSN:EGMSVAE, VPTKL:EPLT-AA[17]-LYY:EQLSN:GMAVS, TPTKM:EPLT-AA[17]-
LYY:EQLSN:GMVVD, VPARL:EPLT-AA[17]-LYY:EQLSN:DMVVE, VPTRL:EPLT-AA[17]-
LYY:EQLSN:DMVVE, APVKT:EPLT-AA[17]-LYY:EQLSN:MIVEE, VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVRS,
VPQDL:EPLT-AA[17]-LYY:EQLSN:MVVKS, VPTEE:EPLT-AA[17]-LYY:EQLSN:FLQHN, VPTGQ:EPLT-AA[17]-
LYY:EQLSN:LEEHS, SRVHH:EPLT-AA[17]-LYY:EQLSN:RLEEH, TQVQL:EPLT-AA[17]-LYY:EQLSN:TLEDH,
VPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKS, VPQEL:EPLT-AA[17]-
LYY:EQLSN:EMVKS, VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VPQQL:EPLT-AA[17]-
LYY:EQLSN:NMVKS, VPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKS, VPQKL:EPLT-AA[17]-
LYY:EQLSN:GMVKS, VPQKM:EPLT-AA[17]-LYY:EQLSN:GMVKS, VPQRL:EPLT-AA[17]-
LYY:EQLSN:DMVKS, VPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS,
VPQDL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPQEE:EPLT-AA[17]-LYY:EQLSN:FLVKS, VPQGQ:EPLT-AA[17]-
LYY:EQLSN:LEVKS, VPQHH:EPLT-AA[17]-LYY:EQLSN:RLVKS, VPQQL:EPLT-AA[17]-LYY:EQLSN:TLVKS,
VSQDL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPTEL:SNIT-AA[17]-QIM:IGEMS:DMQHN, VPTKM:SNIT-AA[17]-
QIM:IGEMS:NMQHN, VPTEL:SNIT-AA[17]-QIM:IGEMS:EMQHN, VPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHN,
VPTQL:SNIT-AA[17]-QIM:IGEMS:NMQHN, VPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSQHN, VPTKL:SNIT-AA[17]-
QIM:IGEMS:GMQHN, VPTKM:SNIT-AA[17]-QIM:IGEMS:GMQHN, VPTRL:SNIT-AA[17]-
QIM:IGEMS:DMQHN, VPTKT:SNIT-AA[17]-QIM:IGEMS:MIQHN, VPTAL:SNIT-AA[17]-QIM:IGEMS:MIQHN,

VPTDL:SNIT-AA[17]-QIM:IGEMS:MIQHN, VPTDL:SNIT-AA[17]-QIM:IGEMS:MVQHN, VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEQHN, VPTEE:SNIT-AA[17]-QIM:IGEMS:FLQHN, VPTHH:SNIT-AA[17]-QIM:IGEMS:RLQHN, VPTQL:SNIT-AA[17]-QIM:IGEMS:TLQHN, VPTEL:SNIT-AA[17]-QIM:IGEMS:DMVVE, VPEKM:SNIT-AA[17]-QIM:IGEMS:NMTVE, VPTEL:SNIT-AA[17]-QIM:IGEMS:EMVVE, APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVR, APTQL:SNIT-AA[17]-QIM:IGEMS:NMVVR, APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVK, VPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSVAE, VPTKL:SNIT-AA[17]-QIM:IGEMS:GMAVS, TPTKM:SNIT-AA[17]-QIM:IGEMS:GMVVD, VPARL:SNIT-AA[17]-QIM:IGEMS:DMVVE, VPTRL:SNIT-AA[17]-QIM:IGEMS:DMVVE, APVKT:SNIT-AA[17]-QIM:IGEMS:MIVEE, VPQAL:SNIT-AA[17]-QIM:IGEMS:MIVRS, VSQDL:SNIT-AA[17]-QIM:IGEMS:MIVKS, VPQDL:SNIT-AA[17]-QIM:IGEMS:MVVKS, VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEEHS, SRVHH:SNIT-AA[17]-QIM:IGEMS:RLEEH, TQVQL:SNIT-AA[17]-QIM:IGEMS:TLEDH, VPTEL:SNIT-AA[17]-QIM:LGEMS:DMEHS, VPTKM:SNIT-AA[17]-QIM:LGEMS:NMEHS, VPTEL:SNIT-AA[17]-QIM:LGEMS:EMEHS, VPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHS, VPTQL:SNIT-AA[17]-QIM:LGEMS:NMEHS, VPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSEHS, VPTKL:SNIT-AA[17]-QIM:LGEMS:GMEHS, VPTKM:SNIT-AA[17]-QIM:LGEMS:GMEHS, VPTRL:SNIT-AA[17]-QIM:LGEMS:DMEHS, VPTKT:SNIT-AA[17]-QIM:LGEMS:MIEHS, VPTAL:SNIT-AA[17]-QIM:LGEMS:MIEHS, VPTDL:SNIT-AA[17]-QIM:LGEMS:MIEHS, VPTDL:SNIT-AA[17]-QIM:LGEMS:MVEHS, VPTEE:SNIT-AA[17]-QIM:LGEMS:FLEHS, VPTHH:SNIT-AA[17]-QIM:LGEMS:RLEHS, VPTQL:SNIT-AA[17]-QIM:LGEMS:TLEHS, VPTEL:SNIT-AA[17]-QIM:LGEMS:DMVVE, VPEKM:SNIT-AA[17]-QIM:LGEMS:NMTVE, VPTEL:SNIT-AA[17]-QIM:LGEMS:EMVVE, APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVR, APTQL:SNIT-AA[17]-QIM:LGEMS:NMVVR, APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVK, VPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSVAE, VPTKL:SNIT-AA[17]-QIM:LGEMS:GMAVS, TPTKM:SNIT-AA[17]-QIM:LGEMS:GMVVD, VPARL:SNIT-AA[17]-QIM:LGEMS:DMVVE, VPTRL:SNIT-AA[17]-QIM:LGEMS:DMVVE, APVKT:SNIT-AA[17]-QIM:LGEMS:MIVEE, VPQAL:SNIT-AA[17]-QIM:LGEMS:MIVRS, VSQDL:SNIT-AA[17]-QIM:LGEMS:MIVKS, VPQDL:SNIT-AA[17]-QIM:LGEMS:MVVKS, VPTEE:SNIT-AA[17]-QIM:LGEMS:FLQHN, SRVHH:SNIT-AA[17]-QIM:LGEMS:RLEEH, TQVQL:SNIT-AA[17]-QIM:LGEMS:TLEDH, SRVEL:RSVK-AA[17]-AKV:KEVQV:DMEEH, SRVKM:RSVK-AA[17]-AKV:KEVQV:NMEEH, SRVEL:RSVK-AA[17]-AKV:KEVQV:EMEEH, SRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEH, SRVQL:RSVK-AA[17]-AKV:KEVQV:NMEEH, SRVKL:RSVK-AA[17]-AKV:KEVQV:EGMSEEH, SRVKL:RSVK-AA[17]-AKV:KEVQV:GMEEH, SRVKM:RSVK-AA[17]-AKV:KEVQV:GMEEH, SRVRL:RSVK-AA[17]-AKV:KEVQV:DMEEH, SRVKT:RSVK-AA[17]-AKV:KEVQV:MIEEH, SRVAL:RSVK-AA[17]-AKV:KEVQV:MIEEH, SRVDL:RSVK-AA[17]-AKV:KEVQV:MIEEH, SRVDL:RSVK-AA[17]-AKV:KEVQV:MVEEH, SRVEE:RSVK-AA[17]-AKV:KEVQV:FLEEH, SRVGQ:RSVK-AA[17]-AKV:KEVQV:LEEEH, SRVQL:RSVK-AA[17]-AKV:KEVQV:TLEEH, VPTEL:RSVK-AA[17]-AKV:KEVQV:DMVVE, VPEKM:RSVK-AA[17]-AKV:KEVQV:NMTVE, VPTEL:RSVK-AA[17]-AKV:KEVQV:EMVVE, APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVR, APTQL:RSVK-AA[17]-AKV:KEVQV:NMVVR, APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVK, VPTKL:RSVK-AA[17]-AKV:KEVQV:EGMSVAE, VPTKL:RSVK-AA[17]-AKV:KEVQV:GMAVS, TPTKM:RSVK-AA[17]-AKV:KEVQV:GMVVD, VPARL:RSVK-AA[17]-AKV:KEVQV:DMVVE, VPTRL:RSVK-AA[17]-AKV:KEVQV:DMVVE, APVKT:RSVK-AA[17]-AKV:KEVQV:MIVEE, VPQAL:RSVK-AA[17]-AKV:KEVQV:MIVRS, VSQDL:RSVK-AA[17]-AKV:KEVQV:MIVKS, VPQDL:RSVK-AA[17]-AKV:KEVQV:MVVKS, VPTEE:RSVK-AA[17]-AKV:KEVQV:FLQHN, VPTGQ:RSVK-AA[17]-AKV:KEVQV:LEEHS, TQVQL:RSVK-AA[17]-AKV:KEVQV:TLEDH, TQVEL:RPVQ-AA[17]-RKI:KKATV:DMEDH, TQVKM:RPVQ-AA[17]-RKI:KKATV:NMEDH, TQVEL:RPVQ-AA[17]-

RKI:KKATV:EMEDH, TQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDH, TQVQL:RPVQ-AA[17]-RKI:KKATV:NMEDH, TQVKL:RPVQ-AA[17]-RKI:KKATV:EGMSEDH, TQVKL:RPVQ-AA[17]-RKI:KKATV:GMEDH, TQVKM:RPVQ-AA[17]-RKI:KKATV:GMEDH, TQVRL:RPVQ-AA[17]-RKI:KKATV:DMEDH, TQVKT:RPVQ-AA[17]-RKI:KKATV:MIEDH, TQVAL:RPVQ-AA[17]-RKI:KKATV:MIEDH, TQVDL:RPVQ-AA[17]-RKI:KKATV:MIEDH, TQVDL:RPVQ-AA[17]-RKI:KKATV:MVEDH, TQVEE:RPVQ-AA[17]-RKI:KKATV:FLEDH, TQVGQ:RPVQ-AA[17]-RKI:KKATV:LEEDH, TQVHH:RPVQ-AA[17]-RKI:KKATV:RLEDH, VPTEL:RPVQ-AA[17]-RKI:KKATV:DMVVE, VPEKM:RPVQ-AA[17]-RKI:KKATV:NMTVE, VPTEL:RPVQ-AA[17]-RKI:KKATV:EMVVE, APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVR, APTQL:RPVQ-AA[17]-RKI:KKATV:NMVVR, APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVK, VPTKL:RPVQ-AA[17]-RKI:KKATV:EGMSVAE, VPTKL:RPVQ-AA[17]-RKI:KKATV:GMAVS, TPTKM:RPVQ-AA[17]-RKI:KKATV:GMVVD, VPARL:RPVQ-AA[17]-RKI:KKATV:DMVVE, VPTRL:RPVQ-AA[17]-RKI:KKATV:DMVVE, APVKT:RPVQ-AA[17]-RKI:KKATV:MIVEE, VPQAL:RPVQ-AA[17]-RKI:KKATV:MIVRS, VSQDL:RPVQ-AA[17]-RKI:KKATV:MIVKS, VPQDL:RPVQ-AA[17]-RKI:KKATV:MVVKS, VPTEE:RPVQ-AA[17]-RKI:KKATV:FLQHN, VPTGQ:RPVQ-AA[17]-RKI:KKATV:LEEHS and SRVHH:RPVQ-AA[17]-RKI:KKATV:RLEEH; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T). More particularly, the quadruplet PEP5:PEP12:PEP2:PEP6 is selected from the group consisting of VPTKM:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVVE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:GMVVE, VPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVE, VPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVE, VPTKT:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTAL:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTDL:SAIS-AA[17]-LYL:LKNYQ:MIVVE, VPTDL:SAIS-AA[17]-LYL:LKNYQ:MVVVE, VPEKM:SAIS-AA[17]-LYL:LKNYQ:NMTVE, APTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVR, APTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVR, APTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVK, VPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVAE, VPTKL:SAIS-AA[17]-LYL:LKNYQ:GMAVS, TPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVD, VPARL:SAIS-AA[17]-LYL:LKNYQ:DMVVE, APVKT:SAIS-AA[17]-LYL:LKNYQ:MIVEE, VPQAL:SAIS-AA[17]-LYL:LKNYQ:MIVRS, VSQDL:SAIS-AA[17]-LYL:LKNYQ:MIVKS, VPQDL:SAIS-AA[17]-LYL:LKNYQ:MVVKS, VPTEE:SAIS-AA[17]-LYL:LKNYQ:FLQHN, VPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEEHS, SRVHH:SAIS-AA[17]-LYL:LKNYQ:RLEEH, TQVQL:SAIS-AA[17]-LYL:LKNYQ:TLEDH, VPEEL:SSLS-AA[17]-LFF:LKVYP:DMTVE, VPEEL:SSLS-AA[17]-LFF:LKVYP:EMTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE, VPEQL:SSLS-AA[17]-LFF:LKVYP:NMTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:EGMSTVE, VPEKL:SSLS-AA[17]-LFF:LKVYP:GMTVE, VPEKM:SSLS-AA[17]-LFF:LKVYP:GMTVE, VPERL:SSLS-AA[17]-LFF:LKVYP:DMTVE, VPEKT:SSLS-AA[17]-LFF:LKVYP:MITVE, VPEAL:SSLS-AA[17]-LFF:LKVYP:MITVE, VPEDL:SSLS-AA[17]-LFF:LKVYP:MITVE, VPEDL:SSLS-AA[17]-LFF:LKVYP:MVTVE, VPTEL:SSLS-AA[17]-LFF:LKVYP:DMVVE, VPTEL:SSLS-AA[17]-LFF:LKVYP:EMVVE, APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVR, APTQL:SSLS-AA[17]-LFF:LKVYP:NMVVR, APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVK, VPTKL:SSLS-AA[17]-LFF:LKVYP:EGMSVAE, VPTKL:SSLS-AA[17]-LFF:LKVYP:GMAVS, TPTKM:SSLS-AA[17]-LFF:LKVYP:GMVVD, VPARL:SSLS-AA[17]-LFF:LKVYP:DMVVE, VPTRL:SSLS-AA[17]-LFF:LKVYP:DMVVE, APVKT:SSLS-AA[17]-LFF:LKVYP:MIVEE, VPQAL:SSLS-AA[17]-LFF:LKVYP:MIVRS, VSQDL:SSLS-AA[17]-LFF:LKVYP:MIVKS, VPQDL:SSLS-AA[17]-LFF:LKVYP:MVVKS, VPTEE:SSLS-AA[17]-LFF:LKVYP:FLQHN, VPTGQ:SSLS-AA[17]-LFF:LKVYP:LEEHS, SRVHH:SSLS-AA[17]-LFF:LKVYP:RLEEH, TQVQL:SSLS-AA[17]-LFF:LKVYP:TLEDH, APTEL:NAIS-AA[17]-LYF:LKKYR:DMVVR, APTKM:NAIS-AA[17]-LYF:LKKYR:NMVVR, APTEL:NAIS-AA[17]-LYF:LKKYR:EMVVR, APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR, APTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVVR, APTKL:NAIS-AA[17]-

LYF:LKKYR:GMVVR, APTKM:NAIS-AA[17]-LYF:LKKYR:GMVVR, APTRL:NAIS-AA[17]-LYF:LKKYR:DMVVR, APTKT:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTAL:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTDL:NAIS-AA[17]-LYF:LKKYR:MIVVR, APTDL:NAIS-AA[17]-LYF:LKKYR:MVVVR, VPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVE, VPEKM:NAIS-AA[17]-LYF:LKKYR:NMTVE, VPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVE, APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVK, VPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVAE, VPTKL:NAIS-AA[17]-LYF:LKKYR:GMAVS, TPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVD, VPARL:NAIS-AA[17]-LYF:LKKYR:DMVVE, VPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVE, APVKT:NAIS-AA[17]-LYF:LKKYR:MIVEE, VPQAL:NAIS-AA[17]-LYF:LKKYR:MIVRS, VSQDL:NAIS-AA[17]-LYF:LKKYR:MIVKS, VPQDL:NAIS-AA[17]-LYF:LKKYR:MVVKS, VPTEE:NAIS-AA[17]-LYF:LKKYR:FLQHN, VPTGQ:NAIS-AA[17]-LYF:LKKYR:LEEHS, SRVHH:NAIS-AA[17]-LYF:LKKYR:RLEEH, TQVQL:NAIS-AA[17]-LYF:LKKYR:TLEDH, APTEL:SATS-AA[17]-LYY:LRKHR:DMVVK, APTKM:SATS-AA[17]-LYY:LRKHR:NMVVK, APTEL:SATS-AA[17]-LYY:LRKHR:EMVVK, APTKL:SATS-AA[17]-LYY:LRKHR:NMVVK, APTQL:SATS-AA[17]-LYY:LRKHR:NMVVK, APTKL:SATS-AA[17]-LYY:LRKHR:EGMSVVK, APTKL:SATS-AA[17]-LYY:LRKHR:GMVVK, APTKM:SATS-AA[17]-LYY:LRKHR:GMVVK, APTRL:SATS-AA[17]-LYY:LRKHR:DMVVK, APTKT:SATS-AA[17]-LYY:LRKHR:MIVVK, APTAL:SATS-AA[17]-LYY:LRKHR:MIVVK, APTDL:SATS-AA[17]-LYY:LRKHR:MIVVK, APTDL:SATS-AA[17]-LYY:LRKHR:MVVVK, VPTEL:SATS-AA[17]-LYY:LRKHR:DMVVE, VPEKM:SATS-AA[17]-LYY:LRKHR:NMTVE, VPTEL:SATS-AA[17]-LYY:LRKHR:EMVVE, APTKL:SATS-AA[17]-LYY:LRKHR:NMVVR, APTQL:SATS-AA[17]-LYY:LRKHR:NMVVR, VPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVAE, VPTKL:SATS-AA[17]-LYY:LRKHR:GMAVS, TPTKM:SATS-AA[17]-LYY:LRKHR:GMVVD, VPARL:SATS-AA[17]-LYY:LRKHR:DMVVE, VPTRL:SATS-AA[17]-LYY:LRKHR:DMVVE, APVKT:SATS-AA[17]-LYY:LRKHR:MIVEE, VPQAL:SATS-AA[17]-LYY:LRKHR:MIVRS, VSQDL:SATS-AA[17]-LYY:LRKHR:MIVKS, VPQDL:SATS-AA[17]-LYY:LRKHR:MVVKS, VPTEE:SATS-AA[17]-LYY:LRKHR:FLQHN, VPTGQ:SATS-AA[17]-LYY:LRKHR:LEEHS, SRVHH:SATS-AA[17]-LYY:LRKHR:RLEEH, TQVQL:SATS-AA[17]-LYY:LRKHR:TLEDH, VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVAE, VPTKM:SPIS-AA[17]-LYK:LKYHY:NMVAE, VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVAE, VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE, VPTQL:SPIS-AA[17]-LYK:LKYHY:NMVAE, VPTKL:SPIS-AA[17]-LYK:LKYHY:GMVAE, VPTKM:SPIS-AA[17]-LYK:LKYHY:GMVAE, VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAE, VPTKT:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTAL:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTDL:SPIS-AA[17]-LYK:LKYHY:MIVAE, VPTDL:SPIS-AA[17]-LYK:LKYHY:MVVAE, VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVVE, VPEKM:SPIS-AA[17]-LYK:LKYHY:NMTVE, VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVVE, APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVR, APTQL:SPIS-AA[17]-LYK:LKYHY:NMVVR, APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVK, VPTKL:SPIS-AA[17]-LYK:LKYHY:GMAVS, TPTKM:SPIS-AA[17]-LYK:LKYHY:GMVVD, VPARL:SPIS-AA[17]-LYK:LKYHY:DMVVE, VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVVE, APVKT:SPIS-AA[17]-LYK:LKYHY:MIVEE, VPQAL:SPIS-AA[17]-LYK:LKYHY:MIVRS, VSQDL:SPIS-AA[17]-LYK:LKYHY:MIVKS, VPQDL:SPIS-AA[17]-LYK:LKYHY:MVVKS, VPTEE:SPIS-AA[17]-LYK:LKYHY:FLQHN, VPTGQ:SPIS-AA[17]-LYK:LKYHY:LEEHS, SRVHH:SPIS-AA[17]-LYK:LKYHY:RLEEH, TQVQL:SPIS-AA[17]-LYK:LKYHY:TLEDH, VPTEL:EPIS-AA[17]-LYL:KFKYE:DMAVS, VPTKM:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTEL:EPIS-AA[17]-LYL:KFKYE:EMAVS, VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTQL:EPIS-AA[17]-LYL:KFKYE:NMAVS, VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSAVS, VPTKM:EPIS-AA[17]-LYL:KFKYE:GMAVS, VPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVS, VPTKT:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTAL:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTDL:EPIS-AA[17]-LYL:KFKYE:MIAVS, VPTDL:EPIS-AA[17]-LYL:KFKYE:MVAVS, VPTEL:EPIS-AA[17]-LYL:KFKYE:DMVVE, VPEKM:EPIS-AA[17]-LYL:KFKYE:NMTVE, VPTEL:EPIS-AA[17]-LYL:KFKYE:EMVVE,

APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVR, APTQL:EPIS-AA[17]-LYL:KFKYE:NMVVR, APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVK, VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSVAE, TPTKM:EPIS-AA[17]-LYL:KFKYE:GMVVD, VPARL:EPIS-AA[17]-LYL:KFKYE:DMVVE, VPTRL:EPIS-AA[17]-LYL:KFKYE:DMVVE, APVKT:EPIS-AA[17]-LYL:KFKYE:MIVEE, VPQAL:EPIS-AA[17]-LYL:KFKYE:MIVRS, VSQDL:EPIS-AA[17]-LYL:KFKYE:MIVKS, VPQDL:EPIS-AA[17]-LYL:KFKYE:MVVKS, VPTEE:EPIS-AA[17]-LYL:KFKYE:FLQHN, VPTGQ:EPIS-AA[17]-LYL:KFKYE:LEEHS, SRVHH:EPIS-AA[17]-LYL:KFKYE:RLEEH, TQVQL:EPIS-AA[17]-LYL:KFKYE:TLEDH, TPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVD, TPTKM:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVVD, TPTKL:SPIN-AA[17]-LYF:YGKIP:GMVVD, TPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVD, TPTKT:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTAL:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTDL:SPIN-AA[17]-LYF:YGKIP:MIVVD, TPTDL:SPIN-AA[17]-LYF:YGKIP:MVVVD, VPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVE, VPEKM:SPIN-AA[17]-LYF:YGKIP:NMTVE, VPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVE, APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVR, APTQL:SPIN-AA[17]-LYF:YGKIP:NMVVR, APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVK, VPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVAE, VPTKL:SPIN-AA[17]-LYF:YGKIP:GMAVS, VPARL:SPIN-AA[17]-LYF:YGKIP:DMVVE, VPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVE, APVKT:SPIN-AA[17]-LYF:YGKIP:MIVEE, VPQAL:SPIN-AA[17]-LYF:YGKIP:MIVRS, VSQDL:SPIN-AA[17]-LYF:YGKIP:MIVKS, VPQDL:SPIN-AA[17]-LYF:YGKIP:MVVKS, VPTEE:SPIN-AA[17]-LYF:YGKIP:FLQHN, VPTGQ:SPIN-AA[17]-LYF:YGKIP:LEEHS, SRVHH:SPIN-AA[17]-LYF:YGKIP:RLEEH, TQVQL:SPIN-AA[17]-LYF:YGKIP:TLEDH, VPAEL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPAKM:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAEL:SPIS-AA[17]-LYI:YKQYE:EMVVE, VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAQL:SPIS-AA[17]-LYI:YKQYE:NMVVE, VPAKL:SPIS-AA[17]-LYI:YKQYE:EGMSVVE, VPAKL:SPIS-AA[17]-LYI:YKQYE:GMVVE, VPAKM:SPIS-AA[17]-LYI:YKQYE:GMVVE, VPARL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPAKT:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPAAL:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPADL:SPIS-AA[17]-LYI:YKQYE:MIVVE, VPADL:SPIS-AA[17]-LYI:YKQYE:MVVVE, VPTEL:SPIS-AA[17]-LYI:YKQYE:DMVVE, VPEKM:SPIS-AA[17]-LYI:YKQYE:NMTVE, VPTEL:SPIS-AA[17]-LYI:YKQYE:EMVVE, APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVR, APTQL:SPIS-AA[17]-LYI:YKQYE:NMVVR, APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVK, VPTKL:SPIS-AA[17]-LYI:YKQYE:EGMSVAE, VPTKL:SPIS-AA[17]-LYI:YKQYE:GMAVS, TPTKM:SPIS-AA[17]-LYI:YKQYE:GMVVD, VPTRL:SPIS-AA[17]-LYI:YKQYE:DMVVE, APVKT:SPIS-AA[17]-LYI:YKQYE:MIVEE, VPQAL:SPIS-AA[17]-LYI:YKQYE:MIVRS, VSQDL:SPIS-AA[17]-LYI:YKQYE:MIVKS, VPQDL:SPIS-AA[17]-LYI:YKQYE:MVVKS, VPTEE:SPIS-AA[17]-LYI:YKQYE:FLQHN, VPTGQ:SPIS-AA[17]-LYI:YKQYE:LEEHS, SRVHH:SPIS-AA[17]-LYI:YKQYE:RLEEH, TQVQL:SPIS-AA[17]-LYI:YKQYE:TLEDH, VPTEL:SPIS-AA[17]-LFI:YKQYE:DMVVE, VPTKM:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTEL:SPIS-AA[17]-LFI:YKQYE:EMVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVVE, VPTKL:SPIS-AA[17]-LFI:YKQYE:GMVVE, VPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVE, VPTRL:SPIS-AA[17]-LFI:YKQYE:DMVVE, VPTKT:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTAL:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTDL:SPIS-AA[17]-LFI:YKQYE:MIVVE, VPTDL:SPIS-AA[17]-LFI:YKQYE:MVVVE, VPEKM:SPIS-AA[17]-LFI:YKQYE:NMTVE, APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVR, APTQL:SPIS-AA[17]-LFI:YKQYE:NMVVR, APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVK, VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVAE, VPTKL:SPIS-AA[17]-LFI:YKQYE:GMAVS, TPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVD, VPARL:SPIS-AA[17]-LFI:YKQYE:DMVVE, APVKT:SPIS-AA[17]-LFI:YKQYE:MIVEE, VPQAL:SPIS-AA[17]-LFI:YKQYE:MIVRS, VSQDL:SPIS-AA[17]-LFI:YKQYE:MIVKS, VPQDL:SPIS-AA[17]-LFI:YKQYE:MVVKS, VPTEE:SPIS-AA[17]-LFI:YKQYE:FLQHN, VPTGQ:SPIS-AA[17]-LFI:YKQYE:LEEHS,

SRVHH:SPIS-AA[17]-LFI:YKQYE:RLEEH, TQVQL:SPIS-AA[17]-LFI:YKQYE:TLEDH, APVEL:KPLS-AA[17]-LYV:DHHKD:DMVEE, APVKM:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVEL:KPLS-AA[17]-LYV:DHHKD:EMVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVQL:KPLS-AA[17]-LYV:DHHKD:NMVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:EGMSVEE, APVKL:KPLS-AA[17]-LYV:DHHKD:GMVEE, APVKM:KPLS-AA[17]-LYV:DHHKD:GMVEE, APVRL:KPLS-AA[17]-LYV:DHHKD:DMVEE, APVAL:KPLS-AA[17]-LYV:DHHKD:MIVEE, APVDL:KPLS-AA[17]-LYV:DHHKD:MIVEE, APVDL:KPLS-AA[17]-LYV:DHHKD:MVVEE, VPTEL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPEKM:KPLS-AA[17]-LYV:DHHKD:NMTVE, VPTEL:KPLS-AA[17]-LYV:DHHKD:EMVVE, APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVR, APTQL:KPLS-AA[17]-LYV:DHHKD:NMVVR, APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVK, VPTKL:KPLS-AA[17]-LYV:DHHKD:EGMSVAE, VPTKL:KPLS-AA[17]-LYV:DHHKD:GMAVS, TPTKM:KPLS-AA[17]-LYV:DHHKD:GMVVD, VPARL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPTRL:KPLS-AA[17]-LYV:DHHKD:DMVVE, VPQAL:KPLS-AA[17]-LYV:DHHKD:MIVRS, VSQDL:KPLS-AA[17]-LYV:DHHKD:MIVKS, VPQDL:KPLS-AA[17]-LYV:DHHKD:MVVKS, VPTEE:KPLS-AA[17]-LYV:DHHKD:FLQHN, VPTGQ:KPLS-AA[17]-LYV:DHHKD:LEEHS, SRVHH:KPLS-AA[17]-LYV:DHHKD:RLEEH, TQVQL:KPLS-AA[17]-LYV:DHHKD:TLEDH, VPQEL:EPLP-AA[17]-VYY:EQLSN:DMVRS, VPQKM:EPLP-AA[17]-VYY:EQLSN:NMVRS, VPQEL:EPLP-AA[17]-VYY:EQLSN:EMVRS, VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS, VPQQL:EPLP-AA[17]-VYY:EQLSN:NMVRS, VPQKL:EPLP-AA[17]-VYY:EQLSN:EGMSVRS, VPQKL:EPLP-AA[17]-VYY:EQLSN:GMVRS, VPQKM:EPLP-AA[17]-VYY:EQLSN:GMVRS, VPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRS, VPQKT:EPLP-AA[17]-VYY:EQLSN:MIVRS, VPQDL:EPLP-AA[17]-VYY:EQLSN:MIVRS, VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVRS, VPTEL:EPLP-AA[17]-VYY:EQLSN:DMVVE, VPEKM:EPLP-AA[17]-VYY:EQLSN:NMTVE, VPTEL:EPLP-AA[17]-VYY:EQLSN:EMVVE, APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVR, APTQL:EPLP-AA[17]-VYY:EQLSN:NMVVR, APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVK, VPTKL:EPLP-AA[17]-VYY:EQLSN:EGMSVAE, VPTKL:EPLP-AA[17]-VYY:EQLSN:GMAVS, TPTKM:EPLP-AA[17]-VYY:EQLSN:GMVVD, VPARL:EPLP-AA[17]-VYY:EQLSN:DMVVE, VPTRL:EPLP-AA[17]-VYY:EQLSN:DMVVE, APVKT:EPLP-AA[17]-VYY:EQLSN:MIVEE, VSQDL:EPLP-AA[17]-VYY:EQLSN:MIVKS, VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVKS, VPTEE:EPLP-AA[17]-VYY:EQLSN:FLQHN, VPTGQ:EPLP-AA[17]-VYY:EQLSN:LEEHS, SRVHH:EPLP-AA[17]-VYY:EQLSN:RLEEH, TQVQL:EPLP-AA[17]-VYY:EQLSN:TLEDH, VSQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VSQKM:EPLT-AA[17]-LYY:EQLSN:NMVKS, VSQEL:EPLT-AA[17]-LYY:EQLSN:EMVKS, VSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VSQQL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VSQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKS, VSQKL:EPLT-AA[17]-LYY:EQLSN:GMVKS, VSQKM:EPLT-AA[17]-LYY:EQLSN:GMVKS, VSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VSQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS, VSQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VSQDL:EPLT-AA[17]-LYY:EQLSN:MVVKS, VPTEL:EPLT-AA[17]-LYY:EQLSN:DMVVE, VPEKM:EPLT-AA[17]-LYY:EQLSN:NMTVE, VPTEL:EPLT-AA[17]-LYY:EQLSN:EMVVE, APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVR, APTQL:EPLT-AA[17]-LYY:EQLSN:NMVVR, APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVK, VPTKL:EPLT-AA[17]-LYY:EQLSN:EGMSVAE, VPTKL:EPLT-AA[17]-LYY:EQLSN:GMAVS, TPTKM:EPLT-AA[17]-LYY:EQLSN:GMVVD, VPARL:EPLT-AA[17]-LYY:EQLSN:DMVVE, VPTRL:EPLT-AA[17]-LYY:EQLSN:DMVVE, APVKT:EPLT-AA[17]-LYY:EQLSN:MIVEE, VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVRS, VPTEE:EPLT-AA[17]-LYY:EQLSN:FLQHN, VPTGQ:EPLT-AA[17]-LYY:EQLSN:LEEHS, SRVHH:EPLT-AA[17]-

LYY:EQLSN:RLEEH, TQVQL:EPLT-AA[17]-LYY:EQLSN:TLEDH, VPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKS, VPQEL:EPLT-AA[17]-LYY:EQLSN:EMVKS, VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VPQQL:EPLT-AA[17]-LYY:EQLSN:NMVKS, VPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKS, VPQKL:EPLT-AA[17]-LYY:EQLSN:GMVKS, VPQKM:EPLT-AA[17]-LYY:EQLSN:GMVKS, VPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS, VPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPQDL:EPLT-AA[17]-LYY:EQLSN:MIVKS, VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEQHN, VPTEL:SNIT-AA[17]-QIM:IGEMS:DMVVE, VPEKM:SNIT-AA[17]-QIM:IGEMS:NMTVE, VPTEL:SNIT-AA[17]-QIM:IGEMS:EMVVE, APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVR, APTQL:SNIT-AA[17]-QIM:IGEMS:NMVVR, APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVK, VPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSVAE, VPTKL:SNIT-AA[17]-QIM:IGEMS:GMAVS, TPTKM:SNIT-AA[17]-QIM:IGEMS:GMVVD, VPARL:SNIT-AA[17]-QIM:IGEMS:DMVVE, VPTRL:SNIT-AA[17]-QIM:IGEMS:DMVVE, APVKT:SNIT-AA[17]-QIM:IGEMS:MIVEE, VPQAL:SNIT-AA[17]-QIM:IGEMS:MIVRS, VSQDL:SNIT-AA[17]-QIM:IGEMS:MIVKS, VPQDL:SNIT-AA[17]-QIM:IGEMS:MVVKS, VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEEHS, SRVHH:SNIT-AA[17]-QIM:IGEMS:RLEEH, TQVQL:SNIT-AA[17]-QIM:IGEMS:TLEDH, VPTEE:SNIT-AA[17]-QIM:LGEMS:FLEHS, VPTEL:SNIT-AA[17]-QIM:LGEMS:DMVVE, VPEKM:SNIT-AA[17]-QIM:LGEMS:NMTVE, VPTEL:SNIT-AA[17]-QIM:LGEMS:EMVVE, APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVR, APTQL:SNIT-AA[17]-QIM:LGEMS:NMVVR, APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVK, VPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSVAE, VPTKL:SNIT-AA[17]-QIM:LGEMS:GMAVS, TPTKM:SNIT-AA[17]-QIM:LGEMS:GMVVD, VPARL:SNIT-AA[17]-QIM:LGEMS:DMVVE, VPTRL:SNIT-AA[17]-QIM:LGEMS:DMVVE, APVKT:SNIT-AA[17]-QIM:LGEMS:MIVEE, VPQAL:SNIT-AA[17]-QIM:LGEMS:MIVRS, VSQDL:SNIT-AA[17]-QIM:LGEMS:MIVKS, VPQDL:SNIT-AA[17]-QIM:LGEMS:MVVKS, VPTEE:SNIT-AA[17]-QIM:LGEMS:FLQHN, SRVHH:SNIT-AA[17]-QIM:LGEMS:RLEEH, TQVQL:SNIT-AA[17]-QIM:LGEMS:TLEDH, SRVQL:RSVK-AA[17]-AKV:KEVQV:TLEEH, VPTEL:RSVK-AA[17]-AKV:KEVQV:DMVVE, VPEKM:RSVK-AA[17]-AKV:KEVQV:NMTVE, VPTEL:RSVK-AA[17]-AKV:KEVQV:EMVVE, APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVR, APTQL:RSVK-AA[17]-AKV:KEVQV:NMVVR, APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVK, VPTKL:RSVK-AA[17]-AKV:KEVQV:EGMSVAE, VPTKL:RSVK-AA[17]-AKV:KEVQV:GMAVS, TPTKM:RSVK-AA[17]-AKV:KEVQV:GMVVD, VPARL:RSVK-AA[17]-AKV:KEVQV:DMVVE, VPTRL:RSVK-AA[17]-AKV:KEVQV:DMVVE, APVKT:RSVK-AA[17]-AKV:KEVQV:MIVEE, VPQAL:RSVK-AA[17]-AKV:KEVQV:MIVRS, VSQDL:RSVK-AA[17]-AKV:KEVQV:MIVKS, VPQDL:RSVK-AA[17]-AKV:KEVQV:MVVKS, VPTEE:RSVK-AA[17]-AKV:KEVQV:FLQHN, VPTGQ:RSVK-AA[17]-AKV:KEVQV:LEEHS, TQVQL:RSVK-AA[17]-AKV:KEVQV:TLEDH, TQVHH:RPVQ-AA[17]-RKI:KKATV:RLEDH, VPTEL:RPVQ-AA[17]-RKI:KKATV:DMVVE, VPEKM:RPVQ-AA[17]-RKI:KKATV:NMTVE, VPTEL:RPVQ-AA[17]-RKI:KKATV:EMVVE, APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVR, APTQL:RPVQ-AA[17]-RKI:KKATV:NMVVR, APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVK, VPTKL:RPVQ-AA[17]-RKI:KKATV:EGMSVAE, VPTKL:RPVQ-AA[17]-RKI:KKATV:GMAVS, TPTKM:RPVQ-AA[17]-RKI:KKATV:GMVVD, VPARL:RPVQ-AA[17]-RKI:KKATV:DMVVE, VPTRL:RPVQ-AA[17]-RKI:KKATV:DMVVE, APVKT:RPVQ-AA[17]-RKI:KKATV:MIVEE, VPQAL:RPVQ-AA[17]-RKI:KKATV:MIVRS, VSQDL:RPVQ-AA[17]-RKI:KKATV:MIVKS, VPQDL:RPVQ-AA[17]-RKI:KKATV:MVVKS, VPTEE:RPVQ-AA[17]-RKI:KKATV:FLQHN, VPTGQ:RPVQ-AA[17]-RKI:KKATV:LEEHS and SRVHH:RPVQ-AA[17]-RKI:KKATV:RLEEH; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the quadruplet PEP9:PEP1:PEP2:PEP10 is selected from the group consisting of GIPEPXXVPTKM:SAIS:LKNYQ:NMVVESXAXR, SIPKAXXVPTEL:SAIS:LKNYQ:EMVVEGXGXR, HVTKPTXVPTKL:SAIS:LKNYQ:NMVVESXGXH, YVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, TVPKPXXVPTQL:SAIS:LKNYQ:NMVVEAXGXH, AVPKAXXVPTKL:SAIS:LKNYQ:NMVVEAXGXH, KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVVEXGXR, KASKAXXVPTKL:SAIS:LKNYQ:GMVVEEXGXR, GSAGPXXVPTKM:SAIS:LKNYQ:GMVVERXGXS, AAPASXXVPTRL:SAIS:LKNYQ:DMVVEAXGXR, STPPTXXVPTRL:SAIS:LKNYQ:DMVVESXGXR, HVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, RVPSTXXVPTKT:SAIS:LKNYQ:MIVVEXGXL, ASAAPXXVPTAL:SAIS:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS:LKNYQ:MVVVEXKXS, NDEGLEXVPTEE:SAIS:LKNYQ:FLVVEKXEXR, NDEGLEXVPTGQ:SAIS:LKNYQ:LEVVEQXEXR, SSVKXQPVPTHH:SAIS:LKNYQ:RLVVELEXAXA, RNVQXRPVPTQL:SAIS:LKNYQ:TLVVELAXKXE, GIPEPXXVPEKM:SAIS:LKNYQ:NMTVESXAXR, HVTKPTXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, YVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, TVPKPXXAPTQL:SAIS:LKNYQ:NMVVRAXGXH, AVPKAXXAPTKL:SAIS:LKNYQ:NMVVKAXGXH, KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVAEXGXR, KASKAXXVPTKL:SAIS:LKNYQ:GMAVSEXGXR, GSAGPXXTPTKM:SAIS:LKNYQ:GMVVDRXGXS, AAPASXXVPARL:SAIS:LKNYQ:DMVVEAXGXR, HVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, RVPSTXXAPVKT:SAIS:LKNYQ:MIVEEXGXL, ASAAPXXVPQAL:SAIS:LKNYQ:MIVRSXKXS, ASASPXXVSQDL:SAIS:LKNYQ:MIVKSXKXS, ASASPXXVPQDL:SAIS:LKNYQ:MVVKSXKXS, NDEGLEXVPTEE:SAIS:LKNYQ:FLQHNKXEXR, NDEGLEXVPTGQ:SAIS:LKNYQ:LEEHSQXEXR, SSVKXQPSRVHH:SAIS:LKNYQ:RLEEHLEXAXA, RNVQXRPTQVQL:SAIS:LKNYQ:TLEDHLAXKXE, KIPKAXXVPEEL:SSLS:LKVYP:DMTVEGXGXR, SIPKAXXVPEEL:SSLS:LKVYP:EMTVEGXGXR, HVTKPTXVPEKL:SSLS:LKVYP:NMTVESXGXH, YVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH, TVPKPXXVPEQL:SSLS:LKVYP:NMTVEAXGXH, AVPKAXXVPEKL:SSLS:LKVYP:NMTVEAXGXH, KVGKAXXVPEKL:SSLS:LKVYP:EGMSTVEXGXR, KASKAXXVPEKL:SSLS:LKVYP:GMTVEEXGXR, GSAGPXXVPEKM:SSLS:LKVYP:GMTVERXGXS, AAPASXXVPERL:SSLS:LKVYP:DMTVEAXGXR, STPPTXXVPERL:SSLS:LKVYP:DMTVESXGXR, HVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH, RVPSTXXVPEKT:SSLS:LKVYP:MITVEXGXL, ASAAPXXVPEAL:SSLS:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS:LKVYP:MVTVEXKXS, NDEGLEXVPEEE:SSLS:LKVYP:FLTVEKXEXR, NDEGLEXVPEGQ:SSLS:LKVYP:LETVEQXEXR, SSVKXQPVPEHH:SSLS:LKVYP:RLTVELEXAXA, RNVQXRPVPEQL:SSLS:LKVYP:TLTVELAXKXE, KIPKAXXVPTEL:SSLS:LKVYP:DMVVEGXGXR, SIPKAXXVPTEL:SSLS:LKVYP:EMVVEGXGXR, HVTKPTXAPTKL:SSLS:LKVYP:NMVVRSXGXH, YVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH, TVPKPXXAPTQL:SSLS:LKVYP:NMVVRAXGXH, AVPKAXXAPTKL:SSLS:LKVYP:NMVVKAXGXH, KVGKAXXVPTKL:SSLS:LKVYP:EGMSVAEXGXR, KASKAXXVPTKL:SSLS:LKVYP:GMAVSEXGXR, GSAGPXXTPTKM:SSLS:LKVYP:GMVVDRXGXS, AAPASXXVPARL:SSLS:LKVYP:DMVVEAXGXR, STPPTXXVPTRL:SSLS:LKVYP:DMVVESXGXR, HVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH, RVPSTXXAPVKT:SSLS:LKVYP:MIVEEXGXL, ASAAPXXVPQAL:SSLS:LKVYP:MIVRSXKXS, ASASPXXVSQDL:SSLS:LKVYP:MIVKSXKXS, ASASPXXVPQDL:SSLS:LKVYP:MVVKSXKXS, NDEGLEXVPTEE:SSLS:LKVYP:FLQHNKXEXR, NDEGLEXVPTGQ:SSLS:LKVYP:LEEHSQXEXR, SSVKXQPSRVHH:SSLS:LKVYP:RLEEHLEXAXA, RNVQXRPTQVQL:SSLS:LKVYP:TLEDHLAXKXE, KIPKAXXVPTEL:SAIS:LKNYQ:DMVVEGXGXR, KIPKAXXAPTEL:NAIS:LKKYR:DMVVRGXGXR, GIPEPXXAPTKM:NAIS:LKKYR:NMVVRSXAXR,

SIPKAXXAPTEL:NAIS:LKKYR:EMVVRGXGXR,
TVPKPXXAPTQL:NAIS:LKKYR:NMVVRAXGXH,
KVGKAXXAPTKL:NAIS:LKKYR:EGMSVVRXGXR,
GSAGPXXAPTKM:NAIS:LKKYR:GMVVRRXGXS,
STPPTXXAPTRL:NAIS:LKKYR:DMVVRSXGXR,
RVPSTXXAPTKT:NAIS:LKKYR:MIVVRXGXL,
ASASPXXAPTDL:NAIS:LKKYR:MIVVRXKXS,
NDEGLESAPTEE:NAIS:LKKYR:FLVVRKXEXR,
SSVKXQPAPTHH:NAIS:LKKYR:RLVVRLEXAXA,
KIPKAXXVPTEL:NAIS:LKKYR:DMVVEGXGXR,
SIPKAXXVPTEL:NAIS:LKKYR:EMVVEGXGXR,
KVGKAXXVPTKL:NAIS:LKKYR:EGMSVAEXGXR,
GSAGPXXTPTKM:NAIS:LKKYR:GMVVDRXGXS,
STPPTXXVPTRL:NAIS:LKKYR:DMVVESXGXR,
ASAAPXXVPQAL:NAIS:LKKYR:MIVRSXKXS,
ASASPXXVPQDL:NAIS:LKKYR:MVVKSXKXS,
NDEGLESAPTEE:SATS:LRKHR:FLVVKKXEXR,
SSVKXQPAPTHH:SATS:LRKHR:RLVVKLEXAXA,
KIPKAXXVPTEL:SATS:LRKHR:DMVVEGXGXR,
SIPKAXXVPTEL:SATS:LRKHR:EMVVEGXGXR,
YVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH,
KVGKAXXVPTKL:SATS:LRKHR:EGMSVAEXGXR,
GSAGPXXTPTKM:SATS:LRKHR:GMVVDRXGXS,
STPPTXXVPTRL:SATS:LRKHR:DMVVESXGXR,
RVPSTXXAPVKT:SATS:LRKHR:MIVEEXGXL,
ASASPXXVSQDL:SATS:LRKHR:MIVKSXKXS,
NDEGLEXVPTEE:SATS:LRKHR:FLQHNKXEXR,
SSVKXQPSRVHH:SATS:LRKHR:RLEEHLEXAXA,
KIPKAXXVPTEL:SPIS:LKYHY:DMVAEGXGXR,
SIPKAXXVPTEL:SPIS:LKYHY:EMVAEGXGXR,
YVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH,
AVPKAXXVPTKL:SPIS:LKYHY:NMVAEAXGXH,

YVPKPXXAPTKL:NAIS:LKKYR:NMVVRSXGXH,
AVPKAXXAPTKL:NAIS:LKKYR:NMVVRAXGXH,
KASKAXXAPTKL:NAIS:LKKYR:GMVVREXGXR,
AAPASXXAPTRL:NAIS:LKKYR:DMVVRAXGXR,
HVPKPXXAPTKL:NAIS:LKKYR:NMVVRSXGXH,
ASAAPXXAPTAL:NAIS:LKKYR:MIVVRXKXS,
ASASPXXAPTDL:NAIS:LKKYR:MVVVRXKXS,
NDEGLESAPTGQ:NAIS:LKKYR:LEVVRQXEXR,
RNVQXRPAPTQL:NAIS:LKKYR:TLVVRLAXKXE,
GIPEPXXVPEKM:NAIS:LKKYR:NMTVESXAXR,
AVPKAXXAPTKL:NAIS:LKKYR:NMVVKAXGXH,
KASKAXXVPTKL:NAIS:LKKYR:GMAVSEXGXR,
AAPASXXVPARL:NAIS:LKKYR:DMVVEAXGXR,
RVPSTXXAPVKT:NAIS:LKKYR:MIVEEXGXL,
ASASPXXVSQDL:NAIS:LKKYR:MIVKSXKXS,
NDEGLEXVPTEE:NAIS:LKKYR:FLQHNKXEXR,
NDEGLEXVPTGQ:NAIS:LKKYR:LEEHSQXEXR,
SSVKXQPSRVHH:NAIS:LKKYR:RLEEHLEXAXA,
HVTKPTXAPTKL:NAIS:LKKYR:NMVVRSXGXH,
GIPEPXXAPTKM:SATS:LRKHR:NMVVKSXAXR,
HVTKPTXAPTKL:SATS:LRKHR:NMVVKSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVKAXGXH,
KASKAXXAPTKL:SATS:LRKHR:GMVVKEXGXR,
AAPASXXAPTRL:SATS:LRKHR:DMVVKAXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVKSXGXH,
ASAAPXXAPTAL:SATS:LRKHR:MIVVKXKXS,
ASASPXXAPTDL:SATS:LRKHR:MVVVKXKXS,
NDEGLESAPTGQ:SATS:LRKHR:LEVVKQXEXR,
RNVQXRPAPTQL:SATS:LRKHR:TLVVKLAXKXE,
GIPEPXXVPEKM:SATS:LRKHR:NMTVESXAXR,
HVTKPTXAPTKL:SATS:LRKHR:NMVVRSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVRAXGXH,
KASKAXXVPTKL:SATS:LRKHR:GMAVSEXGXR,
AAPASXXVPARL:SATS:LRKHR:DMVVEAXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH,
ASAAPXXVPQAL:SATS:LRKHR:MIVRSXKXS,
ASASPXXVPQDL:SATS:LRKHR:MVVKSXKXS,
NDEGLEXVPTGQ:SATS:LRKHR:LEEHSQXEXR,
RNVQXRPTQVQL:SATS:LRKHR:TLEDHLAXKXE,
GIPEPXXVPTKM:SPIS:LKYHY:NMVAESXAXR,
HVTKPTXVPTKL:SPIS:LKYHY:NMVAESXGXH,
TVPKPXXVPTQL:SPIS:LKYHY:NMVAEAXGXH,
KASKAXXVPTKL:SPIS:LKYHY:GMVAEEXGXR,

GSAGPXXVPTKM:SPIS:LKYHY:GMVAERXGXS, AAPASXXVPTRL:SPIS:LKYHY:DMVAEAXGXR,
STPPTXXVPTRL:SPIS:LKYHY:DMVAESXGXR, HVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH,
RVPSTXXVPTKT:SPIS:LKYHY:MIVAEXGXL, ASAAPXXVPTAL:SPIS:LKYHY:MIVAEXKXS,
ASASPXXVPTDL:SPIS:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS:LKYHY:MVVAEXKXS,
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HVTKPTXAPTKL:SNIT:IGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT:IGEMS:NMVVRSXGXH,
TVPKPXXAPTQL:SNIT:IGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT:IGEMS:NMVVKAXGXH,
KVGKAXXVPTKL:SNIT:IGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT:IGEMS:GMAVSEXGXR,
GSAGPXXTPTKM:SNIT:IGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT:IGEMS:DMVVEAXGXR,
STPPTXXVPTRL:SNIT:IGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT:IGEMS:NMVVRSXGXH,
RVPSTXXAPVKT:SNIT:IGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT:IGEMS:MIVRSXKXS,
ASASPXXVSQDL:SNIT:IGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT:IGEMS:MVVKSXKXS,
NDEGLEXVPTGQ:SNIT:IGEMS:LEEHSQXEXR, SSVKXQPSRVHH:SNIT:IGEMS:RLEEHLEXAXA,
RNVQXRPTQVQL:SNIT:IGEMS:TLEDHLAXKXE, KIPKAXXVPTEL:SNIT:LGEMS:DMEHXGXGSR,
GIPEPXXVPTKM:SNIT:LGEMS:NMEHSSXAXR, SIPKAXXVPTEL:SNIT:LGEMS:EMEHXGXGSR,
HVTKPTXVPTKL:SNIT:LGEMS:NMEHSSXGXH, YVPKPXXVPTKL:SNIT:LGEMS:NMEHSSXGXH,
TVPKPXXVPTQL:SNIT:LGEMS:NMEHSAXGXH, AVPKAXXVPTKL:SNIT:LGEMS:NMEHSAXGXH,
KVGKAXXVPTKL:SNIT:LGEMS:EGMSEHSXGXR, KASKAXXVPTKL:SNIT:LGEMS:GMEHSEXGXR,
GSAGPXXVPTKM:SNIT:LGEMS:GMEHSRXGXS, AAPASXXVPTRL:SNIT:LGEMS:DMEHSAXGXR,
STPPTXXVPTRL:SNIT:LGEMS:DMEHSSXGXR, HVPKPXXVPTKL:SNIT:LGEMS:NMEHSSXGXH,
RVPSTXXVPTKT:SNIT:LGEMS:MIEHSXGXL, ASAAPXXVPTAL:SNIT:LGEMS:MIEHSXKXS,
ASASPXXVPTDL:SNIT:LGEMS:MIEHSXKXS, ASASPXXVPTDL:SNIT:LGEMS:MVEHSXKXS,
NDEGLEXVPTEE:SNIT:LGEMS:FLEHXKXESR, SSVKXQPVPTHH:SNIT:LGEMS:RLEHSLEXAXA,
RNVQXRPVPTQL:SNIT:LGEMS:TLEHSLAXKXE, KIPKAXXVPTEL:SNIT:LGEMS:DMVVEGXGXR,
GIPEPXXVPEKM:SNIT:LGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT:LGEMS:EMVVEGXGXR,
HVTKPTXAPTKL:SNIT:LGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT:LGEMS:NMVVRSXGXH,
TVPKPXXAPTQL:SNIT:LGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT:LGEMS:NMVVKAXGXH,
KVGKAXXVPTKL:SNIT:LGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT:LGEMS:GMAVSEXGXR,
GSAGPXXTPTKM:SNIT:LGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT:LGEMS:DMVVEAXGXR,
STPPTXXVPTRL:SNIT:LGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT:LGEMS:NMVVRSXGXH,
RVPSTXXAPVKT:SNIT:LGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT:LGEMS:MIVRSXKXS,
ASASPXXVSQDL:SNIT:LGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT:LGEMS:MVVKSXKXS,
NDEGLEXVPTEE:SNIT:LGEMS:FLQHNKXEXR, SSVKXQPSRVHH:SNIT:LGEMS:RLEEHLEXAXA,
RNVQXRPTQVQL:SNIT:LGEMS:TLEDHLAXKXE, KIPKASSSRVEL:RSVK:KEVQV:DMEEHGXGXR,
GIPEPSSSRVKM:RSVK:KEVQV:NMEEHSXAXR, SIPKASSSRVEL:RSVK:KEVQV:EMEEHGXGXR,
HVTKPTXSRVKL:RSVK:KEVQV:NMEEHSXGXH, YVPKPSSSRVKL:RSVK:KEVQV:NMEEHSXGXH,
TVPKPSSSRVQL:RSVK:KEVQV:NMEEHAXGXH, AVPKASSSRVKL:RSVK:KEVQV:NMEEHAXGXH,
KVGKASSSRVKL:RSVK:KEVQV:EGMSEEHXGXR, KASKASSSRVKL:RSVK:KEVQV:GMEEHEXGXR,
GSAGPSSSRVKM:RSVK:KEVQV:GMEEHRXGXS, AAPASSSSRVRL:RSVK:KEVQV:DMEEHAXGXR,
STPPTSSSRVRL:RSVK:KEVQV:DMEEHSXGXR, HVPKPSSSRVKL:RSVK:KEVQV:NMEEHSXGXH,
RVPSTSSSRVKT:RSVK:KEVQV:MIEEHXGXL, ASAAPSSSRVAL:RSVK:KEVQV:MIEEHXKXS,
ASASPSSSRVDL:RSVK:KEVQV:MIEEHXKXS, ASASPSSSRVDL:RSVK:KEVQV:MVEEHXKXS,
NDEGLESSRVEE:RSVK:KEVQV:FLEEHKXEXR, NDEGLESSRVGQ:RSVK:KEVQV:LEEEHQXEXR,
RNVQXRPSRVQL:RSVK:KEVQV:TLEEHLAXKXE, KIPKAXXVPTEL:RSVK:KEVQV:DMVVEGXGXR,
GIPEPXXVPEKM:RSVK:KEVQV:NMTVESXAXR, SIPKAXXVPTEL:RSVK:KEVQV:EMVVEGXGXR,
HVTKPTXAPTKL:RSVK:KEVQV:NMVVRSXGXH, YVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH,
TVPKPXXAPTQL:RSVK:KEVQV:NMVVRAXGXH, AVPKAXXAPTKL:RSVK:KEVQV:NMVVKAXGXH,

KVGKAXXVPTKL:RSVK:KEVQV:EGMSVAEXGXR, KASKAXXVPTKL:RSVK:KEVQV:GMAVSEXGXR,
GSAGPXXTPTKM:RSVK:KEVQV:GMVVDRXGXS, AAPASXXVPARL:RSVK:KEVQV:DMVVEAXGXR,
STPPTXXVPTRL:RSVK:KEVQV:DMVVESXGXR, HVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH,
RVPSTXXAPVKT:RSVK:KEVQV:MIVEEXGXL, ASAAPXXVPQAL:RSVK:KEVQV:MIVRSXKXS,
ASASPXXVSQDL:RSVK:KEVQV:MIVKSXKXS, ASASPXXVPQDL:RSVK:KEVQV:MVVKSXKXS,
NDEGLEXVPTEE:RSVK:KEVQV:FLQHNKXEXR, NDEGLEXVPTGQ:RSVK:KEVQV:LEEHSQXEXR,
RNVQXRPTQVQL:RSVK:KEVQV:TLEDHLAXKXE, KIPKASSTQVEL:RPVQ:KKATV:DMEDHGXGXR,
GIPEPSSTQVKM:RPVQ:KKATV:NMEDHSXAXR, SIPKASSTQVEL:RPVQ:KKATV:EMEDHGXGXR,
HVTKPTXTQVKL:RPVQ:KKATV:NMEDHSXGXH, YVPKPSSTQVKL:RPVQ:KKATV:NMEDHSXGXH,
TVPKPSSTQVQL:RPVQ:KKATV:NMEDHAXGXH, AVPKASSTQVKL:RPVQ:KKATV:NMEDHAXGXH,
KVGKASSTQVKL:RPVQ:KKATV:EGMSEDHXGXR, KASKASSTQVKL:RPVQ:KKATV:GMEDHEXGXR,
GSAGPSSTQVKM:RPVQ:KKATV:GMEDHRXGXS, AAPASSSTQVRL:RPVQ:KKATV:DMEDHAXGXR,
STPPTSSTQVRL:RPVQ:KKATV:DMEDHSXGXR, HVPKPSSTQVKL:RPVQ:KKATV:NMEDHSXGXH,
RVPSTSSTQVKT:RPVQ:KKATV:MIEDHXGXL, ASAAPSSTQVAL:RPVQ:KKATV:MIEDHXKXS,
ASASPSSTQVDL:RPVQ:KKATV:MIEDHXKXS, ASASPSSTQVDL:RPVQ:KKATV:MVEDHXKXS,
NDEGLESTQVEE:RPVQ:KKATV:FLEDHKXEXR, NDEGLESTQVGQ:RPVQ:KKATV:LEEDHQXEXR,
SSVKXQPTQVHH:RPVQ:KKATV:RLEDHLEXAXA, KIPKAXXVPTEL:RPVQ:KKATV:DMVVEGXGXR,
GIPEPXXVPEKM:RPVQ:KKATV:NMTVESXAXR, SIPKAXXVPTEL:RPVQ:KKATV:EMVVEGXGXR,
HVTKPTXAPTKL:RPVQ:KKATV:NMVVRSXGXH, YVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH,
TVPKPXXAPTQL:RPVQ:KKATV:NMVVRAXGXH, AVPKAXXAPTKL:RPVQ:KKATV:NMVVKAXGXH,
KVGKAXXVPTKL:RPVQ:KKATV:EGMSVAEXGXR, KASKAXXVPTKL:RPVQ:KKATV:GMAVSEXGXR,
GSAGPXXTPTKM:RPVQ:KKATV:GMVVDRXGXS, AAPASXXVPARL:RPVQ:KKATV:DMVVEAXGXR,
STPPTXXVPTRL:RPVQ:KKATV:DMVVESXGXR, HVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH,
RVPSTXXAPVKT:RPVQ:KKATV:MIVEEXGXL, ASAAPXXVPQAL:RPVQ:KKATV:MIVRSXKXS,
ASASPXXVSQDL:RPVQ:KKATV:MIVKSXKXS, ASASPXXVPQDL:RPVQ:KKATV:MVVKSXKXS,
NDEGLEXVPTEE:RPVQ:KKATV:FLQHNKXEXR, NDEGLEXVPTGQ:RPVQ:KKATV:LEEHSQXEXR and
SSVKXQPSRVHH:RPVQ:KKATV:RLEEHLEXAXA. More particularly, the quadruplet
PEP9:PEP1:PEP2:PEP10 is selected from the group consisting of
GIPEPXXVPTKM:SAIS:LKNYQ:NMVVESXAXR, HVTKPTXVPTKL:SAIS:LKNYQ:NMVVESXGXH,
YVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, TVPKPXXVPTQL:SAIS:LKNYQ:NMVVEAXGXH,
AVPKAXXVPTKL:SAIS:LKNYQ:NMVVEAXGXH, KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVVEXGXR,
KASKAXXVPTKL:SAIS:LKNYQ:GMVVEEXGXR, GSAGPXXVPTKM:SAIS:LKNYQ:GMVVERXGXS,
AAPASXXVPTRL:SAIS:LKNYQ:DMVVEAXGXR, STPPTXXVPTRL:SAIS:LKNYQ:DMVVESXGXR,
HVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, RVPSTXXVPTKT:SAIS:LKNYQ:MIVVEXGXL,
ASAAPXXVPTAL:SAIS:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS:LKNYQ:MIVVEXKXS,
ASASPXXVPTDL:SAIS:LKNYQ:MVVVEXKXS, GIPEPXXVPEKM:SAIS:LKNYQ:NMTVESXAXR,
HVTKPTXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, YVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH,
TVPKPXXAPTQL:SAIS:LKNYQ:NMVVRAXGXH, AVPKAXXAPTKL:SAIS:LKNYQ:NMVVKAXGXH,
KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVAEXGXR, KASKAXXVPTKL:SAIS:LKNYQ:GMAVSEXGXR,
GSAGPXXTPTKM:SAIS:LKNYQ:GMVVDRXGXS, AAPASXXVPARL:SAIS:LKNYQ:DMVVEAXGXR,
HVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, RVPSTXXAPVKT:SAIS:LKNYQ:MIVEEXGXL,
ASAAPXXVPQAL:SAIS:LKNYQ:MIVRSXKXS, ASASPSSVSQDL:SAIS:LKNYQ:MIVKSXKXS,

ASASPXXVPQDL:SAIS:LKNYQ:MVVKSXKXS,
NDEGLEXVPTEE:SAIS:LKNYQ:FLQHNKXEXR,
NDEGLEXVPTGQ:SAIS:LKNYQ:LEEHSQXEXR,
SSVKXQPSRVHH:SAIS:LKNYQ:RLEEHLEXAXA,
RNVQXRPTQVQL:SAIS:LKNYQ:TLEDHLAXKXE,
KIPKAXXVPEEL:SSLS:LKVYP:DMTVEGXGXR,
SIPKAXXVPEEL:SSLS:LKVYP:EMTVEGXGXR,
HVTKPTXVPEKL:SSLS:LKVYP:NMTVESXGXH,
YVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH,
TVPKPXXVPEQL:SSLS:LKVYP:NMTVEAXGXH,
AVPKAXXVPEKL:SSLS:LKVYP:NMTVEAXGXH,
KVGKAXXVPEKL:SSLS:LKVYP:EGMSTVEXGXR,
KASKAXXVPEKL:SSLS:LKVYP:GMTVEEXGXR,
GSAGPXXVPEKM:SSLS:LKVYP:GMTVERXGXS,
AAPASXXVPERL:SSLS:LKVYP:DMTVEAXGXR,
STPPTXXVPERL:SSLS:LKVYP:DMTVESXGXR,
HVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH,
RVPSTXXVPEKT:SSLS:LKVYP:MITVEXGXL,
ASAAPXXVPEAL:SSLS:LKVYP:MITVEXKXS,
ASASPXXVPEDL:SSLS:LKVYP:MITVEXKXS,
ASASPXXVPEDL:SSLS:LKVYP:MVTVEXKXS,
KIPKAXXVPTEL:SSLS:LKVYP:DMVVEGXGXR,
SIPKAXXVPTEL:SSLS:LKVYP:EMVVEGXGXR,
HVTKPTXAPTKL:SSLS:LKVYP:NMVVRSXGXH,
YVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH,
TVPKPXXAPTQL:SSLS:LKVYP:NMVVRAXGXH,
AVPKAXXAPTKL:SSLS:LKVYP:NMVVKAXGXH,
KVGKAXXVPTKL:SSLS:LKVYP:EGMSVAEXGXR,
KASKAXXVPTKL:SSLS:LKVYP:GMAVSEXGXR,
GSAGPXXTPTKM:SSLS:LKVYP:GMVVDRXGXS,
AAPASXXVPARL:SSLS:LKVYP:DMVVEAXGXR,
STPPTXXVPTRL:SSLS:LKVYP:DMVVESXGXR,
HVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH,
RVPSTXXAPVKT:SSLS:LKVYP:MIVEEXGXL,
ASAAPXXVPQAL:SSLS:LKVYP:MIVRSXKXS,
ASASPSSVSQDL:SSLS:LKVYP:MIVKSXKXS,
ASASPXXVPQDL:SSLS:LKVYP:MVVKSXKXS,
NDEGLEXVPTEE:SSLS:LKVYP:FLQHNKXEXR,
NDEGLEXVPTGQ:SSLS:LKVYP:LEEHSQXEXR,
SSVKXQPSRVHH:SSLS:LKVYP:RLEEHLEXAXA,
RNVQXRPTQVQL:SSLS:LKVYP:TLEDHLAXKXE,
KIPKAXXAPTEL:NAIS:LKKYR:DMVVRGXGXR,
GIPEPXXAPTKM:NAIS:LKKYR:NMVVRSXAXR,
SIPKAXXAPTEL:NAIS:LKKYR:EMVVRGXGXR,
AVPKAXXAPTKL:NAIS:LKKYR:NMVVRAXGXH,
KVGKAXXAPTKL:NAIS:LKKYR:EGMSVVRXGXR,
KASKAXXAPTKL:NAIS:LKKYR:GMVVREXGXR,
GSAGPXXAPTKM:NAIS:LKKYR:GMVVRRXGXS,
AAPASXXAPTRL:NAIS:LKKYR:DMVVRAXGXR,
STPPTXXAPTRL:NAIS:LKKYR:DMVVRSXGXR,
RVPSTXXAPTKT:NAIS:LKKYR:MIVVRXGXL,
ASAAPXXAPTAL:NAIS:LKKYR:MIVVRXKXS,
ASASPXXAPTDL:NAIS:LKKYR:MIVVRXKXS,
ASASPXXAPTDL:NAIS:LKKYR:MVVVRXKXS,
KIPKAXXVPTEL:NAIS:LKKYR:DMVVEGXGXR,
GIPEPXXVPEKM:NAIS:LKKYR:NMTVESXAXR,
SIPKAXXVPTEL:NAIS:LKKYR:EMVVEGXGXR,
AVPKAXXAPTKL:NAIS:LKKYR:NMVVKAXGXH,
KVGKAXXVPTKL:NAIS:LKKYR:EGMSVAEXGXR,
KASKAXXVPTKL:NAIS:LKKYR:GMAVSEXGXR,
GSAGPXXTPTKM:NAIS:LKKYR:GMVVDRXGXS,
AAPASXXVPARL:NAIS:LKKYR:DMVVEAXGXR,
STPPTXXVPTRL:NAIS:LKKYR:DMVVESXGXR,
RVPSTXXAPVKT:NAIS:LKKYR:MIVEEXGXL,
ASAAPXXVPQAL:NAIS:LKKYR:MIVRSXKXS,
ASASPSSVSQDL:NAIS:LKKYR:MIVKSXKXS,
ASASPXXVPQDL:NAIS:LKKYR:MVVKSXKXS,
NDEGLEXVPTEE:NAIS:LKKYR:FLQHNKXEXR,
NDEGLEXVPTGQ:NAIS:LKKYR:LEEHSQXEXR,
SSVKXQPSRVHH:NAIS:LKKYR:RLEEHLEXAXA,
RNVQXRPTQVQL:NAIS:LKKYR:TLEDHLAXKXE,
KIPKAXXAPTEL:SATS:LRKHR:DMVVKGXGXR,
GIPEPXXAPTKM:SATS:LRKHR:NMVVKSXAXR,
SIPKAXXAPTEL:SATS:LRKHR:EMVVKGXGXR,
HVTKPTXAPTKL:SATS:LRKHR:NMVVKSXGXH,
YVPKPXXAPTKL:SATS:LRKHR:NMVVKSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVKAXGXH,
KVGKAXXAPTKL:SATS:LRKHR:EGMSVVKXGXR,
KASKAXXAPTKL:SATS:LRKHR:GMVVKEXGXR,
GSAGPXXAPTKM:SATS:LRKHR:GMVVKRXGXS,
AAPASXXAPTRL:SATS:LRKHR:DMVVKAXGXR,
STPPTXXAPTRL:SATS:LRKHR:DMVVKSXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVKSXGXH,
RVPSTXXAPTKT:SATS:LRKHR:MIVVKXGXL,

ASAAPXXAPTAL:SATS:LRKHR:MIVVKXKXS,
ASASPXXAPTDL:SATS:LRKHR:MIVVKXKXS,
ASASPXXAPTDL:SATS:LRKHR:MVVVKXKXS,
KIPKAXXVPTEL:SATS:LRKHR:DMVVEGXGXR,
GIPEPXXVPEKM:SATS:LRKHR:NMTVESXAXR,
SIPKAXXVPTEL:SATS:LRKHR:EMVVEGXGXR,
HVTKPTXAPTKL:SATS:LRKHR:NMVVRSXGXH,
YVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVRAXGXH,
KVGKAXXVPTKL:SATS:LRKHR:EGMSVAEXGXR,
KASKAXXVPTKL:SATS:LRKHR:GMAVSEXGXR,
GSAGPXXTPTKM:SATS:LRKHR:GMVVDRXGXS,
AAPASXXVPARL:SATS:LRKHR:DMVVEAXGXR,
STPPTXXVPTRL:SATS:LRKHR:DMVVESXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH,
RVPSTXXAPVKT:SATS:LRKHR:MIVEEXGXL,
ASAAPXXVPQAL:SATS:LRKHR:MIVRSXKXS,
ASASPSSVSQDL:SATS:LRKHR:MIVKSXKXS,
ASASPXXVPQDL:SATS:LRKHR:MVVKSXKXS,
NDEGLEXVPTEE:SATS:LRKHR:FLQHNKXEXR,
NDEGLEXVPTGQ:SATS:LRKHR:LEEHSQXEXR,
SSVKXQPSRVHH:SATS:LRKHR:RLEEHLEXAXA,
RNVQXRPTQVQL:SATS:LRKHR:TLEDHLAXKXE,
KIPKAXXVPTEL:SPIS:LKYHY:DMVAEGXGXR,
GIPEPXXVPTKM:SPIS:LKYHY:NMVAESXAXR,
SIPKAXXVPTEL:SPIS:LKYHY:EMVAEGXGXR,
HVTKPTXVPTKL:SPIS:LKYHY:NMVAESXGXH,
YVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH,
TVPKPXXVPTQL:SPIS:LKYHY:NMVAEAXGXH,
AVPKAXXVPTKL:SPIS:LKYHY:NMVAEAXGXH,
KASKAXXVPTKL:SPIS:LKYHY:GMVAEEXGXR,
GSAGPXXVPTKM:SPIS:LKYHY:GMVAERXGXS,
AAPASXXVPTRL:SPIS:LKYHY:DMVAEAXGXR,
STPPTXXVPTRL:SPIS:LKYHY:DMVAESXGXR,
HVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH,
RVPSTXXVPTKT:SPIS:LKYHY:MIVAEXGXL,
ASAAPXXVPTAL:SPIS:LKYHY:MIVAEXKXS,
ASASPXXVPTDL:SPIS:LKYHY:MIVAEXKXS,
ASASPXXVPTDL:SPIS:LKYHY:MVVAEXKXS,
KIPKAXXVPTEL:SPIS:LKYHY:DMVVEGXGXR,
GIPEPXXVPEKM:SPIS:LKYHY:NMTVESXAXR,
SIPKAXXVPTEL:SPIS:LKYHY:EMVVEGXGXR,
HVTKPTXAPTKL:SPIS:LKYHY:NMVVRSXGXH,
YVPKPXXAPTKL:SPIS:LKYHY:NMVVRSXGXH,
TVPKPXXAPTQL:SPIS:LKYHY:NMVVRAXGXH,
AVPKAXXAPTKL:SPIS:LKYHY:NMVVKAXGXH,
KASKAXXVPTKL:SPIS:LKYHY:GMAVSEXGXR,
GSAGPXXTPTKM:SPIS:LKYHY:GMVVDRXGXS,
AAPASXXVPARL:SPIS:LKYHY:DMVVEAXGXR,
STPPTXXVPTRL:SPIS:LKYHY:DMVVESXGXR,
HVPKPXXAPTKL:SPIS:LKYHY:NMVVRSXGXH,
RVPSTXXAPVKT:SPIS:LKYHY:MIVEEXGXL,
ASAAPXXVPQAL:SPIS:LKYHY:MIVRSXKXS,
ASASPSSVSQDL:SPIS:LKYHY:MIVKSXKXS,
ASASPXXVPQDL:SPIS:LKYHY:MVVKSXKXS,
NDEGLEXVPTEE:SPIS:LKYHY:FLQHNKXEXR,
NDEGLEXVPTGQ:SPIS:LKYHY:LEEHSQXEXR,
SSVKXQPSRVHH:SPIS:LKYHY:RLEEHLEXAXA,
RNVQXRPTQVQL:SPIS:LKYHY:TLEDHLAXKXE,
KIPKAXXVPTEL:EPIS:KFKYE:DMAVXGXGSR,
GIPEPXXVPTKM:EPIS:KFKYE:NMAVSSXAXR,
SIPKAXXVPTEL:EPIS:KFKYE:EMAVXGXGSR,
HVTKPTXVPTKL:EPIS:KFKYE:NMAVSSXGXH,
YVPKPXXVPTKL:EPIS:KFKYE:NMAVSSXGXH,
TVPKPXXVPTQL:EPIS:KFKYE:NMAVSAXGXH,
AVPKAXXVPTKL:EPIS:KFKYE:NMAVSAXGXH,
KVGKAXXVPTKL:EPIS:KFKYE:EGMSAVSXGXR,
GSAGPXXVPTKM:EPIS:KFKYE:GMAVSRXGXS,
AAPASXXVPTRL:EPIS:KFKYE:DMAVSAXGXR,
STPPTXXVPTRL:EPIS:KFKYE:DMAVSSXGXR,
HVPKPXXVPTKL:EPIS:KFKYE:NMAVSSXGXH,
RVPSTXXVPTKT:EPIS:KFKYE:MIAVSXGXL,
ASAAPXXVPTAL:EPIS:KFKYE:MIAVSXKXS,
ASASPXXVPTDL:EPIS:KFKYE:MIAVSXKXS,
ASASPXXVPTDL:EPIS:KFKYE:MVAVSXKXS,
KIPKAXXVPTEL:EPIS:KFKYE:DMVVEGXGXR,
GIPEPXXVPEKM:EPIS:KFKYE:NMTVESXAXR,
SIPKAXXVPTEL:EPIS:KFKYE:EMVVEGXGXR,
HVTKPTXAPTKL:EPIS:KFKYE:NMVVRSXGXH,
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TVPKPXXAPTQL:EPIS:KFKYE:NMVVRAXGXH,
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KASKAXXVPTKL:SNIT:LGEMS:GMAVSEXGXR,

GSAGPXXTPTKM:SNIT:LGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT:LGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT:LGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT:LGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT:LGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT:LGEMS:MIVRSXKXS, ASASPSSVSQDL:SNIT:LGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT:LGEMS:MVVKSXKXS, NDEGLEXVPTEE:SNIT:LGEMS:FLQHNKXEXR, SSVKXQPSRVHH:SNIT:LGEMS:RLEEHLEXAXA, RNVQXRPTQVQL:SNIT:LGEMS:TLEDHLAXKXE, RNVQXRPSRVQL:RSVK:KEVQV:TLEEHLAXKXE, KIPKAXXVPTEL:RSVK:KEVQV:DMVVEGXGXR, GIPEPXXVPEKM:RSVK:KEVQV:NMTVESXAXR, SIPKAXXVPTEL:RSVK:KEVQV:EMVVEGXGXR, HVTKPTXAPTKL:RSVK:KEVQV:NMVVRSXGXH, YVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH, TVPKPXXAPTQL:RSVK:KEVQV:NMVVRAXGXH, AVPKAXXAPTKL:RSVK:KEVQV:NMVVKAXGXH, KVGKAXXVPTKL:RSVK:KEVQV:EGMSVAEXGXR, KASKAXXVPTKL:RSVK:KEVQV:GMAVSEXGXR, GSAGPXXTPTKM:RSVK:KEVQV:GMVVDRXGXS, STPPTXXVPTRL:RSVK:KEVQV:DMVVESXGXR, AAPASXXVPARL:RSVK:KEVQV:DMVVEAXGXR, HVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH, RVPSTXXAPVKT:RSVK:KEVQV:MIVEEXGXL, ASAAPXXVPQAL:RSVK:KEVQV:MIVRSXKXS, ASASPSSVSQDL:RSVK:KEVQV:MIVKSXKXS, ASASPXXVPQDL:RSVK:KEVQV:MVVKSXKXS, NDEGLEXVPTEE:RSVK:KEVQV:FLQHNKXEXR, NDEGLEXVPTGQ:RSVK:KEVQV:LEEHSQXEXR, RNVQXRPTQVQL:RSVK:KEVQV:TLEDHLAXKXE, SSVKXQPTQVHH:RPVQ:KKATV:RLEDHLEXAXA, KIPKAXXVPTEL:RPVQ:KKATV:DMVVEGXGXR, GIPEPXXVPEKM:RPVQ:KKATV:NMTVESXAXR, SIPKAXXVPTEL:RPVQ:KKATV:EMVVEGXGXR, HVTKPTXAPTKL:RPVQ:KKATV:NMVVRSXGXH, YVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH, TVPKPXXAPTQL:RPVQ:KKATV:NMVVRAXGXH, AVPKAXXAPTKL:RPVQ:KKATV:NMVVKAXGXH, KVGKAXXVPTKL:RPVQ:KKATV:EGMSVAEXGXR, KASKAXXVPTKL:RPVQ:KKATV:GMAVSEXGXR, GSAGPXXTPTKM:RPVQ:KKATV:GMVVDRXGXS, AAPASXXVPARL:RPVQ:KKATV:DMVVEAXGXR, STPPTXXVPTRL:RPVQ:KKATV:DMVVESXGXR, HVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH, RVPSTXXAPVKT:RPVQ:KKATV:MIVEEXGXL, ASAAPXXVPQAL:RPVQ:KKATV:MIVRSXKXS, ASASPSSVSQDL:RPVQ:KKATV:MIVKSXKXS, ASASPXXVPQDL:RPVQ:KKATV:MVVKSXKXS, NDEGLEXVPTEE:RPVQ:KKATV:FLQHNKXEXR, NDEGLEXVPTGQ:RPVQ:KKATV:LEEHSQXEXR and SSVKXQPSRVHH:RPVQ:KKATV:RLEEHLEXAXA.

In particular, in certain embodiments, the quadruplet PEP9:PEP12:PEP2:PEP10 is selected from the group consisting of GIPEPXXVPTKM:SAIS-AA[17]-LYL:LKNYQ:NMVVESXAXR, SIPKAXXVPTEL:SAIS-AA[17]-LYL:LKNYQ:EMVVEGXGXR, HVTKPTXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, YVPKPXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, TVPKPXXVPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVEAXGXH, AVPKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVEAXGXH, KVGKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVVEXGXR, KASKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:GMVVEEXGXR, GSAGPXXVPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVERXGXS, AAPASXXVPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVEAXGXR, STPPTXXVPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVESXGXR, HVPKPXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, RVPSTXXVPTKT:SAIS-AA[17]-LYL:LKNYQ:MIVVEXGXL, ASAAPXXVPTAL:SAIS-AA[17]-LYL:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS-AA[17]-LYL:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS-AA[17]-LYL:LKNYQ:MVVVEXKXS, NDEGLEXVPTEE:SAIS-AA[17]-LYL:LKNYQ:FLVVEKXEXR, NDEGLEXVPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEVVEQXEXR, SSVKXQPVPTHH:SAIS-AA[17]-LYL:LKNYQ:RLVVELEXAXA, RNVQXRPVPTQL:SAIS-AA[17]-

LYL:LKNYQ:TLVVELAXKXE, GIPEPXXVPEKM:SAIS-AA[17]-LYL:LKNYQ:NMTVESXAXR, HVTKPTXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, YVPKPXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, TVPKPXXAPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVRAXGXH, AVPKAXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVKAXGXH, KVGKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVAEXGXR, KASKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:GMAVSEXGXR, GSAGPXXTPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVDRXGXS, AAPASXXVPARL:SAIS-AA[17]-LYL:LKNYQ:DMVVEAXGXR, HVPKPXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, RVPSTXXAPVKT:SAIS-AA[17]-LYL:LKNYQ:MIVEEXGXL, ASAAPXXVPQAL:SAIS-AA[17]-LYL:LKNYQ:MIVRSXKXS, ASASPXXVSQDL:SAIS-AA[17]-LYL:LKNYQ:MIVKSXKXS, ASASPXXVPQDL:SAIS-AA[17]-LYL:LKNYQ:MVVKSXKXS, NDEGLEXVPTEE:SAIS-AA[17]-LYL:LKNYQ:FLQHNKXEXR, NDEGLEXVPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEEHSQXEXR, SSVKXQPSRVHH:SAIS-AA[17]-LYL:LKNYQ:RLEEHLEXAXA, RNVQXRPTQVQL:SAIS-AA[17]-LYL:LKNYQ:TLEDHLAXKXE, KIPKAXXVPEEL:SSLS-AA[17]-LFF:LKVYP:DMTVEGXGXR, SIPKAXXVPEEL:SSLS-AA[17]-LFF:LKVYP:EMTVEGXGXR, HVTKPTXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, YVPKPXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, TVPKPXXVPEQL:SSLS-AA[17]-LFF:LKVYP:NMTVEAXGXH, AVPKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVEAXGXH, KVGKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:EGMSTVEXGXR, KASKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:GMTVEEXGXR, GSAGPXXVPEKM:SSLS-AA[17]-LFF:LKVYP:GMTVERXGXS, AAPASXXVPERL:SSLS-AA[17]-LFF:LKVYP:DMTVEAXGXR, STPPTXXVPERL:SSLS-AA[17]-LFF:LKVYP:DMTVESXGXR, HVPKPXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, RVPSTXXVPEKT:SSLS-AA[17]-LFF:LKVYP:MITVEXGXL, ASAAPXXVPEAL:SSLS-AA[17]-LFF:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS-AA[17]-LFF:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS-AA[17]-LFF:LKVYP:MVTVEXKXS, NDEGLEXVPEEE:SSLS-AA[17]-LFF:LKVYP:FLTVEKXEXR, NDEGLEXVPEGQ:SSLS-AA[17]-LFF:LKVYP:LETVEQXEXR, SSVKXQPVPEHH:SSLS-AA[17]-LFF:LKVYP:RLTVELEXAXA, RNVQXRPVPEQL:SSLS-AA[17]-LFF:LKVYP:TLTVELAXKXE, KIPKAXXVPTEL:SSLS-AA[17]-LFF:LKVYP:DMVVEGXGXR, SIPKAXXVPTEL:SSLS-AA[17]-LFF:LKVYP:EMVVEGXGXR, HVTKPTXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVRSXGXH, YVPKPXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVRSXGXH, TVPKPXXAPTQL:SSLS-AA[17]-LFF:LKVYP:NMVVRAXGXH, AVPKAXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVKAXGXH, KVGKAXXVPTKL:SSLS-AA[17]-LFF:LKVYP:EGMSVAEXGXR, KASKAXXVPTKL:SSLS-AA[17]-LFF:LKVYP:GMAVSEXGXR, GSAGPXXTPTKM:SSLS-AA[17]-LFF:LKVYP:GMVVDRXGXS, AAPASXXVPARL:SSLS-AA[17]-LFF:LKVYP:DMVVEAXGXR, STPPTXXVPTRL:SSLS-AA[17]-LFF:LKVYP:DMVVESXGXR, HVPKPXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVRSXGXH, RVPSTXXAPVKT:SSLS-AA[17]-LFF:LKVYP:MIVEEXGXL, ASAAPXXVPQAL:SSLS-AA[17]-LFF:LKVYP:MIVRSXKXS, ASASPXXVSQDL:SSLS-AA[17]-LFF:LKVYP:MIVKSXKXS, ASASPXXVPQDL:SSLS-AA[17]-LFF:LKVYP:MVVKSXKXS, NDEGLEXVPTEE:SSLS-AA[17]-LFF:LKVYP:FLQHNKXEXR, NDEGLEXVPTGQ:SSLS-AA[17]-LFF:LKVYP:LEEHSQXEXR, SSVKXQPSRVHH:SSLS-AA[17]-LFF:LKVYP:RLEEHLEXAXA, RNVQXRPTQVQL:SSLS-AA[17]-LFF:LKVYP:TLEDHLAXKXE, KIPKAXXVPTEL:SAIS-AA[17]-LYL:LKNYQ:DMVVEGXGXR, KIPKAXXAPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVRGXGXR, GIPEPXXAPTKM:NAIS-AA[17]-LYF:LKKYR:NMVVRSXAXR, SIPKAXXAPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVRGXGXR, YVPKPXXAPTKL:NAIS-AA[17]-

LYF:LKKYR:NMVVRSXGXH, TVPKPXXAPTQL:NAIS-AA[17]-LYF:LKKYR:NMVVRAXGXH, AVPKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVRAXGXH, KVGKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVVRXGXR, KASKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:GMVVREXGXR, GSAGPXXAPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVRRXGXS, AAPASXXAPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVRAXGXR, STPPTXXAPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVRSXGXR, HVPKPXXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVRSXGXH, RVPSTXXAPTKT:NAIS-AA[17]-LYF:LKKYR:MIVVRXGXL, ASAAPXXAPTAL:NAIS-AA[17]-LYF:LKKYR:MIVVRXKXS, ASASPXXAPTDL:NAIS-AA[17]-LYF:LKKYR:MIVVRXKXS, ASASPXXAPTDL:NAIS-AA[17]-LYF:LKKYR:MVVVRXKXS, NDEGLESAPTEE:NAIS-AA[17]-LYF:LKKYR:FLVVRKXEXR, NDEGLESAPTGQ:NAIS-AA[17]-LYF:LKKYR:LEVVRQXEXR, SSVKXQPAPTHH:NAIS-AA[17]-LYF:LKKYR:RLVVRLEXAXA, RNVQXRPAPTQL:NAIS-AA[17]-LYF:LKKYR:TLVVRLAXKXE, KIPKAXXVPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVEGXGXR, GIPEPXXVPEKM:NAIS-AA[17]-LYF:LKKYR:NMTVESXAXR, SIPKAXXVPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVEGXGXR, AVPKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVKAXGXH, KVGKAXXVPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVAEXGXR, KASKAXXVPTKL:NAIS-AA[17]-LYF:LKKYR:GMAVSEXGXR, GSAGPXXTPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVDRXGXS, AAPASXXVPARL:NAIS-AA[17]-LYF:LKKYR:DMVVEAXGXR, STPPTXXVPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVESXGXR, RVPSTXXAPVKT:NAIS-AA[17]-LYF:LKKYR:MIVEEXGXL, ASAAPXXVPQAL:NAIS-AA[17]-LYF:LKKYR:MIVRSXKXS, ASASPXXVSQDL:NAIS-AA[17]-LYF:LKKYR:MIVKSXKXS, ASASPXXVPQDL:NAIS-AA[17]-LYF:LKKYR:MVVKSXKXS, NDEGLEXVPTEE:NAIS-AA[17]-LYF:LKKYR:FLQHNKXEXR, NDEGLEXVPTGQ:NAIS-AA[17]-LYF:LKKYR:LEEHSQXEXR, SSVKXQPSRVHH:NAIS-AA[17]-LYF:LKKYR:RLEEHLEXAXA, RNVQXRPTQVQL:NAIS-AA[17]-LYF:LKKYR:TLEDHLAXKXE, HVTKPTXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVRSXGXH, KIPKAXXAPTEL:SATS-AA[17]-LYY:LRKHR:DMVVKGXGXR, GIPEPXXAPTKM:SATS-AA[17]-LYY:LRKHR:NMVVKSXAXR, SIPKAXXAPTEL:SATS-AA[17]-LYY:LRKHR:EMVVKGXGXR, HVTKPTXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, YVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, TVPKPXXAPTQL:SATS-AA[17]-LYY:LRKHR:NMVVKAXGXH, KVGKAXXAPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVVKXGXR, KASKAXXAPTKL:SATS-AA[17]-LYY:LRKHR:GMVVKEXGXR, GSAGPXXAPTKM:SATS-AA[17]-LYY:LRKHR:GMVVKRXGXS, AAPASXXAPTRL:SATS-AA[17]-LYY:LRKHR:DMVVKAXGXR, STPPTXXAPTRL:SATS-AA[17]-LYY:LRKHR:DMVVKSXGXR, HVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, RVPSTXXAPTKT:SATS-AA[17]-LYY:LRKHR:MIVVKXGXL, ASAAPXXAPTAL:SATS-AA[17]-LYY:LRKHR:MIVVKXKXS, ASASPXXAPTDL:SATS-AA[17]-LYY:LRKHR:MIVVKXKXS, ASASPXXAPTDL:SATS-AA[17]-LYY:LRKHR:MVVVKXKXS, NDEGLESAPTEE:SATS-AA[17]-LYY:LRKHR:FLVVKKXEXR, NDEGLESAPTGQ:SATS-AA[17]-LYY:LRKHR:LEVVKQXEXR, SSVKXQPAPTHH:SATS-AA[17]-LYY:LRKHR:RLVVKLEXAXA, RNVQXRPAPTQL:SATS-AA[17]-LYY:LRKHR:TLVVKLAXKXE, KIPKAXXVPTEL:SATS-AA[17]-LYY:LRKHR:DMVVEGXGXR, GIPEPXXVPEKM:SATS-AA[17]-LYY:LRKHR:NMTVESXAXR, SIPKAXXVPTEL:SATS-AA[17]-LYY:LRKHR:EMVVEGXGXR, HVTKPTXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, YVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, TVPKPXXAPTQL:SATS-AA[17]-LYY:LRKHR:NMVVRAXGXH, KVGKAXXVPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVAEXGXR, KASKAXXVPTKL:SATS-AA[17]-LYY:LRKHR:GMAVSEXGXR, GSAGPXXTPTKM:SATS-AA[17]-

LYY:LRKHR:GMVVDRXGXS, AAPASXXVPARL:SATS-AA[17]-LYY:LRKHR:DMVVEAXGXR, STPPTXXVPTRL:SATS-AA[17]-LYY:LRKHR:DMVVESXGXR, HVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, RVPSTXXAPVKT:SATS-AA[17]-LYY:LRKHR:MIVEEXGXL, ASAAPXXVPQAL:SATS-AA[17]-LYY:LRKHR:MIVRSXKXS, ASASPXXVSQDL:SATS-AA[17]-LYY:LRKHR:MIVKSXKXS, ASASPXXVPQDL:SATS-AA[17]-LYY:LRKHR:MVVKSXKXS, NDEGLEXVPTEE:SATS-AA[17]-LYY:LRKHR:FLQHNKXEXR, NDEGLEXVPTGQ:SATS-AA[17]-LYY:LRKHR:LEEHSQXEXR, SSVKXQPSRVHH:SATS-AA[17]-LYY:LRKHR:RLEEHLEXAXA, RNVQXRPTQVQL:SATS-AA[17]-LYY:LRKHR:TLEDHLAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:DMVAEGXGXR, GIPEPXXVPTKM:SPIS-AA[17]-LYK:LKYHY:NMVAESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:EMVAEGXGXR, HVTKPTXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, YVPKPXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, TVPKPXXVPTQL:SPIS-AA[17]-LYK:LKYHY:NMVAEAXGXH, AVPKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAEAXGXH, KASKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:GMVAEEXGXR, GSAGPXXVPTKM:SPIS-AA[17]-LYK:LKYHY:GMVAERXGXS, AAPASXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAEAXGXR, STPPTXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAESXGXR, HVPKPXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, RVPSTXXVPTKT:SPIS-AA[17]-LYK:LKYHY:MIVAEXGXL, ASAAPXXVPTAL:SPIS-AA[17]-LYK:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LYK:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LYK:LKYHY:MVVAEXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LYK:LKYHY:FLVAEKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LYK:LKYHY:LEVAEQXEXR, SSVKXQPVPTHH:SPIS-AA[17]-LYK:LKYHY:RLVAELEXAXA, RNVQXRPVPTQL:SPIS-AA[17]-LYK:LKYHY:TLVAELAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:DMVVEGXGXR, GIPEPXXVPEKM:SPIS-AA[17]-LYK:LKYHY:NMTVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:EMVVEGXGXR, HVTKPTXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LYK:LKYHY:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVKAXGXH, KASKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LYK:LKYHY:GMVVDRXGXS, AAPASXXVPARL:SPIS-AA[17]-LYK:LKYHY:DMVVEAXGXR, STPPTXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVVESXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LYK:LKYHY:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LYK:LKYHY:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LYK:LKYHY:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LYK:LKYHY:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LYK:LKYHY:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LYK:LKYHY:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LYK:LKYHY:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LYK:LKYHY:TLEDHLAXKXE, KIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:DMAVXGXGSR, GIPEPXXVPTKM:EPIS-AA[17]-LYL:KFKYE:NMAVSSXAXR, SIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:EMAVXGXGSR, HVTKPTXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSSXGXH, YVPKPXXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSSXGXH, TVPKPXXVPTQL:EPIS-AA[17]-LYL:KFKYE:NMAVSAXGXH, AVPKAXXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSAXGXH, KVGKAXXVPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSAVSXGXR, GSAGPXXVPTKM:EPIS-AA[17]-LYL:KFKYE:GMAVSRXGXS, AAPASXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVSAXGXR, STPPTXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVSSXGXR, HVPKPXXVPTKL:EPIS-AA[17]-

LYL:KFKYE:NMAVSSXGXH, RVPSTXXVPTKT:EPIS-AA[17]-LYL:KFKYE:MIAVSXGXL, ASAAPXXVPTAL:EPIS-AA[17]-LYL:KFKYE:MIAVSXKXS, ASASPXXVPTDL:EPIS-AA[17]-LYL:KFKYE:MIAVSXKXS, ASASPXXVPTDL:EPIS-AA[17]-LYL:KFKYE:MVAVSXKXS, NDEGLEXVPTEE:EPIS-AA[17]-LYL:KFKYE:FLAVXKXESR, NDEGLEXVPTGQ:EPIS-AA[17]-LYL:KFKYE:LEAVSQXEXR, SSVKXQPVPTHH:EPIS-AA[17]-LYL:KFKYE:RLAVSLEXAXA, RNVQXRPVPTQL:EPIS-AA[17]-LYL:KFKYE:TLAVSLAXKXE, KIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:DMVVEGXGXR, GIPEPXXVPEKM:EPIS-AA[17]-LYL:KFKYE:NMTVESXAXR, SIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:EMVVEGXGXR, HVTKPTXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, YVPKPXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, TVPKPXXAPTQL:EPIS-AA[17]-LYL:KFKYE:NMVVRAXGXH, AVPKAXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVKAXGXH, KVGKAXXVPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSVAEXGXR, GSAGPXXTPTKM:EPIS-AA[17]-LYL:KFKYE:GMVVDRXGXS, AAPASXXVPARL:EPIS-AA[17]-LYL:KFKYE:DMVVEAXGXR, STPPTXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMVVESXGXR, HVPKPXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, RVPSTXXAPVKT:EPIS-AA[17]-LYL:KFKYE:MIVEEXGXL, ASAAPXXVPQAL:EPIS-AA[17]-LYL:KFKYE:MIVRSXKXS, ASASPXXVSQDL:EPIS-AA[17]-LYL:KFKYE:MIVKSXKXS, ASASPXXVPQDL:EPIS-AA[17]-LYL:KFKYE:MVVKSXKXS, NDEGLEXVPTEE:EPIS-AA[17]-LYL:KFKYE:FLQHNKXEXR, NDEGLEXVPTGQ:EPIS-AA[17]-LYL:KFKYE:LEEHSQXEXR, SSVKXQPSRVHH:EPIS-AA[17]-LYL:KFKYE:RLEEHLEXAXA, RNVQXRPTQVQL:EPIS-AA[17]-LYL:KFKYE:TLEDHLAXKXE, KIPKASSTPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVDGXGXR, GIPEPXXTPTKM:SPIN-AA[17]-LYF:YGKIP:NMVVDSXAXR, SIPKASSTPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVDGXGXR, HVTKPTSTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, YVPKPXXTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, TVPKPXXTPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVDAXGXH, AVPKASSTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDAXGXH, KVGKASSTPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVVDXGXR, KASKASSTPTKL:SPIN-AA[17]-LYF:YGKIP:GMVVDEXGXR, AAPASSSTPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVDAXGXR, STPPTSSTPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVDSXGXR, HVPKPXXTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, RVPSTSSTPTKT:SPIN-AA[17]-LYF:YGKIP:MIVVDXGXL, ASAAPXXTPTAL:SPIN-AA[17]-LYF:YGKIP:MIVVDXKXS, ASASPXXTPTDL:SPIN-AA[17]-LYF:YGKIP:MIVVDXKXS, ASASPXXTPTDL:SPIN-AA[17]-LYF:YGKIP:MVVVDXKXS, NDEGLESTPTEE:SPIN-AA[17]-LYF:YGKIP:FLVVDKXEXR, NDEGLESTPTGQ:SPIN-AA[17]-LYF:YGKIP:LEVVDQXEXR, SSVKXQPTPTHH:SPIN-AA[17]-LYF:YGKIP:RLVVDLEXAXA, RNVQXRPTPTQL:SPIN-AA[17]-LYF:YGKIP:TLVVDLAXKXE, KIPKAXXVPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVEGXGXR, GIPEPXXVPEKM:SPIN-AA[17]-LYF:YGKIP:NMTVESXAXR, SIPKAXXVPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVEGXGXR, HVTKPTXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, YVPKPXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, TVPKPXXAPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVRAXGXH, AVPKAXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVKAXGXH, KVGKAXXVPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVAEXGXR, KASKAXXVPTKL:SPIN-AA[17]-LYF:YGKIP:GMAVSEXGXR, AAPASXXVPARL:SPIN-AA[17]-LYF:YGKIP:DMVVEAXGXR, STPPTXXVPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVESXGXR, HVPKPXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, RVPSTXXAPVKT:SPIN-AA[17]-LYF:YGKIP:MIVEEXGXL, ASAAPXXVPQAL:SPIN-AA[17]-LYF:YGKIP:MIVRSXKXS, ASASPXXVSQDL:SPIN-AA[17]-

LYF:YGKIP:MIVKSXKXS, ASASPXXVPQDL:SPIN-AA[17]-LYF:YGKIP:MVVKSXKXS, NDEGLEXVPTEE:SPIN-AA[17]-LYF:YGKIP:FLQHNKXEXR, NDEGLEXVPTGQ:SPIN-AA[17]-LYF:YGKIP:LEEHSQXEXR, SSVKXQPSRVHH:SPIN-AA[17]-LYF:YGKIP:RLEEHLEXAXA, RNVQXRPTQVQL:SPIN-AA[17]-LYF:YGKIP:TLEDHLAXKXE, KIPKAXXVPAEL:SPIS-AA[17]-LYI:YKQYE:DMVVEGXGXR, GIPEPXXVPAKM:SPIS-AA[17]-LYI:YKQYE:NMVVESXAXR, SIPKAXXVPAEL:SPIS-AA[17]-LYI:YKQYE:EMVVEGXGXR, HVTKPTXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, YVPKPXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, TVPKPXXVPAQL:SPIS-AA[17]-LYI:YKQYE:NMVVEAXGXH, AVPKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVEAXGXH, KVGKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:EGMSVVEXGXR, KASKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:GMVVEEXGXR, GSAGPXXVPAKM:SPIS-AA[17]-LYI:YKQYE:GMVVERXGXS, STPPTXXVPARL:SPIS-AA[17]-LYI:YKQYE:DMVVESXGXR, HVPKPXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, RVPSTXXVPAKT:SPIS-AA[17]-LYI:YKQYE:MIVVEXGXL, ASAAPXXVPAAL:SPIS-AA[17]-LYI:YKQYE:MIVVEXKXS, ASASPXXVPADL:SPIS-AA[17]-LYI:YKQYE:MIVVEXKXS, ASASPXXVPADL:SPIS-AA[17]-LYI:YKQYE:MVVVEXKXS, NDEGLEXVPAEE:SPIS-AA[17]-LYI:YKQYE:FLVVEKXEXR, NDEGLEXVPAGQ:SPIS-AA[17]-LYI:YKQYE:LEVVEQXEXR, SSVKXQPVPAHH:SPIS-AA[17]-LYI:YKQYE:RLVVELEXAXA, RNVQXRPVPAQL:SPIS-AA[17]-LYI:YKQYE:TLVVELAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LYI:YKQYE:DMVVEGXGXR, GIPEPXXVPEKM:SPIS-AA[17]-LYI:YKQYE:NMTVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYI:YKQYE:EMVVEGXGXR, HVTKPTXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LYI:YKQYE:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVKAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LYI:YKQYE:EGMSVAEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LYI:YKQYE:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LYI:YKQYE:GMVVDRXGXS, STPPTXXVPTRL:SPIS-AA[17]-LYI:YKQYE:DMVVESXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LYI:YKQYE:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LYI:YKQYE:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LYI:YKQYE:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LYI:YKQYE:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LYI:YKQYE:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LYI:YKQYE:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LYI:YKQYE:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LYI:YKQYE:TLEDHLAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LFI:YKQYE:DMVVEGXGXR, GIPEPXXVPTKM:SPIS-AA[17]-LFI:YKQYE:NMVVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LFI:YKQYE:EMVVEGXGXR, HVTKPTXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, YVPKPXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, TVPKPXXVPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVEAXGXH, AVPKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVEAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVVEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:GMVVEEXGXR, GSAGPXXVPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVERXGXS, AAPASXXVPTRL:SPIS-AA[17]-LFI:YKQYE:DMVVEAXGXR, HVPKPXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, RVPSTXXVPTKT:SPIS-AA[17]-LFI:YKQYE:MIVVEXGXL, ASAAPXXVPTAL:SPIS-AA[17]-LFI:YKQYE:MIVVEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LFI:YKQYE:MIVVEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LFI:YKQYE:MVVVEXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LFI:YKQYE:FLVVEKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-

LFI:YKQYE:LEVVEQXEXR, SSVKXQPVPTHH:SPIS-AA[17]-LFI:YKQYE:RLVVELEXAXA, RNVQXRPVPTQL:SPIS-AA[17]-LFI:YKQYE:TLVVELAXKXE, GIPEPXXVPEKM:SPIS-AA[17]-LFI:YKQYE:NMTVESXAXR, HVTKPTXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVKAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVAEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVDRXGXS, AAPASXXVPARL:SPIS-AA[17]-LFI:YKQYE:DMVVEAXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LFI:YKQYE:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LFI:YKQYE:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LFI:YKQYE:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LFI:YKQYE:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LFI:YKQYE:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LFI:YKQYE:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LFI:YKQYE:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LFI:YKQYE:TLEDHLAXKXE, KIPKAXXAPVEL:KPLS-AA[17]-LYV:DHHKD:DMVEEGXGXR, GIPEPXXAPVKM:KPLS-AA[17]-LYV:DHHKD:NMVEESXAXR, SIPKAXXAPVEL:KPLS-AA[17]-LYV:DHHKD:EMVEEGXGXR, HVTKPTXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, YVPKPXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, TVPKPXXAPVQL:KPLS-AA[17]-LYV:DHHKD:NMVEEAXGXH, AVPKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEEAXGXH, KVGKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:EGMSVEEXGXR, KASKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:GMVEEEXGXR, GSAGPXXAPVKM:KPLS-AA[17]-LYV:DHHKD:GMVEERXGXS, AAPASXXAPVRL:KPLS-AA[17]-LYV:DHHKD:DMVEEAXGXR, STPPTXXAPVRL:KPLS-AA[17]-LYV:DHHKD:DMVEESXGXR, HVPKPXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, ASAAPXXAPVAL:KPLS-AA[17]-LYV:DHHKD:MIVEEXKXS, ASASPXXAPVDL:KPLS-AA[17]-LYV:DHHKD:MIVEEXKXS, ASASPXXAPVDL:KPLS-AA[17]-LYV:DHHKD:MVVEEXKXS, NDEGLESAPVEE:KPLS-AA[17]-LYV:DHHKD:FLVEEKXEXR, NDEGLESAPVGQ:KPLS-AA[17]-LYV:DHHKD:LEVEEQXEXR, SSVKXQPAPVHH:KPLS-AA[17]-LYV:DHHKD:RLVEELEXAXA, RNVQXRPAPVQL:KPLS-AA[17]-LYV:DHHKD:TLVEELAXKXE, KIPKAXXVPTEL:KPLS-AA[17]-LYV:DHHKD:DMVVEGXGXR, GIPEPXXVPEKM:KPLS-AA[17]-LYV:DHHKD:NMTVESXAXR, SIPKAXXVPTEL:KPLS-AA[17]-LYV:DHHKD:EMVVEGXGXR, HVTKPTXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, YVPKPXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, TVPKPXXAPTQL:KPLS-AA[17]-LYV:DHHKD:NMVVRAXGXH, AVPKAXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVKAXGXH, KVGKAXXVPTKL:KPLS-AA[17]-LYV:DHHKD:EGMSVAEXGXR, KASKAXXVPTKL:KPLS-AA[17]-LYV:DHHKD:GMAVSEXGXR, GSAGPXXTPTKM:KPLS-AA[17]-LYV:DHHKD:GMVVDRXGXS, AAPASXXVPARL:KPLS-AA[17]-LYV:DHHKD:DMVVEAXGXR, STPPTXXVPTRL:KPLS-AA[17]-LYV:DHHKD:DMVVESXGXR, HVPKPXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, ASAAPXXVPQAL:KPLS-AA[17]-LYV:DHHKD:MIVRSXKXS, ASASPXXVSQDL:KPLS-AA[17]-LYV:DHHKD:MIVKSXKXS, ASASPXXVPQDL:KPLS-AA[17]-LYV:DHHKD:MVVKSXKXS, NDEGLEXVPTEE:KPLS-AA[17]-LYV:DHHKD:FLQHNKXEXR, NDEGLEXVPTGQ:KPLS-AA[17]-LYV:DHHKD:LEEHSQXEXR, SSVKXQPSRVHH:KPLS-AA[17]-LYV:DHHKD:RLEEHLEXAXA, RNVQXRPTQVQL:KPLS-AA[17]-LYV:DHHKD:TLEDHLAXKXE, KIPKAXXVPQEL:EPLP-AA[17]-VYY:EQLSN:DMVRXGXGSR, GIPEPXXVPQKM:EPLP-AA[17]-VYY:EQLSN:NMVRSSXAXR, SIPKAXXVPQEL:EPLP-AA[17]-

VYY:EQLSN:EMVRXGXGSR, HVTKPTXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, YVPKPXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, TVPKPXXVPQQL:EPLP-AA[17]-VYY:EQLSN:NMVRSAXGXH, AVPKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSAXGXH, KVGKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:EGMSVRSXGXR, KASKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:GMVRSEXGXR, GSAGPXXVPQKM:EPLP-AA[17]-VYY:EQLSN:GMVRSRXGXS, AAPASXXVPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRSAXGXR, STPPTXXVPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRSSXGXR, HVPKPXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, RVPSTXXVPQKT:EPLP-AA[17]-VYY:EQLSN:MIVRSXGXL, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MIVRSXKXS, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MVVRSXKXS, NDEGLEXVPQEE:EPLP-AA[17]-VYY:EQLSN:FLVRXKXESR, NDEGLEXVPQGQ:EPLP-AA[17]-VYY:EQLSN:LEVRSQXEXR, SSVKXQPVPQHH:EPLP-AA[17]-VYY:EQLSN:RLVRSLEXAXA, RNVQXRPVPQQL:EPLP-AA[17]-VYY:EQLSN:TLVRSLAXKXE, KIPKAXXVPTEL:EPLP-AA[17]-VYY:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLP-AA[17]-VYY:EQLSN:NMTVESXAXR, SIPKAXXVPTEL:EPLP-AA[17]-VYY:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, YVPKPXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, TVPKPXXAPTQL:EPLP-AA[17]-VYY:EQLSN:NMVVRAXGXH, AVPKAXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVKAXGXH, KVGKAXXVPTKL:EPLP-AA[17]-VYY:EQLSN:EGMSVAEXGXR, KASKAXXVPTKL:EPLP-AA[17]-VYY:EQLSN:GMAVSEXGXR, GSAGPXXTPTKM:EPLP-AA[17]-VYY:EQLSN:GMVVDRXGXS, AAPASXXVPARL:EPLP-AA[17]-VYY:EQLSN:DMVVEAXGXR, STPPTXXVPTRL:EPLP-AA[17]-VYY:EQLSN:DMVVESXGXR, HVPKPXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLP-AA[17]-VYY:EQLSN:MIVEEXGXL, ASASPXXVSQDL:EPLP-AA[17]-VYY:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MVVKSXKXS, NDEGLEXVPTEE:EPLP-AA[17]-VYY:EQLSN:FLQHNKXEXR, NDEGLEXVPTGQ:EPLP-AA[17]-VYY:EQLSN:LEEHSQXEXR, SSVKXQPSRVHH:EPLP-AA[17]-VYY:EQLSN:RLEEHLEXAXA, RNVQXRPTQVQL:EPLP-AA[17]-VYY:EQLSN:TLEDHLAXKXE, KIPKASSVSQEL:EPLT-AA[17]-LYY:EQLSN:DMVKXGXGSR, GIPEPXXVSQKM:EPLT-AA[17]-LYY:EQLSN:NMVKSSXAXR, SIPKASSVSQEL:EPLT-AA[17]-LYY:EQLSN:EMVKXGXGSR, HVTKPTXVSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, YVPKPXXVSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, TVPKPXXVSQQL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, AVPKASSVSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, KVGKASSVSQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKSXGXR, KASKASSVSQKL:EPLT-AA[17]-LYY:EQLSN:GMVKSEXGXR, GSAGPXXVSQKM:EPLT-AA[17]-LYY:EQLSN:GMVKSRXGXS, AAPASSSVSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSAXGXR, STPPTSSVSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSSXGXR, HVPKPXXVSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, RVPSTSSVSQKT:EPLT-AA[17]-LYY:EQLSN:MIVKSXGXL, ASAAPXXVSQAL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, ASASPXXVSQDL:EPLT-AA[17]-LYY:EQLSN:MVVKSXKXS, NDEGLEXVSQEE:EPLT-AA[17]-LYY:EQLSN:FLVKXKXESR, NDEGLEXVSQGQ:EPLT-AA[17]-LYY:EQLSN:LEVKSQXEXR, SSVKXQPVSQHH:EPLT-AA[17]-LYY:EQLSN:RLVKSLEXAXA, RNVQXRPVSQQL:EPLT-AA[17]-LYY:EQLSN:TLVKSLAXKXE, KIPKAXXVPTEL:EPLT-AA[17]-LYY:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLT-AA[17]-LYY:EQLSN:NMTVESXAXR, SIPKAXXVPTEL:EPLT-AA[17]-LYY:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, YVPKPXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, TVPKPXXAPTQL:EPLT-AA[17]-

LYY:EQLSN:NMVVRAXGXH, AVPKAXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVKAXGXH, KVGKAXXVPTKL:EPLT-AA[17]-LYY:EQLSN:EGMSVAEXGXR, KASKAXXVPTKL:EPLT-AA[17]-LYY:EQLSN:GMAVSEXGXR, GSAGPXXTPTKM:EPLT-AA[17]-LYY:EQLSN:GMVVDRXGXS, AAPASXXVPARL:EPLT-AA[17]-LYY:EQLSN:DMVVEAXGXR, STPPTXXVPTRL:EPLT-AA[17]-LYY:EQLSN:DMVVESXGXR, HVPKPXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLT-AA[17]-LYY:EQLSN:MIVEEXGXL, ASAAPXXVPQAL:EPLT-AA[17]-LYY:EQLSN:MIVRSXKXS, ASASPXXVPQDL:EPLT-AA[17]-LYY:EQLSN:MVVKSXKXS, NDEGLEXVPTEE:EPLT-AA[17]-LYY:EQLSN:FLQHNKXEXR, NDEGLEXVPTGQ:EPLT-AA[17]-LYY:EQLSN:LEEHSQXEXR, SSVKXQPSRVHH:EPLT-AA[17]-LYY:EQLSN:RLEEHLEXAXA, RNVQXRPTQVQL:EPLT-AA[17]-LYY:EQLSN:TLEDHLAXKXE, KIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKXGXGSR, GIPEPXXVPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKSSXAXR, SIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:EMVKXGXGSR, HVTKPTXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, YVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, TVPKPXXVPQQL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, AVPKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, KVGKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKSXGXR, KASKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:GMVKSEXGXR, GSAGPXXVPQKM:EPLT-AA[17]-LYY:EQLSN:GMVKSRXGXS, AAPASXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSAXGXR, STPPTXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSSXGXR, HVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, RVPSTXXVPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKSXGXL, ASAAPXXVPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, NDEGLEXVPQEE:EPLT-AA[17]-LYY:EQLSN:FLVKXKXESR, NDEGLEXVPQGQ:EPLT-AA[17]-LYY:EQLSN:LEVKSQXEXR, SSVKXQPVPQHH:EPLT-AA[17]-LYY:EQLSN:RLVKSLEXAXA, RNVQXRPVPQQL:EPLT-AA[17]-LYY:EQLSN:TLVKSLAXKXE, ASASPXXVSQDL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, KIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:DMQHNGXGXR, GIPEPXXVPTKM:SNIT-AA[17]-QIM:IGEMS:NMQHNSXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:EMQHNGXGXR, HVTKPTXVPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHNSXGXH, YVPKPXXVPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHNSXGXH, TVPKPXXVPTQL:SNIT-AA[17]-QIM:IGEMS:NMQHNAXGXH, AVPKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHNAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSQHNXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:GMQHNEXGXR, GSAGPXXVPTKM:SNIT-AA[17]-QIM:IGEMS:GMQHNRXGXS, AAPASXXVPTRL:SNIT-AA[17]-QIM:IGEMS:DMQHNAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:IGEMS:DMQHNSXGXR, HVPKPXXVPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHNSXGXH, RVPSTXXVPTKT:SNIT-AA[17]-QIM:IGEMS:MIQHNXGXL, ASAAPXXVPTAL:SNIT-AA[17]-QIM:IGEMS:MIQHNXKXS, ASASPXXVPTDL:SNIT-AA[17]-QIM:IGEMS:MIQHNXKXS, ASASPXXVPTDL:SNIT-AA[17]-QIM:IGEMS:MVQHNXKXS, NDEGLEXVPTGQ:SNIT-AA[17]-QIM:IGEMS:LEQHNQXEXR, NDEGLEXVPTEE:SNIT-AA[17]-QIM:IGEMS:FLQHNKXEXR, SSVKXQPVPTHH:SNIT-AA[17]-QIM:IGEMS:RLQHNLEXAXA, RNVQXRPVPTQL:SNIT-AA[17]-QIM:IGEMS:TLQHNLAXKXE, KIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:DMVVEGXGXR, GIPEPXXVPEKM:SNIT-AA[17]-QIM:IGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:EMVVEGXGXR, HVTKPTXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, TVPKPXXAPTQL:SNIT-AA[17]-QIM:IGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT-AA[17]-

QIM:IGEMS:NMVVKAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:GMAVSEXGXR, GSAGPXXTPTKM:SNIT-AA[17]-QIM:IGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT-AA[17]-QIM:IGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:IGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT-AA[17]-QIM:IGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT-AA[17]-QIM:IGEMS:MIVRSXKXS, ASASPXXVSQDL:SNIT-AA[17]-QIM:IGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT-AA[17]-QIM:IGEMS:MVVKSXKXS, NDEGLEXVPTGQ:SNIT-AA[17]-QIM:IGEMS:LEEHSQXEXR, SSVKXQPSRVHH:SNIT-AA[17]-QIM:IGEMS:RLEEHLEXAXA, RNVQXRPTQVQL:SNIT-AA[17]-QIM:IGEMS:TLEDHLAXKXE, KIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:DMEHXGXGSR, GIPEPXXVPTKM:SNIT-AA[17]-QIM:LGEMS:NMEHSSXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:EMEHXGXGSR, HVTKPTXVPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHSSXGXH, YVPKPXXVPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHSSXGXH, TVPKPXXVPTQL:SNIT-AA[17]-QIM:LGEMS:NMEHSAXGXH, AVPKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHSAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSEHSXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:GMEHSEXGXR, GSAGPXXVPTKM:SNIT-AA[17]-QIM:LGEMS:GMEHSRXGXS, AAPASXXVPTRL:SNIT-AA[17]-QIM:LGEMS:DMEHSAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:LGEMS:DMEHSSXGXR, HVPKPXXVPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHSSXGXH, RVPSTXXVPTKT:SNIT-AA[17]-QIM:LGEMS:MIEHSXGXL, ASAAPXXVPTAL:SNIT-AA[17]-QIM:LGEMS:MIEHSXKXS, ASASPXXVPTDL:SNIT-AA[17]-QIM:LGEMS:MIEHSXKXS, ASASPXXVPTDL:SNIT-AA[17]-QIM:LGEMS:MVEHSXKXS, NDEGLEXVPTEE:SNIT-AA[17]-QIM:LGEMS:FLEHXKXESR, SSVKXQPVPTHH:SNIT-AA[17]-QIM:LGEMS:RLEHSLEXAXA, RNVQXRPVPTQL:SNIT-AA[17]-QIM:LGEMS:TLEHSLAXKXE, KIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:DMVVEGXGXR, GIPEPXXVPEKM:SNIT-AA[17]-QIM:LGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:EMVVEGXGXR, HVTKPTXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, TVPKPXXAPTQL:SNIT-AA[17]-QIM:LGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVKAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:GMAVSEXGXR, GSAGPXXTPTKM:SNIT-AA[17]-QIM:LGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT-AA[17]-QIM:LGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:LGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT-AA[17]-QIM:LGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT-AA[17]-QIM:LGEMS:MIVRSXKXS, ASASPXXVSQDL:SNIT-AA[17]-QIM:LGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT-AA[17]-QIM:LGEMS:MVVKSXKXS, NDEGLEXVPTEE:SNIT-AA[17]-QIM:LGEMS:FLQHNKXEXR, SSVKXQPSRVHH:SNIT-AA[17]-QIM:LGEMS:RLEEHLEXAXA, RNVQXRPTQVQL:SNIT-AA[17]-QIM:LGEMS:TLEDHLAXKXE, KIPKASSSRVEL:RSVK-AA[17]-AKV:KEVQV:DMEEHGXGXR, GIPEPXXSRVKM:RSVK-AA[17]-AKV:KEVQV:NMEEHSXAXR, SIPKASSSRVEL:RSVK-AA[17]-AKV:KEVQV:EMEEHGXGXR, HVTKPTSSRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEHSXGXH, YVPKPXXSRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEHSXGXH, TVPKPXXSRVQL:RSVK-AA[17]-AKV:KEVQV:NMEEHAXGXH, AVPKASSSRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEHAXGXH, KVGKASSSRVKL:RSVK-AA[17]-AKV:KEVQV:EGMSEEHXGXR, KASKASSSRVKL:RSVK-AA[17]-AKV:KEVQV:GMEEHEXGXR, GSAGPXXSRVKM:RSVK-AA[17]-

AKV:KEVQV:GMEEHRXGXS, AAPASSSSRVRL:RSVK-AA[17]-AKV:KEVQV:DMEEHAXGXR, STPPTSSSRVRL:RSVK-AA[17]-AKV:KEVQV:DMEEHSXGXR, HVPKPXXSRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEHSXGXH, RVPSTSSSRVKT:RSVK-AA[17]-AKV:KEVQV:MIEEHXGXL, ASAAPXXSRVAL:RSVK-AA[17]-AKV:KEVQV:MIEEHXKXS, ASASPXXSRVDL:RSVK-AA[17]-AKV:KEVQV:MIEEHXKXS, ASASPXXSRVDL:RSVK-AA[17]-AKV:KEVQV:MVEEHXKXS, NDEGLESSRVEE:RSVK-AA[17]-AKV:KEVQV:FLEEHKXEXR, NDEGLESSRVGQ:RSVK-AA[17]-AKV:KEVQV:LEEEHQXEXR, RNVQXRPSRVQL:RSVK-AA[17]-AKV:KEVQV:TLEEHLAXKXE, KIPKAXXVPTEL:RSVK-AA[17]-AKV:KEVQV:DMVVEGXGXR, GIPEPXXVPEKM:RSVK-AA[17]-AKV:KEVQV:NMTVESXAXR, SIPKAXXVPTEL:RSVK-AA[17]-AKV:KEVQV:EMVVEGXGXR, HVTKPTXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, YVPKPXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, TVPKPXXAPTQL:RSVK-AA[17]-AKV:KEVQV:NMVVRAXGXH, AVPKAXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVKAXGXH, KVGKAXXVPTKL:RSVK-AA[17]-AKV:KEVQV:EGMSVAEXGXR, KASKAXXVPTKL:RSVK-AA[17]-AKV:KEVQV:GMAVSEXGXR, GSAGPXXTPTKM:RSVK-AA[17]-AKV:KEVQV:GMVVDRXGXS, AAPASXXVPARL:RSVK-AA[17]-AKV:KEVQV:DMVVEAXGXR, STPPTXXVPTRL:RSVK-AA[17]-AKV:KEVQV:DMVVESXGXR, HVPKPXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, RVPSTXXAPVKT:RSVK-AA[17]-AKV:KEVQV:MIVEEXGXL, ASAAPXXVPQAL:RSVK-AA[17]-AKV:KEVQV:MIVRSXKXS, ASASPXXVSQDL:RSVK-AA[17]-AKV:KEVQV:MIVKSXKXS, ASASPXXVPQDL:RSVK-AA[17]-AKV:KEVQV:MVVKSXKXS, NDEGLEXVPTEE:RSVK-AA[17]-AKV:KEVQV:FLQHNKXEXR, NDEGLEXVPTGQ:RSVK-AA[17]-AKV:KEVQV:LEEHSQXEXR, RNVQXRPTQVQL:RSVK-AA[17]-AKV:KEVQV:TLEDHLAXKXE, KIPKASSTQVEL:RPVQ-AA[17]-RKI:KKATV:DMEDHGXGXR, GIPEPXXTQVKM:RPVQ-AA[17]-RKI:KKATV:NMEDHSXAXR, SIPKASSTQVEL:RPVQ-AA[17]-RKI:KKATV:EMEDHGXGXR, HVTKPTSTQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDHSXGXH, YVPKPXXTQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDHSXGXH, TVPKPXXTQVQL:RPVQ-AA[17]-RKI:KKATV:NMEDHAXGXH, AVPKASSTQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDHAXGXH, KVGKASSTQVKL:RPVQ-AA[17]-RKI:KKATV:EGMSEDHXGXR, KASKASSTQVKL:RPVQ-AA[17]-RKI:KKATV:GMEDHEXGXR, GSAGPXXTQVKM:RPVQ-AA[17]-RKI:KKATV:GMEDHRXGXS, AAPASSSTQVRL:RPVQ-AA[17]-RKI:KKATV:DMEDHAXGXR, STPPTSSTQVRL:RPVQ-AA[17]-RKI:KKATV:DMEDHSXGXR, HVPKPXXTQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDHSXGXH, RVPSTSSTQVKT:RPVQ-AA[17]-RKI:KKATV:MIEDHXGXL, ASAAPXXTQVAL:RPVQ-AA[17]-RKI:KKATV:MIEDHXKXS, ASASPXXTQVDL:RPVQ-AA[17]-RKI:KKATV:MIEDHXKXS, ASASPXXTQVDL:RPVQ-AA[17]-RKI:KKATV:MVEDHXKXS, NDEGLESTQVEE:RPVQ-AA[17]-RKI:KKATV:FLEDHKXEXR, NDEGLESTQVGQ:RPVQ-AA[17]-RKI:KKATV:LEEDHQXEXR, SSVKXQPTQVHH:RPVQ-AA[17]-RKI:KKATV:RLEDHLEXAXA, KIPKAXXVPTEL:RPVQ-AA[17]-RKI:KKATV:DMVVEGXGXR, GIPEPXXVPEKM:RPVQ-AA[17]-RKI:KKATV:NMTVESXAXR, SIPKAXXVPTEL:RPVQ-AA[17]-RKI:KKATV:EMVVEGXGXR, HVTKPTXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVRSXGXH, YVPKPXXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVRSXGXH, TVPKPXXAPTQL:RPVQ-AA[17]-RKI:KKATV:NMVVRAXGXH, AVPKAXXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVKAXGXH, KVGKAXXVPTKL:RPVQ-AA[17]-RKI:KKATV:EGMSVAEXGXR, KASKAXXVPTKL:RPVQ-AA[17]-RKI:KKATV:GMAVSEXGXR, GSAGPXXTPTKM:RPVQ-AA[17]-RKI:KKATV:GMVVDRXGXS, AAPASXXVPARL:RPVQ-AA[17]-RKI:KKATV:DMVVEAXGXR, STPPTXXVPTRL:RPVQ-AA[17]-RKI:KKATV:DMVVESXGXR, HVPKPXXAPTKL:RPVQ-AA[17]-

RKI:KKATV:NMVVRSXGXH, RVPSTXXAPVKT:RPVQ-AA[17]-RKI:KKATV:MIVEEXGXL, ASAAPXXVPQAL:RPVQ-AA[17]-RKI:KKATV:MIVRSXKXS, ASASPXXVSQDL:RPVQ-AA[17]-RKI:KKATV:MIVKSXKXS, ASASPXXVPQDL:RPVQ-AA[17]-RKI:KKATV:MVVKSXKXS, NDEGLEXVPTEE:RPVQ-AA[17]-RKI:KKATV:FLQHNKXEXR, NDEGLEXVPTGQ:RPVQ-AA[17]-RKI:KKATV:LEEHSQXEXR and SSVKXQPSRVHH:RPVQ-AA[17]-RKI:KKATV:RLEEHLEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T). More particularly, the quadruplet PEP9:PEP12:PEP2:PEP10 is selected from the group consisting of GIPEPXXVPTKM:SAIS-AA[17]-LYL:LKNYQ:NMVVESXAXR, HVTKPTXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, YVPKPXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, TVPKPXXVPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVEAXGXH, AVPKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVEAXGXH, KVGKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVVEXGXR, KASKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:GMVVEEXGXR, GSAGPXXVPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVERXGXS, AAPASXXVPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVEAXGXR, STPPTXXVPTRL:SAIS-AA[17]-LYL:LKNYQ:DMVVESXGXR, HVPKPXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVESXGXH, RVPSTXXVPTKT:SAIS-AA[17]-LYL:LKNYQ:MIVVEXGXL, ASAAPXXVPTAL:SAIS-AA[17]-LYL:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS-AA[17]-LYL:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS-AA[17]-LYL:LKNYQ:MVVVEXKXS, GIPEPXXVPEKM:SAIS-AA[17]-LYL:LKNYQ:NMTVESXAXR, HVTKPTXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, YVPKPXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, TVPKPXXAPTQL:SAIS-AA[17]-LYL:LKNYQ:NMVVRAXGXH, AVPKAXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVKAXGXH, KVGKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:EGMSVAEXGXR, KASKAXXVPTKL:SAIS-AA[17]-LYL:LKNYQ:GMAVSEXGXR, GSAGPXXTPTKM:SAIS-AA[17]-LYL:LKNYQ:GMVVDRXGXS, AAPASXXVPARL:SAIS-AA[17]-LYL:LKNYQ:DMVVEAXGXR, HVPKPXXAPTKL:SAIS-AA[17]-LYL:LKNYQ:NMVVRSXGXH, RVPSTXXAPVKT:SAIS-AA[17]-LYL:LKNYQ:MIVEEXGXL, ASAAPXXVPQAL:SAIS-AA[17]-LYL:LKNYQ:MIVRSXKXS, ASASPXXVSQDL:SAIS-AA[17]-LYL:LKNYQ:MIVKSXKXS, ASASPXXVPQDL:SAIS-AA[17]-LYL:LKNYQ:MVVKSXKXS, NDEGLEXVPTEE:SAIS-AA[17]-LYL:LKNYQ:FLQHNKXEXR, NDEGLEXVPTGQ:SAIS-AA[17]-LYL:LKNYQ:LEEHSQXEXR, SSVKXQPSRVHH:SAIS-AA[17]-LYL:LKNYQ:RLEEHLEXAXA, RNVQXRPTQVQL:SAIS-AA[17]-LYL:LKNYQ:TLEDHLAXKXE, KIPKAXXVPEEL:SSLS-AA[17]-LFF:LKVYP:DMTVEGXGXR, SIPKAXXVPEEL:SSLS-AA[17]-LFF:LKVYP:EMTVEGXGXR, HVTKPTXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, YVPKPXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, TVPKPXXVPEQL:SSLS-AA[17]-LFF:LKVYP:NMTVEAXGXH, AVPKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVEAXGXH, KVGKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:EGMSTVEXGXR, KASKAXXVPEKL:SSLS-AA[17]-LFF:LKVYP:GMTVEEXGXR, GSAGPXXVPEKM:SSLS-AA[17]-LFF:LKVYP:GMTVERXGXS, AAPASXXVPERL:SSLS-AA[17]-LFF:LKVYP:DMTVEAXGXR, STPPTXXVPERL:SSLS-AA[17]-LFF:LKVYP:DMTVESXGXR, HVPKPXXVPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVESXGXH, RVPSTXXVPEKT:SSLS-AA[17]-LFF:LKVYP:MITVEXGXL, ASAAPXXVPEAL:SSLS-AA[17]-LFF:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS-AA[17]-LFF:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS-AA[17]-LFF:LKVYP:MVTVEXKXS, KIPKAXXVPTEL:SSLS-AA[17]-LFF:LKVYP:DMVVEGXGXR, SIPKAXXVPTEL:SSLS-AA[17]-LFF:LKVYP:EMVVEGXGXR, HVTKPTXAPTKL:SSLS-AA[17]-

LFF:LKVYP:NMVVRSXGXH, YVPKPXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVRSXGXH, TVPKPXXAPTQL:SSLS-AA[17]-LFF:LKVYP:NMVVRAXGXH, AVPKAXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVKAXGXH, KVGKAXXVPTKL:SSLS-AA[17]-LFF:LKVYP:EGMSVAEXGXR, KASKAXXVPTKL:SSLS-AA[17]-LFF:LKVYP:GMAVSEXGXR, GSAGPXXTPTKM:SSLS-AA[17]-LFF:LKVYP:GMVVDRXGXS, AAPASXXVPARL:SSLS-AA[17]-LFF:LKVYP:DMVVEAXGXR, STPPTXXVPTRL:SSLS-AA[17]-LFF:LKVYP:DMVVESXGXR, HVPKPXXAPTKL:SSLS-AA[17]-LFF:LKVYP:NMVVRSXGXH, RVPSTXXAPVKT:SSLS-AA[17]-LFF:LKVYP:MIVEEXGXL, ASAAPXXVPQAL:SSLS-AA[17]-LFF:LKVYP:MIVRSXKXS, ASASPXXVSQDL:SSLS-AA[17]-LFF:LKVYP:MIVKSXKXS, ASASPXXVPQDL:SSLS-AA[17]-LFF:LKVYP:MVVKSXKXS, NDEGLEXVPTEE:SSLS-AA[17]-LFF:LKVYP:FLQHNKXEXR, NDEGLEXVPTGQ:SSLS-AA[17]-LFF:LKVYP:LEEHSQXEXR, SSVKXQPSRVHH:SSLS-AA[17]-LFF:LKVYP:RLEEHLEXAXA, RNVQXRPTQVQL:SSLS-AA[17]-LFF:LKVYP:TLEDHLAXKXE, KIPKAXXAPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVRGXGXR, GIPEPXXAPTKM:NAIS-AA[17]-LYF:LKKYR:NMVVRSXAXR, SIPKAXXAPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVRGXGXR, AVPKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVRAXGXH, KVGKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVVRXGXR, KASKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:GMVVREXGXR, GSAGPXXAPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVRRXGXS, AAPASXXAPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVRAXGXR, STPPTXXAPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVRSXGXR, RVPSTXXAPTKT:NAIS-AA[17]-LYF:LKKYR:MIVVRXGXL, ASAAPXXAPTAL:NAIS-AA[17]-LYF:LKKYR:MIVVRXKXS, ASASPXXAPTDL:NAIS-AA[17]-LYF:LKKYR:MIVVRXKXS, ASASPXXAPTDL:NAIS-AA[17]-LYF:LKKYR:MVVVRXKXS, KIPKAXXVPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVEGXGXR, GIPEPXXVPEKM:NAIS-AA[17]-LYF:LKKYR:NMTVESXAXR, SIPKAXXVPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVEGXGXR, AVPKAXXAPTKL:NAIS-AA[17]-LYF:LKKYR:NMVVKAXGXH, KVGKAXXVPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVAEXGXR, KASKAXXVPTKL:NAIS-AA[17]-LYF:LKKYR:GMAVSEXGXR, GSAGPXXTPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVDRXGXS, AAPASXXVPARL:NAIS-AA[17]-LYF:LKKYR:DMVVEAXGXR, STPPTXXVPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVESXGXR, RVPSTXXAPVKT:NAIS-AA[17]-LYF:LKKYR:MIVEEXGXL, ASAAPXXVPQAL:NAIS-AA[17]-LYF:LKKYR:MIVRSXKXS, ASASPXXVSQDL:NAIS-AA[17]-LYF:LKKYR:MIVKSXKXS, ASASPXXVPQDL:NAIS-AA[17]-LYF:LKKYR:MVVKSXKXS, NDEGLEXVPTEE:NAIS-AA[17]-LYF:LKKYR:FLQHNKXEXR, NDEGLEXVPTGQ:NAIS-AA[17]-LYF:LKKYR:LEEHSQXEXR, SSVKXQPSRVHH:NAIS-AA[17]-LYF:LKKYR:RLEEHLEXAXA, RNVQXRPTQVQL:NAIS-AA[17]-LYF:LKKYR:TLEDHLAXKXE, KIPKAXXAPTEL:SATS-AA[17]-LYY:LRKHR:DMVVKGXGXR, GIPEPXXAPTKM:SATS-AA[17]-LYY:LRKHR:NMVVKSXAXR, SIPKAXXAPTEL:SATS-AA[17]-LYY:LRKHR:EMVVKGXGXR, HVTKPTXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, YVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, TVPKPXXAPTQL:SATS-AA[17]-LYY:LRKHR:NMVVKAXGXH, KVGKAXXAPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVVKXGXR, KASKAXXAPTKL:SATS-AA[17]-LYY:LRKHR:GMVVKEXGXR, GSAGPXXAPTKM:SATS-AA[17]-LYY:LRKHR:GMVVKRXGXS, AAPASXXAPTRL:SATS-AA[17]-LYY:LRKHR:DMVVKAXGXR, STPPTXXAPTRL:SATS-AA[17]-LYY:LRKHR:DMVVKSXGXR, HVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVKSXGXH, RVPSTXXAPTKT:SATS-AA[17]-LYY:LRKHR:MIVVKXGXL, ASAAPXXAPTAL:SATS-AA[17]-LYY:LRKHR:MIVVKXKXS, ASASPXXAPTDL:SATS-AA[17]-LYY:LRKHR:MIVVKXKXS, ASASPXXAPTDL:SATS-AA[17]-

LYY:LRKHR:MVVVKXKXS, KIPKAXXVPTEL:SATS-AA[17]-LYY:LRKHR:DMVVEGXGXR, GIPEPXXVPEKM:SATS-AA[17]-LYY:LRKHR:NMTVESXAXR, SIPKAXXVPTEL:SATS-AA[17]-LYY:LRKHR:EMVVEGXGXR, HVTKPTXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, YVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, TVPKPXXAPTQL:SATS-AA[17]-LYY:LRKHR:NMVVRAXGXH, KVGKAXXVPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVAEXGXR, KASKAXXVPTKL:SATS-AA[17]-LYY:LRKHR:GMAVSEXGXR, GSAGPXXTPTKM:SATS-AA[17]-LYY:LRKHR:GMVVDRXGXS, AAPASXXVPARL:SATS-AA[17]-LYY:LRKHR:DMVVEAXGXR, STPPTXXVPTRL:SATS-AA[17]-LYY:LRKHR:DMVVESXGXR, HVPKPXXAPTKL:SATS-AA[17]-LYY:LRKHR:NMVVRSXGXH, RVPSTXXAPVKT:SATS-AA[17]-LYY:LRKHR:MIVEEXGXL, ASAAPXXVPQAL:SATS-AA[17]-LYY:LRKHR:MIVRSXKXS, ASASPXXVSQDL:SATS-AA[17]-LYY:LRKHR:MIVKSXKXS, ASASPXXVPQDL:SATS-AA[17]-LYY:LRKHR:MVVKSXKXS, NDEGLEXVPTEE:SATS-AA[17]-LYY:LRKHR:FLQHNKXEXR, NDEGLEXVPTGQ:SATS-AA[17]-LYY:LRKHR:LEEHSQXEXR, SSVKXQPSRVHH:SATS-AA[17]-LYY:LRKHR:RLEEHLEXAXA, RNVQXRPTQVQL:SATS-AA[17]-LYY:LRKHR:TLEDHLAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:DMVAEGXGXR, GIPEPXXVPTKM:SPIS-AA[17]-LYK:LKYHY:NMVAESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:EMVAEGXGXR, HVTKPTXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, YVPKPXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, TVPKPXXVPTQL:SPIS-AA[17]-LYK:LKYHY:NMVAEAXGXH, AVPKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAEAXGXH, KASKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:GMVAEEXGXR, GSAGPXXVPTKM:SPIS-AA[17]-LYK:LKYHY:GMVAERXGXS, AAPASXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAEAXGXR, STPPTXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAESXGXR, HVPKPXXVPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAESXGXH, RVPSTXXVPTKT:SPIS-AA[17]-LYK:LKYHY:MIVAEXGXL, ASAAPXXVPTAL:SPIS-AA[17]-LYK:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LYK:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LYK:LKYHY:MVVAEXKXS, KIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:DMVVEGXGXR, GIPEPXXVPEKM:SPIS-AA[17]-LYK:LKYHY:NMTVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYK:LKYHY:EMVVEGXGXR, HVTKPTXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LYK:LKYHY:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVKAXGXH, KASKAXXVPTKL:SPIS-AA[17]-LYK:LKYHY:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LYK:LKYHY:GMVVDRXGXS, AAPASXXVPARL:SPIS-AA[17]-LYK:LKYHY:DMVVEAXGXR, STPPTXXVPTRL:SPIS-AA[17]-LYK:LKYHY:DMVVESXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LYK:LKYHY:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LYK:LKYHY:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LYK:LKYHY:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LYK:LKYHY:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LYK:LKYHY:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LYK:LKYHY:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LYK:LKYHY:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LYK:LKYHY:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LYK:LKYHY:TLEDHLAXKXE, KIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:DMAVXGXGSR, GIPEPXXVPTKM:EPIS-AA[17]-LYL:KFKYE:NMAVSSXAXR, SIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:EMAVXGXGSR, HVTKPTXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSSXGXH, YVPKPXXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSSXGXH, TVPKPXXVPTQL:EPIS-AA[17]-LYL:KFKYE:NMAVSAXGXH, AVPKAXXVPTKL:EPIS-AA[17]-

LYL:KFKYE:NMAVSAXGXH, KVGKAXXVPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSAVSXGXR, GSAGPXXVPTKM:EPIS-AA[17]-LYL:KFKYE:GMAVSRXGXS, AAPASXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVSAXGXR, STPPTXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVSSXGXR, HVPKPXXVPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVSSXGXH, RVPSTXXVPTKT:EPIS-AA[17]-LYL:KFKYE:MIAVSXGXL, ASAAPXXVPTAL:EPIS-AA[17]-LYL:KFKYE:MIAVSXKXS, ASASPXXVPTDL:EPIS-AA[17]-LYL:KFKYE:MIAVSXKXS, ASASPXXVPTDL:EPIS-AA[17]-LYL:KFKYE:MVAVSXKXS, KIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:DMVVEGXGXR, GIPEPXXVPEKM:EPIS-AA[17]-LYL:KFKYE:NMTVESXAXR, SIPKAXXVPTEL:EPIS-AA[17]-LYL:KFKYE:EMVVEGXGXR, HVTKPTXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, YVPKPXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, TVPKPXXAPTQL:EPIS-AA[17]-LYL:KFKYE:NMVVRAXGXH, AVPKAXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVKAXGXH, KVGKAXXVPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSVAEXGXR, GSAGPXXTPTKM:EPIS-AA[17]-LYL:KFKYE:GMVVDRXGXS, AAPASXXVPARL:EPIS-AA[17]-LYL:KFKYE:DMVVEAXGXR, STPPTXXVPTRL:EPIS-AA[17]-LYL:KFKYE:DMVVESXGXR, HVPKPXXAPTKL:EPIS-AA[17]-LYL:KFKYE:NMVVRSXGXH, RVPSTXXAPVKT:EPIS-AA[17]-LYL:KFKYE:MIVEEXGXL, ASAAPXXVPQAL:EPIS-AA[17]-LYL:KFKYE:MIVRSXKXS, ASASPXXVSQDL:EPIS-AA[17]-LYL:KFKYE:MIVKSXKXS, ASASPXXVPQDL:EPIS-AA[17]-LYL:KFKYE:MVVKSXKXS, NDEGLEXVPTEE:EPIS-AA[17]-LYL:KFKYE:FLQHNKXEXR, NDEGLEXVPTGQ:EPIS-AA[17]-LYL:KFKYE:LEEHSQXEXR, SSVKXQPSRVHH:EPIS-AA[17]-LYL:KFKYE:RLEEHLEXAXA, RNVQXRPTQVQL:EPIS-AA[17]-LYL:KFKYE:TLEDHLAXKXE, KIPKAXXTPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVDGXGXR, GIPEPXXTPTKM:SPIN-AA[17]-LYF:YGKIP:NMVVDSXAXR, SIPKAXXTPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVDGXGXR, HVTKPTSTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, YVPKPXXTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, TVPKPXXTPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVDAXGXH, AVPKAXXTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDAXGXH, KVGKAXXTPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVVDXGXR, KASKAXXTPTKL:SPIN-AA[17]-LYF:YGKIP:GMVVDEXGXR, AAPASXXTPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVDAXGXR, STPPTXXTPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVDSXGXR, HVPKPXXTPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVDSXGXH, RVPSTXXTPTKT:SPIN-AA[17]-LYF:YGKIP:MIVVDXGXL, ASAAPXXTPTAL:SPIN-AA[17]-LYF:YGKIP:MIVVDXKXS, ASASPXXTPTDL:SPIN-AA[17]-LYF:YGKIP:MIVVDXKXS, ASASPXXTPTDL:SPIN-AA[17]-LYF:YGKIP:MVVVDXKXS, KIPKAXXVPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVEGXGXR, GIPEPXXVPEKM:SPIN-AA[17]-LYF:YGKIP:NMTVESXAXR, SIPKAXXVPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVEGXGXR, HVTKPTXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, YVPKPXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, TVPKPXXAPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVRAXGXH, AVPKAXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVKAXGXH, KVGKAXXVPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVAEXGXR, KASKAXXVPTKL:SPIN-AA[17]-LYF:YGKIP:GMAVSEXGXR, AAPASXXVPARL:SPIN-AA[17]-LYF:YGKIP:DMVVEAXGXR, STPPTXXVPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVESXGXR, HVPKPXXAPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVRSXGXH, RVPSTXXAPVKT:SPIN-AA[17]-LYF:YGKIP:MIVEEXGXL, ASAAPXXVPQAL:SPIN-AA[17]-LYF:YGKIP:MIVRSXKXS, ASASPXXVSQDL:SPIN-AA[17]-LYF:YGKIP:MIVKSXKXS, ASASPXXVPQDL:SPIN-AA[17]-LYF:YGKIP:MVVKSXKXS, NDEGLEXVPTEE:SPIN-AA[17]-LYF:YGKIP:FLQHNKXEXR, NDEGLEXVPTGQ:SPIN-AA[17]-

LYF:YGKIP:LEEHSQXEXR, SSVKXQPSRVHH:SPIN-AA[17]-LYF:YGKIP:RLEEHLEXAXA, RNVQXRPTQVQL:SPIN-AA[17]-LYF:YGKIP:TLEDHLAXKXE, KIPKAXXVPAEL:SPIS-AA[17]-LYI:YKQYE:DMVVEGXGXR, GIPEPXXVPAKM:SPIS-AA[17]-LYI:YKQYE:NMVVESXAXR, SIPKAXXVPAEL:SPIS-AA[17]-LYI:YKQYE:EMVVEGXGXR, HVTKPTXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, YVPKPXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, TVPKPXXVPAQL:SPIS-AA[17]-LYI:YKQYE:NMVVEAXGXH, AVPKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVEAXGXH, KVGKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:EGMSVVEXGXR, KASKAXXVPAKL:SPIS-AA[17]-LYI:YKQYE:GMVVEEXGXR, GSAGPXXVPAKM:SPIS-AA[17]-LYI:YKQYE:GMVVERXGXS, STPPTXXVPARL:SPIS-AA[17]-LYI:YKQYE:DMVVESXGXR, HVPKPXXVPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVESXGXH, RVPSTXXVPAKT:SPIS-AA[17]-LYI:YKQYE:MIVVEXGXL, ASAAPXXVPAAL:SPIS-AA[17]-LYI:YKQYE:MIVVEXKXS, ASASPXXVPADL:SPIS-AA[17]-LYI:YKQYE:MIVVEXKXS, ASASPXXVPADL:SPIS-AA[17]-LYI:YKQYE:MVVVEXKXS, KIPKAXXVPTEL:SPIS-AA[17]-LYI:YKQYE:DMVVEGXGXR, GIPEPXXVPEKM:SPIS-AA[17]-LYI:YKQYE:NMTVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LYI:YKQYE:EMVVEGXGXR, HVTKPTXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LYI:YKQYE:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVKAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LYI:YKQYE:EGMSVAEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LYI:YKQYE:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LYI:YKQYE:GMVVDRXGXS, STPPTXXVPTRL:SPIS-AA[17]-LYI:YKQYE:DMVVESXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LYI:YKQYE:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LYI:YKQYE:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LYI:YKQYE:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LYI:YKQYE:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LYI:YKQYE:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LYI:YKQYE:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LYI:YKQYE:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LYI:YKQYE:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LYI:YKQYE:TLEDHLAXKXE, KIPKAXXVPTEL:SPIS-AA[17]-LFI:YKQYE:DMVVEGXGXR, GIPEPXXVPTKM:SPIS-AA[17]-LFI:YKQYE:NMVVESXAXR, SIPKAXXVPTEL:SPIS-AA[17]-LFI:YKQYE:EMVVEGXGXR, HVTKPTXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, YVPKPXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, TVPKPXXVPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVEAXGXH, AVPKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVEAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVVEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:GMVVEEXGXR, GSAGPXXVPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVERXGXS, AAPASXXVPTRL:SPIS-AA[17]-LFI:YKQYE:DMVVEAXGXR, HVPKPXXVPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVESXGXH, RVPSTXXVPTKT:SPIS-AA[17]-LFI:YKQYE:MIVVEXGXL, ASAAPXXVPTAL:SPIS-AA[17]-LFI:YKQYE:MIVVEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LFI:YKQYE:MIVVEXKXS, ASASPXXVPTDL:SPIS-AA[17]-LFI:YKQYE:MVVVEXKXS, GIPEPXXVPEKM:SPIS-AA[17]-LFI:YKQYE:NMTVESXAXR, HVTKPTXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, YVPKPXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, TVPKPXXAPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVRAXGXH, AVPKAXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVKAXGXH, KVGKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVAEXGXR, KASKAXXVPTKL:SPIS-AA[17]-LFI:YKQYE:GMAVSEXGXR, GSAGPXXTPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVDRXGXS, AAPASXXVPARL:SPIS-AA[17]-

LFI:YKQYE:DMVVEAXGXR, HVPKPXXAPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVRSXGXH, RVPSTXXAPVKT:SPIS-AA[17]-LFI:YKQYE:MIVEEXGXL, ASAAPXXVPQAL:SPIS-AA[17]-LFI:YKQYE:MIVRSXKXS, ASASPXXVSQDL:SPIS-AA[17]-LFI:YKQYE:MIVKSXKXS, ASASPXXVPQDL:SPIS-AA[17]-LFI:YKQYE:MVVKSXKXS, NDEGLEXVPTEE:SPIS-AA[17]-LFI:YKQYE:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS-AA[17]-LFI:YKQYE:LEEHSQXEXR, SSVKXQPSRVHH:SPIS-AA[17]-LFI:YKQYE:RLEEHLEXAXA, RNVQXRPTQVQL:SPIS-AA[17]-LFI:YKQYE:TLEDHLAXKXE, KIPKAXXAPVEL:KPLS-AA[17]-LYV:DHHKD:DMVEEGXGXR, GIPEPXXAPVKM:KPLS-AA[17]-LYV:DHHKD:NMVEESXAXR, SIPKAXXAPVEL:KPLS-AA[17]-LYV:DHHKD:EMVEEGXGXR, HVTKPTXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, YVPKPXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, TVPKPXXAPVQL:KPLS-AA[17]-LYV:DHHKD:NMVEEAXGXH, AVPKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEEAXGXH, KVGKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:EGMSVEEXGXR, KASKAXXAPVKL:KPLS-AA[17]-LYV:DHHKD:GMVEEEXGXR, GSAGPXXAPVKM:KPLS-AA[17]-LYV:DHHKD:GMVEERXGXS, AAPASXXAPVRL:KPLS-AA[17]-LYV:DHHKD:DMVEEAXGXR, STPPTXXAPVRL:KPLS-AA[17]-LYV:DHHKD:DMVEESXGXR, HVPKPXXAPVKL:KPLS-AA[17]-LYV:DHHKD:NMVEESXGXH, ASAAPXXAPVAL:KPLS-AA[17]-LYV:DHHKD:MIVEEXKXS, ASASPXXAPVDL:KPLS-AA[17]-LYV:DHHKD:MIVEEXKXS, ASASPXXAPVDL:KPLS-AA[17]-LYV:DHHKD:MVVEEXKXS, KIPKAXXVPTEL:KPLS-AA[17]-LYV:DHHKD:DMVVEGXGXR, GIPEPXXVPEKM:KPLS-AA[17]-LYV:DHHKD:NMTVESXAXR, SIPKAXXVPTEL:KPLS-AA[17]-LYV:DHHKD:EMVVEGXGXR, HVTKPTXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, YVPKPXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, TVPKPXXAPTQL:KPLS-AA[17]-LYV:DHHKD:NMVVRAXGXH, AVPKAXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVKAXGXH, KVGKAXXVPTKL:KPLS-AA[17]-LYV:DHHKD:EGMSVAEXGXR, KASKAXXVPTKL:KPLS-AA[17]-LYV:DHHKD:GMAVSEXGXR, GSAGPXXTPTKM:KPLS-AA[17]-LYV:DHHKD:GMVVDRXGXS, AAPASXXVPARL:KPLS-AA[17]-LYV:DHHKD:DMVVEAXGXR, STPPTXXVPTRL:KPLS-AA[17]-LYV:DHHKD:DMVVESXGXR, HVPKPXXAPTKL:KPLS-AA[17]-LYV:DHHKD:NMVVRSXGXH, ASAAPXXVPQAL:KPLS-AA[17]-LYV:DHHKD:MIVRSXKXS, ASASPXXVSQDL:KPLS-AA[17]-LYV:DHHKD:MIVKSXKXS, ASASPXXVPQDL:KPLS-AA[17]-LYV:DHHKD:MVVKSXKXS, NDEGLEXVPTEE:KPLS-AA[17]-LYV:DHHKD:FLQHNKXEXR, NDEGLEXVPTGQ:KPLS-AA[17]-LYV:DHHKD:LEEHSQXEXR, SSVKXQPSRVHH:KPLS-AA[17]-LYV:DHHKD:RLEEHLEXAXA, RNVQXRPTQVQL:KPLS-AA[17]-LYV:DHHKD:TLEDHLAXKXE, KIPKAXXVPQEL:EPLP-AA[17]-VYY:EQLSN:DMVRXGXGSR, GIPEPXXVPQKM:EPLP-AA[17]-VYY:EQLSN:NMVRSSXAXR, SIPKAXXVPQEL:EPLP-AA[17]-VYY:EQLSN:EMVRXGXGSR, HVTKPTXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, YVPKPXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, TVPKPXXVPQQL:EPLP-AA[17]-VYY:EQLSN:NMVRSAXGXH, AVPKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSAXGXH, KVGKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:EGMSVRSXGXR, KASKAXXVPQKL:EPLP-AA[17]-VYY:EQLSN:GMVRSEXGXR, GSAGPXXVPQKM:EPLP-AA[17]-VYY:EQLSN:GMVRSRXGXS, AAPASXXVPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRSAXGXR, STPPTXXVPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRSSXGXR, HVPKPXXVPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRSSXGXH, RVPSTXXVPQKT:EPLP-AA[17]-VYY:EQLSN:MIVRSXGXL, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MIVRSXKXS, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MVVRSXKXS, KIPKAXXVPTEL:EPLP-AA[17]-VYY:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLP-AA[17]-

VYY:EQLSN:NMTVESXAXR, SIPKAXXVPTEL:EPLP-AA[17]-VYY:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, YVPKPXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, TVPKPXXAPTQL:EPLP-AA[17]-VYY:EQLSN:NMVVRAXGXH, AVPKAXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVKAXGXH, KVGKAXXVPTKL:EPLP-AA[17]-VYY:EQLSN:EGMSVAEXGXR, KASKAXXVPTKL:EPLP-AA[17]-VYY:EQLSN:GMAVSEXGXR, GSAGPXXTPTKM:EPLP-AA[17]-VYY:EQLSN:GMVVDRXGXS, AAPASXXVPARL:EPLP-AA[17]-VYY:EQLSN:DMVVEAXGXR, STPPTXXVPTRL:EPLP-AA[17]-VYY:EQLSN:DMVVESXGXR, HVPKPXXAPTKL:EPLP-AA[17]-VYY:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLP-AA[17]-VYY:EQLSN:MIVEEXGXL, ASASPXXVSQDL:EPLP-AA[17]-VYY:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLP-AA[17]-VYY:EQLSN:MVVKSXKXS, NDEGLEXVPTEE:EPLP-AA[17]-VYY:EQLSN:FLQHNKXEXR, NDEGLEXVPTGQ:EPLP-AA[17]-VYY:EQLSN:LEEHSQXEXR, SSVKXQPSRVHH:EPLP-AA[17]-VYY:EQLSN:RLEEHLEXAXA, RNVQXRPTQVQL:EPLP-AA[17]-VYY:EQLSN:TLEDHLAXKXE, KIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKXGXGSR, GIPEPXXVPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKSSXAXR, SIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:EMVKXGXGSR, HVTKPTXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, YVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, TVPKPXXVPQQL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, AVPKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, KVGKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKSXGXR, KASKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:GMVKSEXGXR, GSAGPXXVPQKM:EPLT-AA[17]-LYY:EQLSN:GMVKSRXGXS, AAPASXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSAXGXR, STPPTXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSSXGXR, HVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, RVPSTXXVPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKSXGXL, ASAAPXXVPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLT-AA[17]-LYY:EQLSN:MVVKSXKXS, KIPKAXXVPTEL:EPLT-AA[17]-LYY:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLT-AA[17]-LYY:EQLSN:NMTVESXAXR, SIPKAXXVPTEL:EPLT-AA[17]-LYY:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, YVPKPXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, TVPKPXXAPTQL:EPLT-AA[17]-LYY:EQLSN:NMVVRAXGXH, AVPKAXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVKAXGXH, KVGKAXXVPTKL:EPLT-AA[17]-LYY:EQLSN:EGMSVAEXGXR, KASKAXXVPTKL:EPLT-AA[17]-LYY:EQLSN:GMAVSEXGXR, GSAGPXXTPTKM:EPLT-AA[17]-LYY:EQLSN:GMVVDRXGXS, AAPASXXVPARL:EPLT-AA[17]-LYY:EQLSN:DMVVEAXGXR, STPPTXXVPTRL:EPLT-AA[17]-LYY:EQLSN:DMVVESXGXR, HVPKPXXAPTKL:EPLT-AA[17]-LYY:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLT-AA[17]-LYY:EQLSN:MIVEEXGXL, ASAAPXXVPQAL:EPLT-AA[17]-LYY:EQLSN:MIVRSXKXS, NDEGLEXVPTEE:EPLT-AA[17]-LYY:EQLSN:FLQHNKXEXR, NDEGLEXVPTGQ:EPLT-AA[17]-LYY:EQLSN:LEEHSQXEXR, SSVKXQPSRVHH:EPLT-AA[17]-LYY:EQLSN:RLEEHLEXAXA, RNVQXRPTQVQL:EPLT-AA[17]-LYY:EQLSN:TLEDHLAXKXE, KIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKXGXGSR, GIPEPXXVPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKSSXAXR, SIPKAXXVPQEL:EPLT-AA[17]-LYY:EQLSN:EMVKXGXGSR, HVTKPTXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, YVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, TVPKPXXVPQQL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, AVPKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSAXGXH, KVGKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKSXGXR, KASKAXXVPQKL:EPLT-AA[17]-LYY:EQLSN:GMVKSEXGXR, GSAGPXXVPQKM:EPLT-AA[17]-

LYY:EQLSN:GMVKSRXGXS, AAPASXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSAXGXR, STPPTXXVPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKSSXGXR, HVPKPXXVPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKSSXGXH, RVPSTXXVPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKSXGXL, ASAAPXXVPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLT-AA[17]-LYY:EQLSN:MIVKSXKXS, NDEGLEXVPTGQ:SNIT-AA[17]-QIM:IGEMS:LEQHNQXEXR, KIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:DMVVEGXGXR, GIPEPXXVPEKM:SNIT-AA[17]-QIM:IGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:IGEMS:EMVVEGXGXR, HVTKPTXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, TVPKPXXAPTQL:SNIT-AA[17]-QIM:IGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVKAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:IGEMS:GMAVSEXGXR, GSAGPXXTPTKM:SNIT-AA[17]-QIM:IGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT-AA[17]-QIM:IGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:IGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT-AA[17]-QIM:IGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT-AA[17]-QIM:IGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT-AA[17]-QIM:IGEMS:MIVRSXKXS, ASASPXXVSQDL:SNIT-AA[17]-QIM:IGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT-AA[17]-QIM:IGEMS:MVVKSXKXS, NDEGLEXVPTGQ:SNIT-AA[17]-QIM:IGEMS:LEEHSQXEXR, SSVKXQPSRVHH:SNIT-AA[17]-QIM:IGEMS:RLEEHLEXAXA, RNVQXRPTQVQL:SNIT-AA[17]-QIM:IGEMS:TLEDHLAXKXE, NDEGLEXVPTEE:SNIT-AA[17]-QIM:LGEMS:FLEHXKXESR, KIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:DMVVEGXGXR, GIPEPXXVPEKM:SNIT-AA[17]-QIM:LGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT-AA[17]-QIM:LGEMS:EMVVEGXGXR, HVTKPTXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, TVPKPXXAPTQL:SNIT-AA[17]-QIM:LGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVKAXGXH, KVGKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSVAEXGXR, KASKAXXVPTKL:SNIT-AA[17]-QIM:LGEMS:GMAVSEXGXR, GSAGPXXTPTKM:SNIT-AA[17]-QIM:LGEMS:GMVVDRXGXS, AAPASXXVPARL:SNIT-AA[17]-QIM:LGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT-AA[17]-QIM:LGEMS:DMVVESXGXR, HVPKPXXAPTKL:SNIT-AA[17]-QIM:LGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT-AA[17]-QIM:LGEMS:MIVEEXGXL, ASAAPXXVPQAL:SNIT-AA[17]-QIM:LGEMS:MIVRSXKXS, ASASPXXVSQDL:SNIT-AA[17]-QIM:LGEMS:MIVKSXKXS, ASASPXXVPQDL:SNIT-AA[17]-QIM:LGEMS:MVVKSXKXS, NDEGLEXVPTEE:SNIT-AA[17]-QIM:LGEMS:FLQHNKXEXR, SSVKXQPSRVHH:SNIT-AA[17]-QIM:LGEMS:RLEEHLEXAXA, RNVQXRPTQVQL:SNIT-AA[17]-QIM:LGEMS:TLEDHLAXKXE, RNVQXRPSRVQL:RSVK-AA[17]-AKV:KEVQV:TLEEHLAXKXE, KIPKAXXVPTEL:RSVK-AA[17]-AKV:KEVQV:DMVVEGXGXR, GIPEPXXVPEKM:RSVK-AA[17]-AKV:KEVQV:NMTVESXAXR, SIPKAXXVPTEL:RSVK-AA[17]-AKV:KEVQV:EMVVEGXGXR, HVTKPTXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, YVPKPXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, TVPKPXXAPTQL:RSVK-AA[17]-AKV:KEVQV:NMVVRAXGXH, AVPKAXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVKAXGXH, KVGKAXXVPTKL:RSVK-AA[17]-AKV:KEVQV:EGMSVAEXGXR, KASKAXXVPTKL:RSVK-AA[17]-AKV:KEVQV:GMAVSEXGXR, GSAGPXXTPTKM:RSVK-AA[17]-AKV:KEVQV:GMVVDRXGXS, AAPASXXVPARL:RSVK-AA[17]-AKV:KEVQV:DMVVEAXGXR, STPPTXXVPTRL:RSVK-AA[17]-AKV:KEVQV:DMVVESXGXR, HVPKPXXAPTKL:RSVK-AA[17]-AKV:KEVQV:NMVVRSXGXH, RVPSTXXAPVKT:RSVK-AA[17]-

AKV:KEVQV:MIVEEXGXL, ASAAPXXVPQAL:RSVK-AA[17]-AKV:KEVQV:MIVRSXKXS, ASASPXXVSQDL:RSVK-AA[17]-AKV:KEVQV:MIVKSXKXS, ASASPXXVPQDL:RSVK-AA[17]-AKV:KEVQV:MVVKSXKXS, NDEGLEXVPTEE:RSVK-AA[17]-AKV:KEVQV:FLQHNKXEXR, NDEGLEXVPTGQ:RSVK-AA[17]-AKV:KEVQV:LEEHSQXEXR, RNVQXRPTQVQL:RSVK-AA[17]-AKV:KEVQV:TLEDHLAXKXE, SSVKXQPTQVHH:RPVQ-AA[17]-RKI:KKATV:RLEDHLEXAXA, KIPKAXXVPTEL:RPVQ-AA[17]-RKI:KKATV:DMVVEGXGXR, GIPEPXXVPEKM:RPVQ-AA[17]-RKI:KKATV:NMTVESXAXR, SIPKAXXVPTEL:RPVQ-AA[17]-RKI:KKATV:EMVVEGXGXR, HVTKPTXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVRSXGXH, YVPKPXXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVRSXGXH, TVPKPXXAPTQL:RPVQ-AA[17]-RKI:KKATV:NMVVRAXGXH, AVPKAXXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVKAXGXH, KVGKAXXVPTKL:RPVQ-AA[17]-RKI:KKATV:EGMSVAEXGXR, KASKAXXVPTKL:RPVQ-AA[17]-RKI:KKATV:GMAVSEXGXR, GSAGPXXTPTKM:RPVQ-AA[17]-RKI:KKATV:GMVVDRXGXS, AAPASXXVPARL:RPVQ-AA[17]-RKI:KKATV:DMVVEAXGXR, STPPTXXVPTRL:RPVQ-AA[17]-RKI:KKATV:DMVVESXGXR, HVPKPXXAPTKL:RPVQ-AA[17]-RKI:KKATV:NMVVRSXGXH, RVPSTXXAPVKT:RPVQ-AA[17]-RKI:KKATV:MIVEEXGXL, ASAAPXXVPQAL:RPVQ-AA[17]-RKI:KKATV:MIVRSXKXS, ASASPXXVSQDL:RPVQ-AA[17]-RKI:KKATV:MIVKSXKXS, ASASPXXVPQDL:RPVQ-AA[17]-RKI:KKATV:MVVKSXKXS, NDEGLEXVPTEE:RPVQ-AA[17]-RKI:KKATV:FLQHNKXEXR, NDEGLEXVPTGQ:RPVQ-AA[17]-RKI:KKATV:LEEHSQXEXR and SSVKXQPSRVHH:RPVQ-AA17-RKI:KKATV:RLEEHLEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the hexaplet PEP7:PEP3:PEP1:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS:LKNYQ:VVE:SXAXR, SIPKAXX:VPT:SAIS:LKNYQ:VVE:GXGXR, HVTKPTX:VPT:SAIS:LKNYQ:VVE:SXGXH, YVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS:LKNYQ:VVE:AXGXH, AVPKAXX:VPT:SAIS:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS:LKNYQ:VVE:XGXR, KASKAXX:VPT:SAIS:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS:LKNYQ:VVE:RXGXS, AAPASXX:VPT:SAIS:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS:LKNYQ:VVE:SXGXR, HVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS:LKNYQ:VVE:XGXL, ASAAPXX:VPT:SAIS:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS:LKNYQ:VVE:XKXS, NDEGLEX:VPT:SAIS:LKNYQ:VVE:KXEXR, NDEGLEX:VPT:SAIS:LKNYQ:VVE:QXEXR, SSVKXQP:VPT:SAIS:LKNYQ:VVE:LEXAXA, RNVQXRP:VPT:SAIS:LKNYQ:VVE:LAXKXE, GIPEPXX:VPE:SAIS:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS:LKNYQ:VVR:SXGXH, YVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS:LKNYQ:VVR:AXGXH, AVPKAXX:APT:SAIS:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS:LKNYQ:VAE:XGXR, KASKAXX:VPT:SAIS:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS:LKNYQ:VVD:RXGXS, AAPASXX:VPA:SAIS:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH, RVPSTXX:APV:SAIS:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS:LKNYQ:VRS:XKXS, ASASPXX:VSQ:SAIS:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS:LKNYQ:VKS:XKXS, NDEGLEX:VPT:SAIS:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS:LKNYQ:EHS:QXEXR, SSVKXQP:SRV:SAIS:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS:LKNYQ:EDH:LAXKXE, KIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR,

HVTKPTX:VPE:SSLS:LKVYP:TVE:SXGXH,
TVPKPXX:VPE:SSLS:LKVYP:TVE:AXGXH,
KVGKAXX:VPE:SSLS:LKVYP:TVE:XGXR,
GSAGPXX:VPE:SSLS:LKVYP:TVE:RXGXS,
STPPTXX:VPE:SSLS:LKVYP:TVE:SXGXR,
RVPSTXX:VPE:SSLS:LKVYP:TVE:XGXL,
ASASPXX:VPE:SSLS:LKVYP:TVE:XKXS,
NDEGLEX:VPE:SSLS:LKVYP:TVE:QXEXR,
RNVQXRP:VPE:SSLS:LKVYP:TVE:LAXKXE,
SIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR,
YVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH,
AVPKAXX:APT:SSLS:LKVYP:VVK:AXGXH,
KASKAXX:VPT:SSLS:LKVYP:AVS:EXGXR,
AAPASXX:VPA:SSLS:LKVYP:VVE:AXGXR,
HVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH,
ASAAPXX:VPQ:SSLS:LKVYP:VRS:XKXS,
ASASPXX:VPQ:SSLS:LKVYP:VKS:XKXS,
NDEGLEX:VPT:SSLS:LKVYP:EHS:QXEXR,
RNVQXRP:TQV:SSLS:LKVYP:EDH:LAXKXE,
KIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
SIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
TVPKPXX:APT:NAIS:LKKYR:VVR:AXGXH,
KVGKAXX:APT:NAIS:LKKYR:VVR:XGXR,
GSAGPXX:APT:NAIS:LKKYR:VVR:RXGXS,
STPPTXX:APT:NAIS:LKKYR:VVR:SXGXR,
RVPSTXX:APT:NAIS:LKKYR:VVR:XGXL,
ASASPXX:APT:NAIS:LKKYR:VVR:XKXS,
NDEGLEX:APT:NAIS:LKKYR:VVR:QXEXR,
RNVQXRP:APT:NAIS:LKKYR:VVR:LAXKXE,
GIPEPXX:VPE:NAIS:LKKYR:TVE:SXAXR,
AVPKAXX:APT:NAIS:LKKYR:VVK:AXGXH,
KASKAXX:VPT:NAIS:LKKYR:AVS:EXGXR,
AAPASXX:VPA:NAIS:LKKYR:VVE:AXGXR,
RVPSTXX:APV:NAIS:LKKYR:VEE:XGXL,
ASASPXX:VSQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:QHN:KXEXR,
SSVKXQP:SRV:NAIS:LKKYR:EEH:LEXAXA,
HVTKPTX:APT:NAIS:LKKYR:VVR:SXGXH,
GIPEPXX:APT:SATS:LRKHR:VVK:SXAXR,
HVTKPTX:APT:SATS:LRKHR:VVK:SXGXH,
TVPKPXX:APT:SATS:LRKHR:VVK:AXGXH,
KASKAXX:APT:SATS:LRKHR:VVK:EXGXR,

YVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
AVPKAXX:VPE:SSLS:LKVYP:TVE:AXGXH,
KASKAXX:VPE:SSLS:LKVYP:TVE:EXGXR,
AAPASXX:VPE:SSLS:LKVYP:TVE:AXGXR,
HVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
ASAAPXX:VPE:SSLS:LKVYP:TVE:XKXS,
NDEGLEX:VPE:SSLS:LKVYP:TVE:KXEXR,
SSVKXQP:VPE:SSLS:LKVYP:TVE:LEXAXA,
KIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR,
HVTKPTX:APT:SSLS:LKVYP:VVR:SXGXH,
TVPKPXX:APT:SSLS:LKVYP:VVR:AXGXH,
KVGKAXX:VPT:SSLS:LKVYP:VAE:XGXR,
GSAGPXX:TPT:SSLS:LKVYP:VVD:RXGXS,
STPPTXX:VPT:SSLS:LKVYP:VVE:SXGXR,
RVPSTXX:APV:SSLS:LKVYP:VEE:XGXL,
ASASPXX:VSQ:SSLS:LKVYP:VKS:XKXS,
NDEGLEX:VPT:SSLS:LKVYP:QHN:KXEXR,
SSVKXQP:SRV:SSLS:LKVYP:EEH:LEXAXA,
KIPKAXX:VPT:SAIS:LKNYQ:VVE:GXGXR,
GIPEPXX:APT:NAIS:LKKYR:VVR:SXAXR,
YVPKPXX:APT:NAIS:LKKYR:VVR:SXGXH,
AVPKAXX:APT:NAIS:LKKYR:VVR:AXGXH,
KASKAXX:APT:NAIS:LKKYR:VVR:EXGXR,
AAPASXX:APT:NAIS:LKKYR:VVR:AXGXR,
HVPKPXX:APT:NAIS:LKKYR:VVR:SXGXH,
ASAAPXX:APT:NAIS:LKKYR:VVR:XKXS,
NDEGLEX:APT:NAIS:LKKYR:VVR:KXEXR,
SSVKXQP:APT:NAIS:LKKYR:VVR:LEXAXA,
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SIPKAXX:VPT:NAIS:LKKYR:VVE:GXGXR,
KVGKAXX:VPT:NAIS:LKKYR:VAE:XGXR,
GSAGPXX:TPT:NAIS:LKKYR:VVD:RXGXS,
STPPTXX:VPT:NAIS:LKKYR:VVE:SXGXR,
ASAAPXX:VPQ:NAIS:LKKYR:VRS:XKXS,
ASASPXX:VPQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:EHS:QXEXR,
RNVQXRP:TQV:NAIS:LKKYR:EDH:LAXKXE,
KIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
SIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
YVPKPXX:APT:SATS:LRKHR:VVK:SXGXH,
KVGKAXX:APT:SATS:LRKHR:VVK:XGXR,
GSAGPXX:APT:SATS:LRKHR:VVK:RXGXS,

AAPASXX:APT:SATS:LRKHR:VVK:AXGXR,
HVPKPXX:APT:SATS:LRKHR:VVK:SXGXH,
ASAAPXX:APT:SATS:LRKHR:VVK:XKXS,
NDEGLEX:APT:SATS:LRKHR:VVK:KXEXR,
SSVKXQP:APT:SATS:LRKHR:VVK:LEXAXA,
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SSVKXQP:SRV:SATS:LRKHR:EEH:LEXAXA,
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GSAGPXX:VPT:SPIS:LKYHY:VAE:RXGXS,
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TVPKPXX:APT:SPIS:LKYHY:VVR:AXGXH,
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AAPASXX:VPT:EPIS:KFKYE:AVS:AXGXR,
HVPKPXX:VPT:EPIS:KFKYE:AVS:SXGXH,
ASAAPXX:VPT:EPIS:KFKYE:AVS:XKXS,

STPPTXX:APT:SATS:LRKHR:VVK:SXGXR,
RVPSTXX:APT:SATS:LRKHR:VVK:XGXL,
ASASPXX:APT:SATS:LRKHR:VVK:XKXS,
NDEGLEX:APT:SATS:LRKHR:VVK:QXEXR,
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GIPEPXX:VPE:SATS:LRKHR:TVE:SXAXR,
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SSVKXQP:VPA:SPIS:YKQYE:VVE:LEXAXA,
KIPKAXX:VPT:SPIS:YKQYE:VVE:GXGXR,

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GIPEPXX:VPE:EPIS:KFKYE:TVE:SXAXR,
HVTKPTX:APT:EPIS:KFKYE:VVR:SXGXH,
TVPKPXX:APT:EPIS:KFKYE:VVR:AXGXH,
KVGKAXX:VPT:EPIS:KFKYE:VAE:XGXR,
AAPASXX:VPA:EPIS:KFKYE:VVE:AXGXR,
HVPKPXX:APT:EPIS:KFKYE:VVR:SXGXH,
ASAAPXX:VPQ:EPIS:KFKYE:VRS:XKXS,
ASASPXX:VPQ:EPIS:KFKYE:VKS:XKXS,
NDEGLEX:VPT:EPIS:KFKYE:EHS:QXEXR,
RNVQXRP:TQV:EPIS:KFKYE:EDH:LAXKXE,
GIPEPXX:TPT:SPIN:YGKIP:VVD:SXAXR,
HVTKPTX:TPT:SPIN:YGKIP:VVD:SXGXH,
TVPKPXX:TPT:SPIN:YGKIP:VVD:AXGXH,
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AAPASXX:TPT:SPIN:YGKIP:VVD:AXGXR,
HVPKPXX:TPT:SPIN:YGKIP:VVD:SXGXH,
ASAAPXX:TPT:SPIN:YGKIP:VVD:XKXS,
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SIPKAXX:VPT:SPIN:YGKIP:VVE:GXGXR,
YVPKPXX:APT:SPIN:YGKIP:VVR:SXGXH,
AVPKAXX:APT:SPIN:YGKIP:VVK:AXGXH,
KASKAXX:VPT:SPIN:YGKIP:AVS:EXGXR,
STPPTXX:VPT:SPIN:YGKIP:VVE:SXGXR,
RVPSTXX:APV:SPIN:YGKIP:VEE:XGXL,
ASASPXX:VSQ:SPIN:YGKIP:VKS:XKXS,
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SIPKAXX:VPA:SPIS:YKQYE:VVE:GXGXR,
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AVPKAXX:VPA:SPIS:YKQYE:VVE:AXGXH,
KASKAXX:VPA:SPIS:YKQYE:VVE:EXGXR,
STPPTXX:VPA:SPIS:YKQYE:VVE:SXGXR,
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GIPEPXX:VPE:SPIS:YKQYE:TVE:SXAXR,

SIPKAXX:VPT:SPIS:YKQYE:VVE:GXGXR, HVTKPTX:APT:SPIS:YKQYE:VVR:SXGXH,
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STPPTXX:VPT:SPIS:YKQYE:VVE:SXGXR, HVPKPXX:APT:SPIS:YKQYE:VVR:SXGXH,
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AVPKAXX:APV:KPLS:DHHKD:VEE:AXGXH, KVGKAXX:APV:KPLS:DHHKD:VEE:XGXR,
KASKAXX:APV:KPLS:DHHKD:VEE:EXGXR, GSAGPXX:APV:KPLS:DHHKD:VEE:RXGXS,
AAPASXX:APV:KPLS:DHHKD:VEE:AXGXR, STPPTXX:APV:KPLS:DHHKD:VEE:SXGXR,
HVPKPXX:APV:KPLS:DHHKD:VEE:SXGXH, ASAAPXX:APV:KPLS:DHHKD:VEE:XKXS,
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GSAGPXX:TPT:KPLS:DHHKD:VVD:RXGXS, AAPASXX:VPA:KPLS:DHHKD:VVE:AXGXR,
STPPTXX:VPT:KPLS:DHHKD:VVE:SXGXR, HVPKPXX:APT:KPLS:DHHKD:VVR:SXGXH,
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STPPTXX:VPQ:EPLP:EQLSN:VRS:SXGXR, HVPKPXX:VPQ:EPLP:EQLSN:VRS:SXGXH,
RVPSTXX:VPQ:EPLP:EQLSN:VRS:XGXL, ASASPXX:VPQ:EPLP:EQLSN:VRS:XKXS,
NDEGLEX:VPQ:EPLP:EQLSN:VRS:KXEXR, NDEGLEX:VPQ:EPLP:EQLSN:VRS:QXEXR,
SSVKXQP:VPQ:EPLP:EQLSN:VRS:LEXAXA, RNVQXRP:VPQ:EPLP:EQLSN:VRS:LAXKXE,
KIPKAXX:VPT:EPLP:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLP:EQLSN:TVE:SXAXR,
SIPKAXX:VPT:EPLP:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLP:EQLSN:VVR:SXGXH,
YVPKPXX:APT:EPLP:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLP:EQLSN:VVR:AXGXH,
AVPKAXX:APT:EPLP:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLP:EQLSN:VAE:XGXR,
KASKAXX:VPT:EPLP:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLP:EQLSN:VVD:RXGXS,
AAPASXX:VPA:EPLP:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLP:EQLSN:VVE:SXGXR,
HVPKPXX:APT:EPLP:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLP:EQLSN:VEE:XGXL,
ASASPXX:VSQ:EPLP:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLP:EQLSN:VKS:XKXS,
NDEGLEX:VPT:EPLP:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLP:EQLSN:EHS:QXEXR,
SSVKXQP:SRV:EPLP:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLP:EQLSN:EDH:LAXKXE,
KIPKAXX:VSQ:EPLT:EQLSN:VKS:GXGXR, GIPEPXX:VSQ:EPLT:EQLSN:VKS:SXAXR,
SIPKAXX:VSQ:EPLT:EQLSN:VKS:GXGXR, HVTKPTX:VSQ:EPLT:EQLSN:VKS:SXGXH,
YVPKPXX:VSQ:EPLT:EQLSN:VKS:SXGXH, TVPKPXX:VSQ:EPLT:EQLSN:VKS:AXGXH,
AVPKAXX:VSQ:EPLT:EQLSN:VKS:AXGXH, KVGKAXX:VSQ:EPLT:EQLSN:VKS:XGXR,
KASKAXX:VSQ:EPLT:EQLSN:VKS:EXGXR, GSAGPXX:VSQ:EPLT:EQLSN:VKS:RXGXS,
AAPASXX:VSQ:EPLT:EQLSN:VKS:AXGXR, STPPTXX:VSQ:EPLT:EQLSN:VKS:SXGXR,
HVPKPXX:VSQ:EPLT:EQLSN:VKS:SXGXH, RVPSTXX:VSQ:EPLT:EQLSN:VKS:XGXL,
ASAAPXX:VSQ:EPLT:EQLSN:VKS:XKXS, ASASPXX:VSQ:EPLT:EQLSN:VKS:XKXS,
NDEGLEX:VSQ:EPLT:EQLSN:VKS:KXEXR, NDEGLEX:VSQ:EPLT:EQLSN:VKS:QXEXR,
SSVKXQP:VSQ:EPLT:EQLSN:VKS:LEXAXA, RNVQXRP:VSQ:EPLT:EQLSN:VKS:LAXKXE,
KIPKAXX:VPT:EPLT:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLT:EQLSN:TVE:SXAXR,
SIPKAXX:VPT:EPLT:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLT:EQLSN:VVR:SXGXH,
YVPKPXX:APT:EPLT:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLT:EQLSN:VVR:AXGXH,
AVPKAXX:APT:EPLT:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLT:EQLSN:VAE:XGXR,
KASKAXX:VPT:EPLT:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLT:EQLSN:VVD:RXGXS,
AAPASXX:VPA:EPLT:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLT:EQLSN:VVE:SXGXR,
HVPKPXX:APT:EPLT:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLT:EQLSN:VEE:XGXL,
ASAAPXX:VPQ:EPLT:EQLSN:VRS:XKXS, ASASPXX:VPQ:EPLT:EQLSN:VKS:XKXS,
NDEGLEX:VPT:EPLT:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLT:EQLSN:EHS:QXEXR,
SSVKXQP:SRV:EPLT:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT:EQLSN:EDH:LAXKXE,
KIPKAXX:VPQ:EPLT:EQLSN:VKS:GXGXR, GIPEPXX:VPQ:EPLT:EQLSN:VKS:SXAXR,
SIPKAXX:VPQ:EPLT:EQLSN:VKS:GXGXR, HVTKPTX:VPQ:EPLT:EQLSN:VKS:SXGXH,
YVPKPXX:VPQ:EPLT:EQLSN:VKS:SXGXH, TVPKPXX:VPQ:EPLT:EQLSN:VKS:AXGXH,
AVPKAXX:VPQ:EPLT:EQLSN:VKS:AXGXH, KVGKAXX:VPQ:EPLT:EQLSN:VKS:XGXR,
KASKAXX:VPQ:EPLT:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT:EQLSN:VKS:RXGXS,
AAPASXX:VPQ:EPLT:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT:EQLSN:VKS:SXGXR,
HVPKPXX:VPQ:EPLT:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT:EQLSN:VKS:XGXL,

ASAAPXX:VPQ:EPLT:EQLSN:VKS:XKXS,
NDEGLEX:VPQ:EPLT:EQLSN:VKS:QXEXR,
RNVQXRP:VPQ:EPLT:EQLSN:VKS:LAXKXE,
GIPEPXX:VPT:SNIT:IGEMS:QHN:SXAXR,
HVTKPTX:VPT:SNIT:IGEMS:QHN:SXGXH,
TVPKPXX:VPT:SNIT:IGEMS:QHN:AXGXH,
KVGKAXX:VPT:SNIT:IGEMS:QHN:XGXR,
GSAGPXX:VPT:SNIT:IGEMS:QHN:RXGXS,
STPPTXX:VPT:SNIT:IGEMS:QHN:SXGXR,
RVPSTXX:VPT:SNIT:IGEMS:QHN:XGXL,
ASASPXX:VPT:SNIT:IGEMS:QHN:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:QHN:KXEXR,
RNVQXRP:VPT:SNIT:IGEMS:QHN:LAXKXE,
GIPEPXX:VPE:SNIT:IGEMS:TVE:SXAXR,
HVTKPTX:APT:SNIT:IGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:IGEMS:VVR:AXGXH,
KVGKAXX:VPT:SNIT:IGEMS:VAE:XGXR,
GSAGPXX:TPT:SNIT:IGEMS:VVD:RXGXS,
STPPTXX:VPT:SNIT:IGEMS:VVE:SXGXR,
RVPSTXX:APV:SNIT:IGEMS:VEE:XGXL,
ASASPXX:VSQ:SNIT:IGEMS:VKS:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:EHS:QXEXR,
RNVQXRP:TQV:SNIT:IGEMS:EDH:LAXKXE,
GIPEPXX:VPT:SNIT:LGEMS:EHS:SXAXR,
HVTKPTX:VPT:SNIT:LGEMS:EHS:SXGXH,
TVPKPXX:VPT:SNIT:LGEMS:EHS:AXGXH,
KVGKAXX:VPT:SNIT:LGEMS:EHS:XGXR,
GSAGPXX:VPT:SNIT:LGEMS:EHS:RXGXS,
STPPTXX:VPT:SNIT:LGEMS:EHS:SXGXR,
RVPSTXX:VPT:SNIT:LGEMS:EHS:XGXL,
ASASPXX:VPT:SNIT:LGEMS:EHS:XKXS,
SSVKXQP:VPT:SNIT:LGEMS:EHS:LEXAXA,
KIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR,
SIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR,
YVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH,
AVPKAXX:APT:SNIT:LGEMS:VVK:AXGXH,
KASKAXX:VPT:SNIT:LGEMS:AVS:EXGXR,
AAPASXX:VPA:SNIT:LGEMS:VVE:AXGXR,
HVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH,
ASAAPXX:VPQ:SNIT:LGEMS:VRS:XKXS,
ASASPXX:VPQ:SNIT:LGEMS:VKS:XKXS,
SSVKXQP:SRV:SNIT:LGEMS:EEH:LEXAXA,

NDEGLEX:VPQ:EPLT:EQLSN:VKS:KXEXR,
SSVKXQP:VPQ:EPLT:EQLSN:VKS:LEXAXA,
KIPKAXX:VPT:SNIT:IGEMS:QHN:GXGXR,
SIPKAXX:VPT:SNIT:IGEMS:QHN:GXGXR,
YVPKPXX:VPT:SNIT:IGEMS:QHN:SXGXH,
AVPKAXX:VPT:SNIT:IGEMS:QHN:AXGXH,
KASKAXX:VPT:SNIT:IGEMS:QHN:EXGXR,
AAPASXX:VPT:SNIT:IGEMS:QHN:AXGXR,
HVPKPXX:VPT:SNIT:IGEMS:QHN:SXGXH,
ASAAPXX:VPT:SNIT:IGEMS:QHN:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:QHN:QXEXR,
SSVKXQP:VPT:SNIT:IGEMS:QHN:LEXAXA,
KIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
SIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
YVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
AVPKAXX:APT:SNIT:IGEMS:VVK:AXGXH,
KASKAXX:VPT:SNIT:IGEMS:AVS:EXGXR,
AAPASXX:VPA:SNIT:IGEMS:VVE:AXGXR,
HVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
ASAAPXX:VPQ:SNIT:IGEMS:VRS:XKXS,
ASASPXX:VPQ:SNIT:IGEMS:VKS:XKXS,
SSVKXQP:SRV:SNIT:IGEMS:EEH:LEXAXA,
KIPKAXX:VPT:SNIT:LGEMS:EHS:GXGXR,
SIPKAXX:VPT:SNIT:LGEMS:EHS:GXGXR,
YVPKPXX:VPT:SNIT:LGEMS:EHS:SXGXH,
AVPKAXX:VPT:SNIT:LGEMS:EHS:AXGXH,
KASKAXX:VPT:SNIT:LGEMS:EHS:EXGXR,
AAPASXX:VPT:SNIT:LGEMS:EHS:AXGXR,
HVPKPXX:VPT:SNIT:LGEMS:EHS:SXGXH,
ASAAPXX:VPT:SNIT:LGEMS:EHS:XKXS,
NDEGLEX:VPT:SNIT:LGEMS:EHS:KXEXR,
RNVQXRP:VPT:SNIT:LGEMS:EHS:LAXKXE,
GIPEPXX:VPE:SNIT:LGEMS:TVE:SXAXR,
HVTKPTX:APT:SNIT:LGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:LGEMS:VVR:AXGXH,
KVGKAXX:VPT:SNIT:LGEMS:VAE:XGXR,
GSAGPXX:TPT:SNIT:LGEMS:VVD:RXGXS,
STPPTXX:VPT:SNIT:LGEMS:VVE:SXGXR,
RVPSTXX:APV:SNIT:LGEMS:VEE:XGXL,
ASASPXX:VSQ:SNIT:LGEMS:VKS:XKXS,
NDEGLEX:VPT:SNIT:LGEMS:QHN:KXEXR,
RNVQXRP:TQV:SNIT:LGEMS:EDH:LAXKXE,

KIPKAXX:SRV:RSVK:KEVQV:EEH:GXGXR, GIPEPXX:SRV:RSVK:KEVQV:EEH:SXAXR,
SIPKAXX:SRV:RSVK:KEVQV:EEH:GXGXR, HVTKPTX:SRV:RSVK:KEVQV:EEH:SXGXH,
YVPKPXX:SRV:RSVK:KEVQV:EEH:SXGXH, TVPKPXX:SRV:RSVK:KEVQV:EEH:AXGXH,
AVPKAXX:SRV:RSVK:KEVQV:EEH:AXGXH, KVGKAXX:SRV:RSVK:KEVQV:EEH:XGXR,
KASKAXX:SRV:RSVK:KEVQV:EEH:EXGXR, GSAGPXX:SRV:RSVK:KEVQV:EEH:RXGXS,
AAPASXX:SRV:RSVK:KEVQV:EEH:AXGXR, STPPTXX:SRV:RSVK:KEVQV:EEH:SXGXR,
HVPKPXX:SRV:RSVK:KEVQV:EEH:SXGXH, RVPSTXX:SRV:RSVK:KEVQV:EEH:XGXL,
ASAAPXX:SRV:RSVK:KEVQV:EEH:XKXS, ASASPXX:SRV:RSVK:KEVQV:EEH:XKXS,
NDEGLEX:SRV:RSVK:KEVQV:EEH:KXEXR, NDEGLEX:SRV:RSVK:KEVQV:EEH:QXEXR,
RNVQXRP:SRV:RSVK:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
GIPEPXX:VPE:RSVK:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
HVTKPTX:APT:RSVK:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
TVPKPXX:APT:RSVK:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK:KEVQV:VVK:AXGXH,
KVGKAXX:VPT:RSVK:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK:KEVQV:AVS:EXGXR,
GSAGPXX:TPT:RSVK:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK:KEVQV:VVE:AXGXR,
STPPTXX:VPT:RSVK:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
RVPSTXX:APV:RSVK:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK:KEVQV:VRS:XKXS,
ASASPXX:VSQ:RSVK:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK:KEVQV:VKS:XKXS,
NDEGLEX:VPT:RSVK:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK:KEVQV:EHS:QXEXR,
RNVQXRP:TQV:RSVK:KEVQV:EDH:LAXKXE, KIPKAXX:TQV:RPVQ:KKATV:EDH:GXGXR,
GIPEPXX:TQV:RPVQ:KKATV:EDH:SXAXR, SIPKAXX:TQV:RPVQ:KKATV:EDH:GXGXR,
HVTKPTX:TQV:RPVQ:KKATV:EDH:SXGXH, YVPKPXX:TQV:RPVQ:KKATV:EDH:SXGXH,
TVPKPXX:TQV:RPVQ:KKATV:EDH:AXGXH, AVPKAXX:TQV:RPVQ:KKATV:EDH:AXGXH,
KVGKAXX:TQV:RPVQ:KKATV:EDH:XGXR, KASKAXX:TQV:RPVQ:KKATV:EDH:EXGXR,
GSAGPXX:TQV:RPVQ:KKATV:EDH:RXGXS, AAPASXX:TQV:RPVQ:KKATV:EDH:AXGXR,
STPPTXX:TQV:RPVQ:KKATV:EDH:SXGXR, HVPKPXX:TQV:RPVQ:KKATV:EDH:SXGXH,
RVPSTXX:TQV:RPVQ:KKATV:EDH:XGXL, ASAAPXX:TQV:RPVQ:KKATV:EDH:XKXS,
ASASPXX:TQV:RPVQ:KKATV:EDH:XKXS, NDEGLEX:TQV:RPVQ:KKATV:EDH:KXEXR,
NDEGLEX:TQV:RPVQ:KKATV:EDH:QXEXR, SSVKXQP:TQV:RPVQ:KKATV:EDH:LEXAXA,
KIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ:KKATV:TVE:SXAXR,
SIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ:KKATV:VVR:SXGXH,
YVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ:KKATV:VVR:AXGXH,
AVPKAXX:APT:RPVQ:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ:KKATV:VAE:XGXR,
KASKAXX:VPT:RPVQ:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ:KKATV:VVD:RXGXS,
AAPASXX:VPA:RPVQ:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ:KKATV:VVE:SXGXR,
HVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ:KKATV:VEE:XGXL,
ASAAPXX:VPQ:RPVQ:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ:KKATV:VKS:XKXS,
ASASPXX:VPQ:RPVQ:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ:KKATV:QHN:KXEXR,
NDEGLEX:VPT:RPVQ:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ:KKATV:EEH:LEXAXA. More particularly, the hexaplet PEP7:PEP3:PEP1:PEP2:PEP4:PEP8 is selected from the group consisting of
GIPEPXX:VPT:SAIS:LKNYQ:VVE:SXAXR, HVTKPTX:VPT:SAIS:LKNYQ:VVE:SXGXH,
YVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS:LKNYQ:VVE:AXGXH,

AVPKAXX:VPT:SAIS:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS:LKNYQ:VVE:XGXR,
KASKAXX:VPT:SAIS:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS:LKNYQ:VVE:RXGXS,
AAPASXX:VPT:SAIS:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS:LKNYQ:VVE:SXGXR,
HVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS:LKNYQ:VVE:XGXL,
ASAAPXX:VPT:SAIS:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS:LKNYQ:VVE:XKXS,
GIPEPXX:VPE:SAIS:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS:LKNYQ:VVR:SXGXH,
YVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS:LKNYQ:VVR:AXGXH,
AVPKAXX:APT:SAIS:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS:LKNYQ:VAE:XGXR,
KASKAXX:VPT:SAIS:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS:LKNYQ:VVD:RXGXS,
AAPASXX:VPA:SAIS:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH,
RVPSTXX:APV:SAIS:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS:LKNYQ:VRS:XKXS,
ASASPXX:VSQ:SAIS:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS:LKNYQ:VKS:XKXS,
NDEGLEX:VPT:SAIS:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS:LKNYQ:EHS:QXEXR,
SSVKXQP:SRV:SAIS:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS:LKNYQ:EDH:LAXKXE,
KIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR,
HVTKPTX:VPE:SSLS:LKVYP:TVE:SXGXH, YVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
TVPKPXX:VPE:SSLS:LKVYP:TVE:AXGXH, AVPKAXX:VPE:SSLS:LKVYP:TVE:AXGXH,
KVGKAXX:VPE:SSLS:LKVYP:TVE:XGXR, KASKAXX:VPE:SSLS:LKVYP:TVE:EXGXR,
GSAGPXX:VPE:SSLS:LKVYP:TVE:RXGXS, AAPASXX:VPE:SSLS:LKVYP:TVE:AXGXR,
STPPTXX:VPE:SSLS:LKVYP:TVE:SXGXR, HVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
RVPSTXX:VPE:SSLS:LKVYP:TVE:XGXL, ASAAPXX:VPE:SSLS:LKVYP:TVE:XKXS,
ASASPXX:VPE:SSLS:LKVYP:TVE:XKXS, KIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR,
SIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR, HVTKPTX:APT:SSLS:LKVYP:VVR:SXGXH,
YVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH, TVPKPXX:APT:SSLS:LKVYP:VVR:AXGXH,
AVPKAXX:APT:SSLS:LKVYP:VVK:AXGXH, KVGKAXX:VPT:SSLS:LKVYP:VAE:XGXR,
KASKAXX:VPT:SSLS:LKVYP:AVS:EXGXR, GSAGPXX:TPT:SSLS:LKVYP:VVD:RXGXS,
AAPASXX:VPA:SSLS:LKVYP:VVE:AXGXR, STPPTXX:VPT:SSLS:LKVYP:VVE:SXGXR,
HVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH, RVPSTXX:APV:SSLS:LKVYP:VEE:XGXL,
ASAAPXX:VPQ:SSLS:LKVYP:VRS:XKXS, ASASPXX:VSQ:SSLS:LKVYP:VKS:XKXS,
ASASPXX:VPQ:SSLS:LKVYP:VKS:XKXS, NDEGLEX:VPT:SSLS:LKVYP:QHN:KXEXR,
NDEGLEX:VPT:SSLS:LKVYP:EHS:QXEXR, SSVKXQP:SRV:SSLS:LKVYP:EEH:LEXAXA,
RNVQXRP:TQV:SSLS:LKVYP:EDH:LAXKXE, KIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
GIPEPXX:APT:NAIS:LKKYR:VVR:SXAXR, SIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
AVPKAXX:APT:NAIS:LKKYR:VVR:AXGXH, KVGKAXX:APT:NAIS:LKKYR:VVR:XGXR,
KASKAXX:APT:NAIS:LKKYR:VVR:EXGXR, GSAGPXX:APT:NAIS:LKKYR:VVR:RXGXS,
AAPASXX:APT:NAIS:LKKYR:VVR:AXGXR, STPPTXX:APT:NAIS:LKKYR:VVR:SXGXR,
RVPSTXX:APT:NAIS:LKKYR:VVR:XGXL, ASAAPXX:APT:NAIS:LKKYR:VVR:XKXS,
ASASPXX:APT:NAIS:LKKYR:VVR:XKXS, KIPKAXX:VPT:NAIS:LKKYR:VVE:GXGXR,
GIPEPXX:VPE:NAIS:LKKYR:TVE:SXAXR, SIPKAXX:VPT:NAIS:LKKYR:VVE:GXGXR,
AVPKAXX:APT:NAIS:LKKYR:VVK:AXGXH, KVGKAXX:VPT:NAIS:LKKYR:VAE:XGXR,
KASKAXX:VPT:NAIS:LKKYR:AVS:EXGXR, GSAGPXX:TPT:NAIS:LKKYR:VVD:RXGXS,
AAPASXX:VPA:NAIS:LKKYR:VVE:AXGXR, STPPTXX:VPT:NAIS:LKKYR:VVE:SXGXR,

RVPSTXX:APV:NAIS:LKKYR:VEE:XGXL,
ASASPXX:VSQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:QHN:KXEXR,
SSVKXQP:SRV:NAIS:LKKYR:EEH:LEXAXA,
KIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
SIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
YVPKPXX:APT:SATS:LRKHR:VVK:SXGXH,
KVGKAXX:APT:SATS:LRKHR:VVK:XGXR,
GSAGPXX:APT:SATS:LRKHR:VVK:RXGXS,
STPPTXX:APT:SATS:LRKHR:VVK:SXGXR,
RVPSTXX:APT:SATS:LRKHR:VVK:XGXL,
ASASPXX:APT:SATS:LRKHR:VVK:XKXS,
GIPEPXX:VPE:SATS:LRKHR:TVE:SXAXR,
HVTKPTX:APT:SATS:LRKHR:VVR:SXGXH,
TVPKPXX:APT:SATS:LRKHR:VVR:AXGXH,
KASKAXX:VPT:SATS:LRKHR:AVS:EXGXR,
AAPASXX:VPA:SATS:LRKHR:VVE:AXGXR,
HVPKPXX:APT:SATS:LRKHR:VVR:SXGXH,
ASAAPXX:VPQ:SATS:LRKHR:VRS:XKXS,
ASASPXX:VPQ:SATS:LRKHR:VKS:XKXS,
NDEGLEX:VPT:SATS:LRKHR:EHS:QXEXR,
SSVKXQP:SRV:SATS:LRKHR:EEH:LEXAXA,
RNVQXRP:TQV:SATS:LRKHR:EDH:LAXKXE,
GIPEPXX:VPT:SPIS:LKYHY:VAE:SXAXR,
HVTKPTX:VPT:SPIS:LKYHY:VAE:SXGXH,
TVPKPXX:VPT:SPIS:LKYHY:VAE:AXGXH,
KASKAXX:VPT:SPIS:LKYHY:VAE:EXGXR,
AAPASXX:VPT:SPIS:LKYHY:VAE:AXGXR,
HVPKPXX:VPT:SPIS:LKYHY:VAE:SXGXH,
ASAAPXX:VPT:SPIS:LKYHY:VAE:XKXS,
KIPKAXX:VPT:SPIS:LKYHY:VVE:GXGXR,
SIPKAXX:VPT:SPIS:LKYHY:VVE:GXGXR,
YVPKPXX:APT:SPIS:LKYHY:VVR:SXGXH,
AVPKAXX:APT:SPIS:LKYHY:VVK:AXGXH,
GSAGPXX:TPT:SPIS:LKYHY:VVD:RXGXS,
STPPTXX:VPT:SPIS:LKYHY:VVE:SXGXR,
RVPSTXX:APV:SPIS:LKYHY:VEE:XGXL,
ASASPXX:VSQ:SPIS:LKYHY:VKS:XKXS,
NDEGLEX:VPT:SPIS:LKYHY:QHN:KXEXR,
SSVKXQP:SRV:SPIS:LKYHY:EEH:LEXAXA,
KIPKAXX:VPT:EPIS:KFKYE:AVS:GXGXR,
SIPKAXX:VPT:EPIS:KFKYE:AVS:GXGXR,
YVPKPXX:VPT:EPIS:KFKYE:AVS:SXGXH,

ASAAPXX:VPQ:NAIS:LKKYR:VRS:XKXS,
ASASPXX:VPQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:EHS:QXEXR,
RNVQXRP:TQV:NAIS:LKKYR:EDH:LAXKXE,
GIPEPXX:APT:SATS:LRKHR:VVK:SXAXR,
HVTKPTX:APT:SATS:LRKHR:VVK:SXGXH,
TVPKPXX:APT:SATS:LRKHR:VVK:AXGXH,
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AAPASXX:APT:SATS:LRKHR:VVK:AXGXR,
HVPKPXX:APT:SATS:LRKHR:VVK:SXGXH,
ASAAPXX:APT:SATS:LRKHR:VVK:XKXS,
KIPKAXX:VPT:SATS:LRKHR:VVE:GXGXR,
SIPKAXX:VPT:SATS:LRKHR:VVE:GXGXR,
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NDEGLEX:VPT:SATS:LRKHR:QHN:KXEXR,
SSVKXQP:SRV:SATS:LRKHR:EEH:LEXAXA,
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SIPKAXX:VPT:SPIS:LKYHY:VAE:GXGXR,
YVPKPXX:VPT:SPIS:LKYHY:VAE:SXGXH,
AVPKAXX:VPT:SPIS:LKYHY:VAE:AXGXH,
GSAGPXX:VPT:SPIS:LKYHY:VAE:RXGXS,
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ASASPXX:VPQ:SPIS:LKYHY:VKS:XKXS,
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GIPEPXX:VPT:EPIS:KFKYE:AVS:SXAXR,
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AVPKAXX:VPT:EPIS:KFKYE:AVS:AXGXH,
GSAGPXX:VPT:EPIS:KFKYE:AVS:RXGXS,
STPPTXX:VPT:EPIS:KFKYE:AVS:SXGXR,
RVPSTXX:VPT:EPIS:KFKYE:AVS:XGXL,
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GIPEPXX:APV:KPLS:DHHKD:VEE:SXAXR, SIPKAXX:APV:KPLS:DHHKD:VEE:GXGXR,
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GSAGPXX:APV:KPLS:DHHKD:VEE:RXGXS, AAPASXX:APV:KPLS:DHHKD:VEE:AXGXR,
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AVPKAXX:APT:KPLS:DHHKD:VVK:AXGXH, KVGKAXX:VPT:KPLS:DHHKD:VAE:XGXR,
KASKAXX:VPT:KPLS:DHHKD:AVS:EXGXR, GSAGPXX:TPT:KPLS:DHHKD:VVD:RXGXS,
AAPASXX:VPA:KPLS:DHHKD:VVE:AXGXR, STPPTXX:VPT:KPLS:DHHKD:VVE:SXGXR,
HVPKPXX:APT:KPLS:DHHKD:VVR:SXGXH, ASAAPXX:VPQ:KPLS:DHHKD:VRS:XKXS,
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SSVKXQP:SRV:KPLS:DHHKD:EEH:LEXAXA, RNVQXRP:TQV:KPLS:DHHKD:EDH:LAXKXE,
KIPKAXX:VPQ:EPLP:EQLSN:VRS:GXGXR, GIPEPXX:VPQ:EPLP:EQLSN:VRS:SXAXR,
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AVPKAXX:VPQ:EPLP:EQLSN:VRS:AXGXH, KVGKAXX:VPQ:EPLP:EQLSN:VRS:XGXR,
KASKAXX:VPQ:EPLP:EQLSN:VRS:EXGXR, GSAGPXX:VPQ:EPLP:EQLSN:VRS:RXGXS,
AAPASXX:VPQ:EPLP:EQLSN:VRS:AXGXR, STPPTXX:VPQ:EPLP:EQLSN:VRS:SXGXR,
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KVGKAXX:VSQ:EPLT:EQLSN:VKS:XGXR, KASKAXX:VSQ:EPLT:EQLSN:VKS:EXGXR,
GSAGPXX:VSQ:EPLT:EQLSN:VKS:RXGXS, AAPASXX:VSQ:EPLT:EQLSN:VKS:AXGXR,
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GIPEPXX:VPE:EPLT:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLT:EQLSN:VVE:GXGXR,
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KVGKAXX:VPT:EPLT:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLT:EQLSN:AVS:EXGXR,
GSAGPXX:TPT:EPLT:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLT:EQLSN:VVE:AXGXR,
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SSVKXQP:SRV:EPLT:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT:EQLSN:EDH:LAXKXE,
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KASKAXX:VPQ:EPLT:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT:EQLSN:VKS:RXGXS,
AAPASXX:VPQ:EPLT:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT:EQLSN:VKS:SXGXR,
HVPKPXX:VPQ:EPLT:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT:EQLSN:VKS:XGXL,
ASAAPXX:VPQ:EPLT:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLT:EQLSN:VKS:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:QHN:QXEXR, KIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
GIPEPXX:VPE:SNIT:IGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
HVTKPTX:APT:SNIT:IGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:IGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT:IGEMS:VVK:AXGXH,
KVGKAXX:VPT:SNIT:IGEMS:VAE:XGXR, KASKAXX:VPT:SNIT:IGEMS:AVS:EXGXR,
GSAGPXX:TPT:SNIT:IGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT:IGEMS:VVE:AXGXR,
STPPTXX:VPT:SNIT:IGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
RVPSTXX:APV:SNIT:IGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT:IGEMS:VRS:XKXS,
ASASPXX:VSQ:SNIT:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT:IGEMS:VKS:XKXS,

NDEGLEX:VPT:SNIT:IGEMS:EHS:QXEXR, SSVKXQP:SRV:SNIT:IGEMS:EEH:LEXAXA,
RNVQXRP:TQV:SNIT:IGEMS:EDH:LAXKXE, NDEGLEX:VPT:SNIT:LGEMS:EHS:KXEXR,
KIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT:LGEMS:TVE:SXAXR,
SIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT:LGEMS:VVR:SXGXH,
YVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT:LGEMS:VVR:AXGXH,
AVPKAXX:APT:SNIT:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT:LGEMS:VAE:XGXR,
KASKAXX:VPT:SNIT:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT:LGEMS:VVD:RXGXS,
AAPASXX:VPA:SNIT:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT:LGEMS:VVE:SXGXR,
HVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT:LGEMS:VEE:XGXL,
ASAAPXX:VPQ:SNIT:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT:LGEMS:VKS:XKXS,
ASASPXX:VPQ:SNIT:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT:LGEMS:QHN:KXEXR,
SSVKXQP:SRV:SNIT:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT:LGEMS:EDH:LAXKXE,
RNVQXRP:SRV:RSVK:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
GIPEPXX:VPE:RSVK:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
HVTKPTX:APT:RSVK:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
TVPKPXX:APT:RSVK:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK:KEVQV:VVK:AXGXH,
KVGKAXX:VPT:RSVK:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK:KEVQV:AVS:EXGXR,
GSAGPXX:TPT:RSVK:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK:KEVQV:VVE:AXGXR,
STPPTXX:VPT:RSVK:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
RVPSTXX:APV:RSVK:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK:KEVQV:VRS:XKXS,
ASASPXX:VSQ:RSVK:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK:KEVQV:VKS:XKXS,
NDEGLEX:VPT:RSVK:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK:KEVQV:EHS:QXEXR,
RNVQXRP:TQV:RSVK:KEVQV:EDH:LAXKXE, SSVKXQP:TQV:RPVQ:KKATV:EDH:LEXAXA,
KIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ:KKATV:TVE:SXAXR,
SIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ:KKATV:VVR:SXGXH,
YVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ:KKATV:VVR:AXGXH,
AVPKAXX:APT:RPVQ:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ:KKATV:VAE:XGXR,
KASKAXX:VPT:RPVQ:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ:KKATV:VVD:RXGXS,
AAPASXX:VPA:RPVQ:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ:KKATV:VVE:SXGXR,
HVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ:KKATV:VEE:XGXL,
ASAAPXX:VPQ:RPVQ:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ:KKATV:VKS:XKXS,
ASASPXX:VPQ:RPVQ:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ:KKATV:QHN:KXEXR,
NDEGLEX:VPT:RPVQ:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ:KKATV:EEH:LEXAXA.

In particular, in certain embodiments, the hexaplet PEP7:PEP3:PEP12:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:SXAXR, SIPKAXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:GXGXR, HVTKPTX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:SXGXH, YVPKPXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:AXGXH, AVPKAXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:XGXR, KASKAXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:RXGXS, AAPASXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS-AA^{17}-LYL:LKNYQ:VVE:SXGXR, HVPKPXX:VPT:SAIS-

AA[17]-LYL:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XGXL, ASAAPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:QXEXR, SSVKXQP:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:LEXAXA, RNVQXRP:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:LAXKXE, GIPEPXX:VPE:SAIS-AA[17]-LYL:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, YVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:AXGXH, AVPKAXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VAE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS-AA[17]-LYL:LKNYQ:VVD:RXGXS, AAPASXX:VPA:SAIS-AA[17]-LYL:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, RVPSTXX:APV:SAIS-AA[17]-LYL:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS-AA[17]-LYL:LKNYQ:VRS:XKXS, ASASPXX:VSQ:SAIS-AA[17]-LYL:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS-AA[17]-LYL:LKNYQ:VKS:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:EHS:QXEXR, SSVKXQP:SRV:SAIS-AA[17]-LYL:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS-AA[17]-LYL:LKNYQ:EDH:LAXKXE, KIPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:GXGXR, HVTKPTX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, YVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, TVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXH, AVPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXH, KVGKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XGXR, KASKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:EXGXR, GSAGPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:RXGXS, AAPASXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXR, STPPTXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXR, HVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, RVPSTXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XGXL, ASAAPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XKXS, NDEGLEX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:KXEXR, NDEGLEX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:QXEXR, SSVKXQP:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:LEXAXA, RNVQXRP:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:LAXKXE, KIPKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VVE:GXGXR, SIPKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VVE:GXGXR, HVTKPTX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, YVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, TVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:AXGXH, AVPKAXX:APT:SSLS-AA[17]-LFF:LKVYP:VVK:AXGXH, KVGKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VAE:XGXR, KASKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:AVS:EXGXR, GSAGPXX:TPT:SSLS-AA[17]-LFF:LKVYP:VVD:RXGXS, AAPASXX:VPA:SSLS-AA[17]-LFF:LKVYP:VVE:AXGXR, STPPTXX:VPT:SSLS-AA[17]-LFF:LKVYP:VVE:SXGXR, HVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, RVPSTXX:APV:SSLS-AA[17]-LFF:LKVYP:VEE:XGXL, ASAAPXX:VPQ:SSLS-AA[17]-LFF:LKVYP:VRS:XKXS, ASASPXX:VSQ:SSLS-AA[17]-LFF:LKVYP:VKS:XKXS, ASASPXX:VPQ:SSLS-AA[17]-LFF:LKVYP:VKS:XKXS, NDEGLEX:VPT:SSLS-AA[17]-LFF:LKVYP:QHN:KXEXR, NDEGLEX:VPT:SSLS-AA[17]-LFF:LKVYP:EHS:QXEXR, SSVKXQP:SRV:SSLS-AA[17]-LFF:LKVYP:EEH:LEXAXA, RNVQXRP:TQV:SSLS-AA[17]-LFF:LKVYP:EDH:LAXKXE, KIPKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:GXGXR, KIPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:GXGXR, GIPEPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXAXR, SIPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:GXGXR, YVPKPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXGXH, TVPKPXX:APT:NAIS-AA[17]-

LYF:LKKYR:VVR:AXGXH, AVPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:AXGXH, KVGKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XGXR, KASKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:EXGXR, GSAGPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:RXGXS, AAPASXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:AXGXR, STPPTXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXGXR, HVPKPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXGXH, RVPSTXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XGXL, ASAAPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XKXS, NDEGLEX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:KXEXR, NDEGLEX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:QXEXR, SSVKXQP:APT:NAIS-AA[17]-LYF:LKKYR:VVR:LEXAXA, RNVQXRP:APT:NAIS-AA[17]-LYF:LKKYR:VVR:LAXKXE, KIPKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:GXGXR, GIPEPXX:VPE:NAIS-AA[17]-LYF:LKKYR:TVE:SXAXR, SIPKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVK:AXGXH, KVGKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VAE:XGXR, KASKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:AVS:EXGXR, GSAGPXX:TPT:NAIS-AA[17]-LYF:LKKYR:VVD:RXGXS, AAPASXX:VPA:NAIS-AA[17]-LYF:LKKYR:VVE:AXGXR, STPPTXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:SXGXR, RVPSTXX:APV:NAIS-AA[17]-LYF:LKKYR:VEE:XGXL, ASAAPXX:VPQ:NAIS-AA[17]-LYF:LKKYR:VRS:XKXS, ASASPXX:VSQ:NAIS-AA[17]-LYF:LKKYR:VKS:XKXS, ASASPXX:VPQ:NAIS-AA[17]-LYF:LKKYR:VKS:XKXS, NDEGLEX:VPT:NAIS-AA[17]-LYF:LKKYR:QHN:KXEXR, NDEGLEX:VPT:NAIS-AA[17]-LYF:LKKYR:EHS:QXEXR, SSVKXQP:SRV:NAIS-AA[17]-LYF:LKKYR:EEH:LEXAXA, RNVQXRP:TQV:NAIS-AA[17]-LYF:LKKYR:EDH:LAXKXE, HVTKPTX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXGXH, KIPKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:GXGXR, GIPEPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXAXR, SIPKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:AXGXH, KVGKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XGXR, KASKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:EXGXR, GSAGPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:RXGXS, AAPASXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:AXGXR, STPPTXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, RVPSTXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XGXL, ASAAPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XKXS, NDEGLEX:APT:SATS-AA[17]-LYY:LRKHR:VVK:KXEXR, NDEGLEX:APT:SATS-AA[17]-LYY:LRKHR:VVK:QXEXR, SSVKXQP:APT:SATS-AA[17]-LYY:LRKHR:VVK:LEXAXA, RNVQXRP:APT:SATS-AA[17]-LYY:LRKHR:VVK:LAXKXE, KIPKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:GXGXR, GIPEPXX:VPE:SATS-AA[17]-LYY:LRKHR:TVE:SXAXR, SIPKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:AXGXH, KVGKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VAE:XGXR, KASKAXX:VPT:SATS-AA[17]-LYY:LRKHR:AVS:EXGXR, GSAGPXX:TPT:SATS-AA[17]-LYY:LRKHR:VVD:RXGXS, AAPASXX:VPA:SATS-AA[17]-LYY:LRKHR:VVE:AXGXR, STPPTXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, RVPSTXX:APV:SATS-AA[17]-LYY:LRKHR:VEE:XGXL, ASAAPXX:VPQ:SATS-AA[17]-LYY:LRKHR:VRS:XKXS, ASASPXX:VSQ:SATS-AA[17]-LYY:LRKHR:VKS:XKXS, ASASPXX:VPQ:SATS-AA[17]-LYY:LRKHR:VKS:XKXS, NDEGLEX:VPT:SATS-AA[17]-LYY:LRKHR:QHN:KXEXR,

NDEGLEX:VPT:SATS-AA[17]-LYY:LRKHR:EHS:QXEXR, SSVKXQP:SRV:SATS-AA[17]-LYY:LRKHR:EEH:LEXAXA, RNVQXRP:TQV:SATS-AA[17]-LYY:LRKHR:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXR, HVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:QXEXR, SSVKXQP:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:LEXAXA, RNVQXRP:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYK:LKYHY:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYK:LKYHY:VVK:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYK:LKYHY:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LYK:LKYHY:VVE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYK:LKYHY:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYK:LKYHY:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYK:LKYHY:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYK:LKYHY:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYK:LKYHY:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYK:LKYHY:EDH:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:GXGXR, GIPEPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:GXGXR, HVTKPTX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, YVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, TVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXH, AVPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XGXR, GSAGPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:RXGXS, AAPASXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXR, HVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, RVPSTXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XGXL, ASAAPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XKXS, NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:QXEXR, SSVKXQP:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:LEXAXA, RNVQXRP:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:GXGXR, GIPEPXX:VPE:EPIS-AA[17]-LYL:KFKYE:TVE:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:GXGXR, HVTKPTX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, YVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, TVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:AXGXH, AVPKAXX:APT:EPIS-AA[17]-LYL:KFKYE:VVK:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VAE:XGXR, GSAGPXX:TPT:EPIS-AA[17]-LYL:KFKYE:VVD:RXGXS, AAPASXX:VPA:EPIS-

AA[17]-LYL:KFKYE:VVE:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:SXGXR, HVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, RVPSTXX:APV:EPIS-AA[17]-LYL:KFKYE:VEE:XGXL, ASAAPXX:VPQ:EPIS-AA[17]-LYL:KFKYE:VRS:XKXS, ASASPXX:VSQ:EPIS-AA[17]-LYL:KFKYE:VKS:XKXS, ASASPXX:VPQ:EPIS-AA[17]-LYL:KFKYE:VKS:XKXS, NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:QHN:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:EHS:QXEXR, SSVKXQP:SRV:EPIS-AA[17]-LYL:KFKYE:EEH:LEXAXA, RNVQXRP:TQV:EPIS-AA[17]-LYL:KFKYE:EDH:LAXKXE, KIPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:GXGXR, GIPEPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXAXR, SIPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:GXGXR, HVTKPTX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, YVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, TVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXH, AVPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXH, KVGKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XGXR, KASKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:EXGXR, AAPASXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXR, STPPTXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXR, HVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, RVPSTXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XGXL, ASAAPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XKXS, NDEGLEX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:KXEXR, NDEGLEX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:QXEXR, SSVKXQP:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:LEXAXA, RNVQXRP:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:LAXKXE, KIPKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:GXGXR, GIPEPXX:VPE:SPIN-AA[17]-LYF:YGKIP:TVE:SXAXR, SIPKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:GXGXR, HVTKPTX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, YVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, TVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:AXGXH, AVPKAXX:APT:SPIN-AA[17]-LYF:YGKIP:VVK:AXGXH, KVGKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VAE:XGXR, KASKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:AVS:EXGXR, AAPASXX:VPA:SPIN-AA[17]-LYF:YGKIP:VVE:AXGXR, STPPTXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:SXGXR, HVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, RVPSTXX:APV:SPIN-AA[17]-LYF:YGKIP:VEE:XGXL, ASAAPXX:VPQ:SPIN-AA[17]-LYF:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN-AA[17]-LYF:YGKIP:VKS:XKXS, ASASPXX:VPQ:SPIN-AA[17]-LYF:YGKIP:VKS:XKXS, NDEGLEX:VPT:SPIN-AA[17]-LYF:YGKIP:QHN:KXEXR, NDEGLEX:VPT:SPIN-AA[17]-LYF:YGKIP:EHS:QXEXR, SSVKXQP:SRV:SPIN-AA[17]-LYF:YGKIP:EEH:LEXAXA, RNVQXRP:TQV:SPIN-AA[17]-LYF:YGKIP:EDH:LAXKXE, KIPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, GIPEPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXAXR, SIPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, HVTKPTX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, YVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, TVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:AXGXH, AVPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:AXGXH, KVGKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XGXR, KASKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:EXGXR, GSAGPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:RXGXS, STPPTXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXR, HVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, RVPSTXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XGXL, ASAAPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XKXS, NDEGLEX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:KXEXR, NDEGLEX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:QXEXR, SSVKXQP:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:LEXAXA, RNVQXRP:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYI:YKQYE:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR,

HVTKPTX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYI:YKQYE:VVD:RXGXS, STPPTXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYI:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYI:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYI:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYI:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYI:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYI:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYI:YKQYE:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXR, HVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:QXEXR, SSVKXQP:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:LEXAXA, RNVQXRP:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:LAXKXE, GIPEPXX:VPE:SPIS-AA[17]-LFI:YKQYE:TVE:SXAXR, HVTKPTX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LFI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LFI:YKQYE:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXR, HVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LFI:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LFI:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LFI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LFI:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LFI:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LFI:YKQYE:EDH:LAXKXE, KIPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:GXGXR, GIPEPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXAXR, SIPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:GXGXR, HVTKPTX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, YVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, TVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXH, AVPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXH, KVGKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XGXR, KASKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:EXGXR, GSAGPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:RXGXS, AAPASXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXR, STPPTXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXR, HVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, ASAAPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XKXS, NDEGLEX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:KXEXR, NDEGLEX:APV:KPLS-

AA[17]-LYV:DHHKD:VEE:QXEXR, SSVKXQP:APV:KPLS-AA[17]-LYV:DHHKD:VEE:LEXAXA, RNVQXRP:APV:KPLS-AA[17]-LYV:DHHKD:VEE:LAXKXE, KIPKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:GXGXR, GIPEPXX:VPE:KPLS-AA[17]-LYV:DHHKD:TVE:SXAXR, SIPKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:GXGXR, HVTKPTX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, YVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, TVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:AXGXH, AVPKAXX:APT:KPLS-AA[17]-LYV:DHHKD:VVK:AXGXH, KVGKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VAE:XGXR, KASKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:AVS:EXGXR, GSAGPXX:TPT:KPLS-AA[17]-LYV:DHHKD:VVD:RXGXS, AAPASXX:VPA:KPLS-AA[17]-LYV:DHHKD:VVE:AXGXR, STPPTXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:SXGXR, HVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, ASAAPXX:VPQ:KPLS-AA[17]-LYV:DHHKD:VRS:XKXS, ASASPXX:VSQ:KPLS-AA[17]-LYV:DHHKD:VKS:XKXS, ASASPXX:VPQ:KPLS-AA[17]-LYV:DHHKD:VKS:XKXS, NDEGLEX:VPT:KPLS-AA[17]-LYV:DHHKD:QHN:KXEXR, NDEGLEX:VPT:KPLS-AA[17]-LYV:DHHKD:EHS:QXEXR, SSVKXQP:SRV:KPLS-AA[17]-LYV:DHHKD:EEH:LEXAXA, RNVQXRP:TQV:KPLS-AA[17]-LYV:DHHKD:EDH:LAXKXE, KIPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:GXGXR, GIPEPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXAXR, SIPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:GXGXR, HVTKPTX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, YVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, TVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXH, AVPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXH, KVGKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XGXR, KASKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:EXGXR, GSAGPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:RXGXS, AAPASXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXR, STPPTXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXR, HVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, RVPSTXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XGXL, ASASPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XKXS, NDEGLEX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:KXEXR, NDEGLEX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:QXEXR, SSVKXQP:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:LEXAXA, RNVQXRP:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:LAXKXE, KIPKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLP-AA[17]-VYY:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLP-AA[17]-VYY:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLP-AA[17]-VYY:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLP-AA[17]-VYY:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLP-AA[17]-VYY:EQLSN:VEE:XGXL, ASASPXX:VSQ:EPLP-AA[17]-VYY:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLP-AA[17]-VYY:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLP-AA[17]-VYY:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLP-AA[17]-VYY:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLP-AA[17]-VYY:EQLSN:EDH:LAXKXE, KIPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, GIPEPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXAXR, SIPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, HVTKPTX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH,

YVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, TVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, AVPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, KVGKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXR, KASKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:EXGXR, GSAGPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:RXGXS, AAPASXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXR, STPPTXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXR, HVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, RVPSTXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXL, ASAAPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, ASASPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, NDEGLEX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:KXEXR, NDEGLEX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:QXEXR, SSVKXQP:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:LEXAXA, RNVQXRP:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:LAXKXE, KIPKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLT-AA[17]-LYY:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLT-AA[17]-LYY:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLT-AA[17]-LYY:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLT-AA[17]-LYY:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLT-AA[17]-LYY:EQLSN:VEE:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VRS:XKXS, ASASPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLT-AA[17]-LYY:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLT-AA[17]-LYY:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLT-AA[17]-LYY:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT-AA[17]-LYY:EQLSN:EDH:LAXKXE, KIPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, GIPEPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXAXR, SIPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, HVTKPTX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, YVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, TVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, AVPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, KVGKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXR, KASKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:RXGXS, AAPASXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXR, HVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, NDEGLEX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:KXEXR, NDEGLEX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:QXEXR, SSVKXQP:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:LEXAXA, RNVQXRP:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:GXGXR, GIPEPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:GXGXR, HVTKPTX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:SXGXH, YVPKPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:SXGXH, TVPKPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:AXGXH, AVPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:EXGXR, GSAGPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:RXGXS, AAPASXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:SXGXR, HVPKPXX:VPT:SNIT-

AA[17]-QIM:IGEMS:QHN:SXGXH, RVPSTXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:XGXL, ASAAPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:QXEXR, NDEGLEX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:KXEXR, SSVKXQP:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:LEXAXA, RNVQXRP:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:IGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:IGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:IGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:IGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:IGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:IGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:IGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:IGEMS:EHS:QXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:IGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:IGEMS:EDH:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:GXGXR, GIPEPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:GXGXR, HVTKPTX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:SXGXH, YVPKPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:SXGXH, TVPKPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:AXGXH, AVPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:EXGXR, GSAGPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:RXGXS, AAPASXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:SXGXR, HVPKPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:SXGXH, RVPSTXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:XGXL, ASAAPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:KXEXR, SSVKXQP:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:LEXAXA, RNVQXRP:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:LGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:LGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:LGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:LGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:LGEMS:QHN:KXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:LGEMS:EDH:LAXKXE, KIPKAXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:GXGXR, GIPEPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:SXAXR, SIPKAXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:GXGXR,

HVTKPTX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:SXGXH, YVPKPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:SXGXH, TVPKPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:AXGXH, AVPKAXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:AXGXH, KVGKAXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:XGXR, KASKAXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:EXGXR, GSAGPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:RXGXS, AAPASXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:AXGXR, STPPTXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:SXGXR, HVPKPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:SXGXH, RVPSTXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:XGXL, ASAAPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:XKXS, ASASPXX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:XKXS, NDEGLEX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:KXEXR, NDEGLEX:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:QXEXR, RNVQXRP:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:GXGXR, GIPEPXX:VPE:RSVK-AA[17]-AKV:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:GXGXR, HVTKPTX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:SXGXH, TVPKPXX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK-AA[17]-AKV:KEVQV:VVK:AXGXH, KVGKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:AVS:EXGXR, GSAGPXX:TPT:RSVK-AA[17]-AKV:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK-AA[17]-AKV:KEVQV:VVE:AXGXR, STPPTXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:SXGXH, RVPSTXX:APV:RSVK-AA[17]-AKV:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK-AA[17]-AKV:KEVQV:VRS:XKXS, ASASPXX:VSQ:RSVK-AA[17]-AKV:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK-AA[17]-AKV:KEVQV:VKS:XKXS, NDEGLEX:VPT:RSVK-AA[17]-AKV:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK-AA[17]-AKV:KEVQV:EHS:QXEXR, RNVQXRP:TQV:RSVK-AA[17]-AKV:KEVQV:EDH:LAXKXE, KIPKAXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:GXGXR, GIPEPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:SXAXR, SIPKAXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:GXGXR, HVTKPTX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:SXGXH, YVPKPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:SXGXH, TVPKPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:AXGXH, AVPKAXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:AXGXH, KVGKAXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:XGXR, KASKAXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:EXGXR, GSAGPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:RXGXS, AAPASXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:AXGXR, STPPTXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:SXGXR, HVPKPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:SXGXH, RVPSTXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:XGXL, ASAAPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:XKXS, ASASPXX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:XKXS, NDEGLEX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:KXEXR, NDEGLEX:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:QXEXR, SSVKXQP:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:LEXAXA, KIPKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ-AA[17]-RKI:KKATV:TVE:SXAXR, SIPKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, YVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:AXGXH, AVPKAXX:APT:RPVQ-AA[17]-RKI:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VAE:XGXR, KASKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ-AA[17]-RKI:KKATV:VVD:RXGXS, AAPASXX:VPA:RPVQ-AA[17]-

RKI:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:SXGXR, HVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ-AA[17]-RKI:KKATV:VEE:XGXL, ASAAPXX:VPQ:RPVQ-AA[17]-RKI:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ-AA[17]-RKI:KKATV:VKS:XKXS, ASASPXX:VPQ:RPVQ-AA[17]-RKI:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ-AA[17]-RKI:KKATV:QHN:KXEXR, NDEGLEX:VPT:RPVQ-AA[17]-RKI:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ-AA[17]-RKI:KKATV:EEH:LEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T). More particularly, the hexaplet PEP7:PEP3:PEP12:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:SXAXR, HVTKPTX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:SXGXH, YVPKPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:AXGXH, AVPKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:RXGXS, AAPASXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:SXGXR, HVPKPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XGXL, ASAAPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VVE:XKXS, GIPEPXX:VPE:SAIS-AA[17]-LYL:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, YVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:AXGXH, AVPKAXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:VAE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS-AA[17]-LYL:LKNYQ:VVD:RXGXS, AAPASXX:VPA:SAIS-AA[17]-LYL:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS-AA[17]-LYL:LKNYQ:VVR:SXGXH, RVPSTXX:APV:SAIS-AA[17]-LYL:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS-AA[17]-LYL:LKNYQ:VRS:XKXS, ASASPXX:VSQ:SAIS-AA[17]-LYL:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS-AA[17]-LYL:LKNYQ:VKS:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:LKNYQ:EHS:QXEXR, SSVKXQP:SRV:SAIS-AA[17]-LYL:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS-AA[17]-LYL:LKNYQ:EDH:LAXKXE, KIPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:GXGXR, HVTKPTX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, YVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, TVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXH, AVPKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXH, KVGKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XGXR, KASKAXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:EXGXR, GSAGPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:RXGXS, AAPASXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:AXGXR, STPPTXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXR, HVPKPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:SXGXH, RVPSTXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XGXL, ASAAPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:LKVYP:TVE:XKXS, KIPKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VVE:GXGXR, SIPKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VVE:GXGXR, HVTKPTX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, YVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, TVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:AXGXH, AVPKAXX:APT:SSLS-AA[17]-LFF:LKVYP:VVK:AXGXH, KVGKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:VAE:XGXR, KASKAXX:VPT:SSLS-AA[17]-LFF:LKVYP:AVS:EXGXR, GSAGPXX:TPT:SSLS-AA[17]-LFF:LKVYP:VVD:RXGXS, AAPASXX:VPA:SSLS-AA[17]-LFF:LKVYP:VVE:AXGXR, STPPTXX:VPT:SSLS-

AA[17]-LFF:LKVYP:VVE:SXGXR, HVPKPXX:APT:SSLS-AA[17]-LFF:LKVYP:VVR:SXGXH, RVPSTXX:APV:SSLS-AA[17]-LFF:LKVYP:VEE:XGXL, ASAAPXX:VPQ:SSLS-AA[17]-LFF:LKVYP:VRS:XKXS, ASASPXX:VSQ:SSLS-AA[17]-LFF:LKVYP:VKS:XKXS, ASASPXX:VPQ:SSLS-AA[17]-LFF:LKVYP:VKS:XKXS, NDEGLEX:VPT:SSLS-AA[17]-LFF:LKVYP:QHN:KXEXR, NDEGLEX:VPT:SSLS-AA[17]-LFF:LKVYP:EHS:QXEXR, SSVKXQP:SRV:SSLS-AA[17]-LFF:LKVYP:EEH:LEXAXA, RNVQXRP:TQV:SSLS-AA[17]-LFF:LKVYP:EDH:LAXKXE, KIPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:GXGXR, GIPEPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXAXR, SIPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:AXGXH, KVGKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XGXR, KASKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:EXGXR, GSAGPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:RXGXS, AAPASXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:AXGXR, STPPTXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:SXGXR, RVPSTXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XGXL, ASAAPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:LKKYR:VVR:XKXS, KIPKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:GXGXR, GIPEPXX:VPE:NAIS-AA[17]-LYF:LKKYR:TVE:SXAXR, SIPKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:LKKYR:VVK:AXGXH, KVGKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:VAE:XGXR, KASKAXX:VPT:NAIS-AA[17]-LYF:LKKYR:AVS:EXGXR, GSAGPXX:TPT:NAIS-AA[17]-LYF:LKKYR:VVD:RXGXS, AAPASXX:VPA:NAIS-AA[17]-LYF:LKKYR:VVE:AXGXR, STPPTXX:VPT:NAIS-AA[17]-LYF:LKKYR:VVE:SXGXR, RVPSTXX:APV:NAIS-AA[17]-LYF:LKKYR:VEE:XGXL, ASAAPXX:VPQ:NAIS-AA[17]-LYF:LKKYR:VRS:XKXS, ASASPXX:VSQ:NAIS-AA[17]-LYF:LKKYR:VKS:XKXS, ASASPXX:VPQ:NAIS-AA[17]-LYF:LKKYR:VKS:XKXS, NDEGLEX:VPT:NAIS-AA[17]-LYF:LKKYR:QHN:KXEXR, NDEGLEX:VPT:NAIS-AA[17]-LYF:LKKYR:EHS:QXEXR, SSVKXQP:SRV:NAIS-AA[17]-LYF:LKKYR:EEH:LEXAXA, RNVQXRP:TQV:NAIS-AA[17]-LYF:LKKYR:EDH:LAXKXE, KIPKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:GXGXR, GIPEPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXAXR, SIPKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:AXGXH, KVGKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XGXR, KASKAXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:EXGXR, GSAGPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:RXGXS, AAPASXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:AXGXR, STPPTXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:SXGXH, RVPSTXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XGXL, ASAAPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:LRKHR:VVK:XKXS, KIPKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:GXGXR, GIPEPXX:VPE:SATS-AA[17]-LYY:LRKHR:TVE:SXAXR, SIPKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:AXGXH, KVGKAXX:VPT:SATS-AA[17]-LYY:LRKHR:VAE:XGXR, KASKAXX:VPT:SATS-AA[17]-LYY:LRKHR:AVS:EXGXR, GSAGPXX:TPT:SATS-AA[17]-LYY:LRKHR:VVD:RXGXS, AAPASXX:VPA:SATS-AA[17]-LYY:LRKHR:VVE:AXGXR, STPPTXX:VPT:SATS-AA[17]-LYY:LRKHR:VVE:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:LRKHR:VVR:SXGXH, RVPSTXX:APV:SATS-AA[17]-LYY:LRKHR:VEE:XGXL, ASAAPXX:VPQ:SATS-AA[17]-LYY:LRKHR:VRS:XKXS, ASASPXX:VSQ:SATS-AA[17]-LYY:LRKHR:VKS:XKXS,

ASASPXX:VPQ:SATS-AA[17]-LYY:LRKHR:VKS:XKXS, NDEGLEX:VPT:SATS-AA[17]-LYY:LRKHR:QHN:KXEXR, NDEGLEX:VPT:SATS-AA[17]-LYY:LRKHR:EHS:QXEXR, SSVKXQP:SRV:SATS-AA[17]-LYY:LRKHR:EEH:LEXAXA, RNVQXRP:TQV:SATS-AA[17]-LYY:LRKHR:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXR, HVPKPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:LKYHY:VAE:XKXS, KIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYK:LKYHY:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYK:LKYHY:VVK:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:LKYHY:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYK:LKYHY:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LYK:LKYHY:VVE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:LKYHY:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYK:LKYHY:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYK:LKYHY:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYK:LKYHY:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYK:LKYHY:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYK:LKYHY:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:LKYHY:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYK:LKYHY:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYK:LKYHY:EDH:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:GXGXR, GIPEPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:GXGXR, HVTKPTX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, YVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, TVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXH, AVPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XGXR, GSAGPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:RXGXS, AAPASXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXR, HVPKPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:SXGXH, RVPSTXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XGXL, ASAAPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:KFKYE:AVS:XKXS, KIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:GXGXR, GIPEPXX:VPE:EPIS-AA[17]-LYL:KFKYE:TVE:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:GXGXR, HVTKPTX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, YVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, TVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:AXGXH, AVPKAXX:APT:EPIS-AA[17]-LYL:KFKYE:VVK:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:KFKYE:VAE:XGXR, GSAGPXX:TPT:EPIS-AA[17]-LYL:KFKYE:VVD:RXGXS, AAPASXX:VPA:EPIS-AA[17]-LYL:KFKYE:VVE:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:KFKYE:VVE:SXGXR, HVPKPXX:APT:EPIS-AA[17]-LYL:KFKYE:VVR:SXGXH, RVPSTXX:APV:EPIS-AA[17]-LYL:KFKYE:VEE:XGXL, ASAAPXX:VPQ:EPIS-AA[17]-LYL:KFKYE:VRS:XKXS, ASASPXX:VSQ:EPIS-AA[17]-LYL:KFKYE:VKS:XKXS, ASASPXX:VPQ:EPIS-AA[17]-LYL:KFKYE:VKS:XKXS,

NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:QHN:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:KFKYE:EHS:QXEXR, SSVKXQP:SRV:EPIS-AA[17]-LYL:KFKYE:EEH:LEXAXA, RNVQXRP:TQV:EPIS-AA[17]-LYL:KFKYE:EDH:LAXKXE, KIPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:GXGXR, GIPEPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXAXR, SIPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:GXGXR, HVTKPTX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, YVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, TVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXH, AVPKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXH, KVGKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XGXR, KASKAXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:EXGXR, AAPASXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:AXGXR, STPPTXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXR, HVPKPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:SXGXH, RVPSTXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XGXL, ASAAPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:YGKIP:VVD:XKXS, KIPKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:GXGXR, GIPEPXX:VPE:SPIN-AA[17]-LYF:YGKIP:TVE:SXAXR, SIPKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:GXGXR, HVTKPTX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, YVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, TVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:AXGXH, AVPKAXX:APT:SPIN-AA[17]-LYF:YGKIP:VVK:AXGXH, KVGKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:VAE:XGXR, KASKAXX:VPT:SPIN-AA[17]-LYF:YGKIP:AVS:EXGXR, AAPASXX:VPA:SPIN-AA[17]-LYF:YGKIP:VVE:AXGXR, STPPTXX:VPT:SPIN-AA[17]-LYF:YGKIP:VVE:SXGXR, HVPKPXX:APT:SPIN-AA[17]-LYF:YGKIP:VVR:SXGXH, RVPSTXX:APV:SPIN-AA[17]-LYF:YGKIP:VEE:XGXL, ASAAPXX:VPQ:SPIN-AA[17]-LYF:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN-AA[17]-LYF:YGKIP:VKS:XKXS, ASASPXX:VPQ:SPIN-AA[17]-LYF:YGKIP:VKS:XKXS, NDEGLEX:VPT:SPIN-AA[17]-LYF:YGKIP:QHN:KXEXR, NDEGLEX:VPT:SPIN-AA[17]-LYF:YGKIP:EHS:QXEXR, SSVKXQP:SRV:SPIN-AA[17]-LYF:YGKIP:EEH:LEXAXA, RNVQXRP:TQV:SPIN-AA[17]-LYF:YGKIP:EDH:LAXKXE, KIPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, GIPEPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXAXR, SIPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, HVTKPTX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, YVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, TVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:AXGXH, AVPKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:AXGXH, KVGKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XGXR, KASKAXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:EXGXR, GSAGPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:RXGXS, STPPTXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXR, HVPKPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXH, RVPSTXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XGXL, ASAAPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:YKQYE:VVE:XKXS, KIPKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYI:YKQYE:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LYI:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYI:YKQYE:VVD:RXGXS, STPPTXX:VPT:SPIS-AA[17]-LYI:YKQYE:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYI:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYI:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYI:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYI:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYI:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-

AA[17]-LYI:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYI:YKQYE:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXR, HVPKPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:YKQYE:VVE:XKXS, GIPEPXX:VPE:SPIS-AA[17]-LFI:YKQYE:TVE:SXAXR, HVTKPTX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LFI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LFI:YKQYE:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LFI:YKQYE:VVE:AXGXR, HVPKPXX:APT:SPIS-AA[17]-LFI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LFI:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LFI:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LFI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LFI:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LFI:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LFI:YKQYE:EDH:LAXKXE, KIPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:GXGXR, GIPEPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXAXR, SIPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:GXGXR, HVTKPTX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, YVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, TVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXH, AVPKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXH, KVGKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XGXR, KASKAXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:EXGXR, GSAGPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:RXGXS, AAPASXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:AXGXR, STPPTXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXR, HVPKPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:SXGXH, ASAAPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:DHHKD:VEE:XKXS, KIPKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:GXGXR, GIPEPXX:VPE:KPLS-AA[17]-LYV:DHHKD:TVE:SXAXR, SIPKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:GXGXR, HVTKPTX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, YVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, TVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:AXGXH, AVPKAXX:APT:KPLS-AA[17]-LYV:DHHKD:VVK:AXGXH, KVGKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:VAE:XGXR, KASKAXX:VPT:KPLS-AA[17]-LYV:DHHKD:AVS:EXGXR, GSAGPXX:TPT:KPLS-AA[17]-LYV:DHHKD:VVD:RXGXS, AAPASXX:VPA:KPLS-AA[17]-LYV:DHHKD:VVE:AXGXR, STPPTXX:VPT:KPLS-AA[17]-LYV:DHHKD:VVE:SXGXR, HVPKPXX:APT:KPLS-AA[17]-LYV:DHHKD:VVR:SXGXH, ASAAPXX:VPQ:KPLS-AA[17]-LYV:DHHKD:VRS:XKXS, ASASPXX:VSQ:KPLS-AA[17]-LYV:DHHKD:VKS:XKXS, ASASPXX:VPQ:KPLS-AA[17]-LYV:DHHKD:VKS:XKXS, NDEGLEX:VPT:KPLS-AA[17]-LYV:DHHKD:QHN:KXEXR, NDEGLEX:VPT:KPLS-AA[17]-LYV:DHHKD:EHS:QXEXR, SSVKXQP:SRV:KPLS-AA[17]-LYV:DHHKD:EEH:LEXAXA, RNVQXRP:TQV:KPLS-AA[17]-

LYV:DHHKD:EDH:LAXKXE, KIPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:GXGXR, GIPEPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXAXR, SIPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:GXGXR, HVTKPTX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, YVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, TVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXH, AVPKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXH, KVGKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XGXR, KASKAXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:EXGXR, GSAGPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:RXGXS, AAPASXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:AXGXR, STPPTXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXR, HVPKPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:SXGXH, RVPSTXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XGXL, ASASPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VRS:XKXS, KIPKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLP-AA[17]-VYY:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLP-AA[17]-VYY:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLP-AA[17]-VYY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLP-AA[17]-VYY:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLP-AA[17]-VYY:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLP-AA[17]-VYY:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLP-AA[17]-VYY:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLP-AA[17]-VYY:EQLSN:VEE:XGXL, ASASPXX:VSQ:EPLP-AA[17]-VYY:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLP-AA[17]-VYY:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLP-AA[17]-VYY:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLP-AA[17]-VYY:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLP-AA[17]-VYY:EQLSN:EDH:LAXKXE, KIPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, GIPEPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXAXR, SIPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, HVTKPTX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, YVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, TVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, AVPKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, KVGKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXR, KASKAXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:EXGXR, GSAGPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:RXGXS, AAPASXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXR, STPPTXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXR, HVPKPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, RVPSTXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXL, ASAAPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, ASASPXX:VSQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, KIPKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLT-AA[17]-LYY:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLT-AA[17]-LYY:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLT-AA[17]-LYY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLT-AA[17]-LYY:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLT-AA[17]-LYY:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLT-AA[17]-LYY:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLT-AA[17]-LYY:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLT-AA[17]-LYY:EQLSN:VEE:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VRS:XKXS,

NDEGLEX:VPT:EPLT-AA[17]-LYY:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLT-AA[17]-LYY:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLT-AA[17]-LYY:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT-AA[17]-LYY:EQLSN:EDH:LAXKXE, KIPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, GIPEPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXAXR, SIPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:GXGXR, HVTKPTX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, YVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, TVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, AVPKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXH, KVGKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXR, KASKAXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:RXGXS, AAPASXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXR, HVPKPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLT-AA[17]-LYY:EQLSN:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:IGEMS:QHN:QXEXR, KIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:IGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:IGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:IGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:IGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:IGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:IGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:IGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:IGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:IGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:IGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:IGEMS:EHS:QXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:IGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:IGEMS:EDH:LAXKXE, NDEGLEX:VPT:SNIT-AA[17]-QIM:LGEMS:EHS:KXEXR, KIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:LGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:LGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:LGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:LGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:LGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:LGEMS:QHN:KXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:LGEMS:EDH:LAXKXE, RNVQXRP:SRV:RSVK-AA[17]-AKV:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:GXGXR, GIPEPXX:VPE:RSVK-AA[17]-AKV:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:GXGXR, HVTKPTX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK-AA[17]-

AKV:KEVQV:VVR:SXGXH, TVPKPXX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK-AA[17]-AKV:KEVQV:VVK:AXGXH, KVGKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK-AA[17]-AKV:KEVQV:AVS:EXGXR, GSAGPXX:TPT:RSVK-AA[17]-AKV:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK-AA[17]-AKV:KEVQV:VVE:AXGXR, STPPTXX:VPT:RSVK-AA[17]-AKV:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK-AA[17]-AKV:KEVQV:VVR:SXGXH, RVPSTXX:APV:RSVK-AA[17]-AKV:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK-AA[17]-AKV:KEVQV:VRS:XKXS, ASASPXX:VSQ:RSVK-AA[17]-AKV:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK-AA[17]-AKV:KEVQV:VKS:XKXS, NDEGLEX:VPT:RSVK-AA[17]-AKV:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK-AA[17]-AKV:KEVQV:EHS:QXEXR, RNVQXRP:TQV:RSVK-AA[17]-AKV:KEVQV:EDH:LAXKXE, SSVKXQP:TQV:RPVQ-AA[17]-RKI:KKATV:EDH:LEXAXA, KIPKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ-AA[17]-RKI:KKATV:TVE:SXAXR, SIPKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, YVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:AXGXH, AVPKAXX:APT:RPVQ-AA[17]-RKI:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:VAE:XGXR, KASKAXX:VPT:RPVQ-AA[17]-RKI:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ-AA[17]-RKI:KKATV:VVD:RXGXS, AAPASXX:VPA:RPVQ-AA[17]-RKI:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ-AA[17]-RKI:KKATV:VVE:SXGXR, HVPKPXX:APT:RPVQ-AA[17]-RKI:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ-AA[17]-RKI:KKATV:VEE:XGXL, ASAAPXX:VPQ:RPVQ-AA[17]-RKI:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ-AA[17]-RKI:KKATV:VKS:XKXS, ASASPXX:VPQ:RPVQ-AA[17]-RKI:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ-AA[17]-RKI:KKATV:QHN:KXEXR, NDEGLEX:VPT:RPVQ-AA[17]-RKI:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ-AA[17]-RKI:KKATV:EEH:LEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the hexaplet PEP7:PEP5:PEP1:PEP2:PEP6:PEP8 is selected from the group consisting of GIPEPXX:VPTKM:SAIS:LKNYQ:NMVVE:SXAXR, SIPKAXX:VPTEL:SAIS:LKNYQ:EMVVE:GXGXR, HVTKPTX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, YVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, TVPKPXX:VPTQL:SAIS:LKNYQ:NMVVE:AXGXH, AVPKAXX:VPTKL:SAIS:LKNYQ:NMVVE:AXGXH, KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVVE:XGXR, KASKAXX:VPTKL:SAIS:LKNYQ:GMVVE:EXGXR, GSAGPXX:VPTKM:SAIS:LKNYQ:GMVVE:RXGXS, AAPASXX:VPTRL:SAIS:LKNYQ:DMVVE:AXGXR, STPPTXX:VPTRL:SAIS:LKNYQ:DMVVE:SXGXR, HVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, RVPSTXX:VPTKT:SAIS:LKNYQ:MIVVE:XGXL, ASAAPXX:VPTAL:SAIS:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS:LKNYQ:MVVVE:XKXS, NDEGLEX:VPTEE:SAIS:LKNYQ:FLVVE:KXEXR, NDEGLEX:VPTGQ:SAIS:LKNYQ:LEVVE:QXEXR, SSVKXQP:VPTHH:SAIS:LKNYQ:RLVVE:LEXAXA, RNVQXRP:VPTQL:SAIS:LKNYQ:TLVVE:LAXKXE, GIPEPXX:VPEKM:SAIS:LKNYQ:NMTVE:SXAXR, HVTKPTX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, YVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, TVPKPXX:APTQL:SAIS:LKNYQ:NMVVR:AXGXH, AVPKAXX:APTKL:SAIS:LKNYQ:NMVVK:AXGXH, KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVAE:XGXR, KASKAXX:VPTKL:SAIS:LKNYQ:GMAVS:EXGXR, GSAGPXX:TPTKM:SAIS:LKNYQ:GMVVD:RXGXS, AAPASXX:VPARL:SAIS:LKNYQ:DMVVE:AXGXR,

HVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, RVPSTXX:APVKT:SAIS:LKNYQ:MIVEE:XGXL,
ASAAPXX:VPQAL:SAIS:LKNYQ:MIVRS:XKXS, ASASPXX:VSQDL:SAIS:LKNYQ:MIVKS:XKXS,
ASASPXX:VPQDL:SAIS:LKNYQ:MVVKS:XKXS, NDEGLEX:VPTEE:SAIS:LKNYQ:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SAIS:LKNYQ:LEEHS:QXEXR, SSVKXQP:SRVHH:SAIS:LKNYQ:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SAIS:LKNYQ:TLEDH:LAXKXE, KIPKAXX:VPEEL:SSLS:LKVYP:DMTVE:GXGXR,
SIPKAXX:VPEEL:SSLS:LKVYP:EMTVE:GXGXR, HVTKPTX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH,
YVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, TVPKPXX:VPEQL:SSLS:LKVYP:NMTVE:AXGXH,
AVPKAXX:VPEKL:SSLS:LKVYP:NMTVE:AXGXH, KVGKAXX:VPEKL:SSLS:LKVYP:EGMSTVE:XGXR,
KASKAXX:VPEKL:SSLS:LKVYP:GMTVE:EXGXR, GSAGPXX:VPEKM:SSLS:LKVYP:GMTVE:RXGXS,
AAPASXX:VPERL:SSLS:LKVYP:DMTVE:AXGXR, STPPTXX:VPERL:SSLS:LKVYP:DMTVE:SXGXR,
HVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, RVPSTXX:VPEKT:SSLS:LKVYP:MITVE:XGXL,
ASAAPXX:VPEAL:SSLS:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS:LKVYP:MITVE:XKXS,
ASASPXX:VPEDL:SSLS:LKVYP:MVTVE:XKXS, NDEGLEX:VPEEE:SSLS:LKVYP:FLTVE:KXEXR,
NDEGLEX:VPEGQ:SSLS:LKVYP:LETVE:QXEXR, SSVKXQP:VPEHH:SSLS:LKVYP:RLTVE:LEXAXA,
RNVQXRP:VPEQL:SSLS:LKVYP:TLTVE:LAXKXE, KIPKAXX:VPTEL:SSLS:LKVYP:DMVVE:GXGXR,
SIPKAXX:VPTEL:SSLS:LKVYP:EMVVE:GXGXR, HVTKPTX:APTKL:SSLS:LKVYP:NMVVR:SXGXH,
YVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, TVPKPXX:APTQL:SSLS:LKVYP:NMVVR:AXGXH,
AVPKAXX:APTKL:SSLS:LKVYP:NMVVK:AXGXH, KVGKAXX:VPTKL:SSLS:LKVYP:EGMSVAE:XGXR,
KASKAXX:VPTKL:SSLS:LKVYP:GMAVS:EXGXR, GSAGPXX:TPTKM:SSLS:LKVYP:GMVVD:RXGXS,
AAPASXX:VPARL:SSLS:LKVYP:DMVVE:AXGXR, STPPTXX:VPTRL:SSLS:LKVYP:DMVVE:SXGXR,
HVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, RVPSTXX:APVKT:SSLS:LKVYP:MIVEE:XGXL,
ASAAPXX:VPQAL:SSLS:LKVYP:MIVRS:XKXS, ASASPXX:VSQDL:SSLS:LKVYP:MIVKS:XKXS,
ASASPXX:VPQDL:SSLS:LKVYP:MVVKS:XKXS, NDEGLEX:VPTEE:SSLS:LKVYP:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SSLS:LKVYP:LEEHS:QXEXR, SSVKXQP:SRVHH:SSLS:LKVYP:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SSLS:LKVYP:TLEDH:LAXKXE, KIPKAXX:VPTEL:SAIS:LKNYQ:DMVVE:GXGXR,
KIPKAXX:APTEL:NAIS:LKKYR:DMVVR:GXGXR, GIPEPXX:APTKM:NAIS:LKKYR:NMVVR:SXAXR,
SIPKAXX:APTEL:NAIS:LKKYR:EMVVR:GXGXR, YVPKPXX:APTKL:NAIS:LKKYR:NMVVR:SXGXH,
TVPKPXX:APTQL:NAIS:LKKYR:NMVVR:AXGXH, AVPKAXX:APTKL:NAIS:LKKYR:NMVVR:AXGXH,
KVGKAXX:APTKL:NAIS:LKKYR:EGMSVVR:XGXR, KASKAXX:APTKL:NAIS:LKKYR:GMVVR:EXGXR,
GSAGPXX:APTKM:NAIS:LKKYR:GMVVR:RXGXS, AAPASXX:APTRL:NAIS:LKKYR:DMVVR:AXGXR,
STPPTXX:APTRL:NAIS:LKKYR:DMVVR:SXGXR, HVPKPXX:APTKL:NAIS:LKKYR:NMVVR:SXGXH,
RVPSTXX:APTKT:NAIS:LKKYR:MIVVR:XGXL, ASAAPXX:APTAL:NAIS:LKKYR:MIVVR:XKXS,
ASASPXX:APTDL:NAIS:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS:LKKYR:MVVVR:XKXS,
NDEGLEX:APTEE:NAIS:LKKYR:FLVVR:KXEXR, NDEGLEX:APTGQ:NAIS:LKKYR:LEVVR:QXEXR,
SSVKXQP:APTHH:NAIS:LKKYR:RLVVR:LEXAXA, RNVQXRP:APTQL:NAIS:LKKYR:TLVVR:LAXKXE,
KIPKAXX:VPTEL:NAIS:LKKYR:DMVVE:GXGXR, GIPEPXX:VPEKM:NAIS:LKKYR:NMTVE:SXAXR,
SIPKAXX:VPTEL:NAIS:LKKYR:EMVVE:GXGXR, AVPKAXX:APTKL:NAIS:LKKYR:NMVVK:AXGXH,
KVGKAXX:VPTKL:NAIS:LKKYR:EGMSVAE:XGXR, KASKAXX:VPTKL:NAIS:LKKYR:GMAVS:EXGXR,
GSAGPXX:TPTKM:NAIS:LKKYR:GMVVD:RXGXS, AAPASXX:VPARL:NAIS:LKKYR:DMVVE:AXGXR,
STPPTXX:VPTRL:NAIS:LKKYR:DMVVE:SXGXR, RVPSTXX:APVKT:NAIS:LKKYR:MIVEE:XGXL,
ASAAPXX:VPQAL:NAIS:LKKYR:MIVRS:XKXS, ASASPXX:VSQDL:NAIS:LKKYR:MIVKS:XKXS,
ASASPXX:VPQDL:NAIS:LKKYR:MVVKS:XKXS, NDEGLEX:VPTEE:NAIS:LKKYR:FLQHN:KXEXR,

NDEGLEX:VPTGQ:NAIS:LKKYR:LEEHS:QXEXR, SSVKXQP:SRVHH:NAIS:LKKYR:RLEEH:LEXAXA,
RNVQXRP:TQVQL:NAIS:LKKYR:TLEDH:LAXKXE, HVTKPTX:APTKL:NAIS:LKKYR:NMVVR:SXGXH,
KIPKAXX:APTEL:SATS:LRKHR:DMVVK:GXGXR, GIPEPXX:APTKM:SATS:LRKHR:NMVVK:SXAXR,
SIPKAXX:APTEL:SATS:LRKHR:EMVVK:GXGXR, HVTKPTX:APTKL:SATS:LRKHR:NMVVK:SXGXH,
YVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH, TVPKPXX:APTQL:SATS:LRKHR:NMVVK:AXGXH,
KVGKAXX:APTKL:SATS:LRKHR:EGMSVVK:XGXR, KASKAXX:APTKL:SATS:LRKHR:GMVVK:EXGXR,
GSAGPXX:APTKM:SATS:LRKHR:GMVVK:RXGXS, AAPASXX:APTRL:SATS:LRKHR:DMVVK:AXGXR,
STPPTXX:APTRL:SATS:LRKHR:DMVVK:SXGXR, HVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH,
RVPSTXX:APTKT:SATS:LRKHR:MIVVK:XGXL, ASAAPXX:APTAL:SATS:LRKHR:MIVVK:XKXS,
ASASPXX:APTDL:SATS:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS:LRKHR:MVVVK:XKXS,
NDEGLEX:APTEE:SATS:LRKHR:FLVVK:KXEXR, NDEGLEX:APTGQ:SATS:LRKHR:LEVVK:QXEXR,
SSVKXQP:APTHH:SATS:LRKHR:RLVVK:LEXAXA, RNVQXRP:APTQL:SATS:LRKHR:TLVVK:LAXKXE,
KIPKAXX:VPTEL:SATS:LRKHR:DMVVE:GXGXR, GIPEPXX:VPEKM:SATS:LRKHR:NMTVE:SXAXR,
SIPKAXX:VPTEL:SATS:LRKHR:EMVVE:GXGXR, HVTKPTX:APTKL:SATS:LRKHR:NMVVR:SXGXH,
YVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH, TVPKPXX:APTQL:SATS:LRKHR:NMVVR:AXGXH,
KVGKAXX:VPTKL:SATS:LRKHR:EGMSVAE:XGXR, KASKAXX:VPTKL:SATS:LRKHR:GMAVS:EXGXR,
GSAGPXX:TPTKM:SATS:LRKHR:GMVVD:RXGXS, AAPASXX:VPARL:SATS:LRKHR:DMVVE:AXGXR,
STPPTXX:VPTRL:SATS:LRKHR:DMVVE:SXGXR, HVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH,
RVPSTXX:APVKT:SATS:LRKHR:MIVEE:XGXL, ASAAPXX:VPQAL:SATS:LRKHR:MIVRS:XKXS,
ASASPXX:VSQDL:SATS:LRKHR:MIVKS:XKXS, ASASPXX:VPQDL:SATS:LRKHR:MVVKS:XKXS,
NDEGLEX:VPTEE:SATS:LRKHR:FLQHN:KXEXR, NDEGLEX:VPTGQ:SATS:LRKHR:LEEHS:QXEXR,
SSVKXQP:SRVHH:SATS:LRKHR:RLEEH:LEXAXA, RNVQXRP:TQVQL:SATS:LRKHR:TLEDH:LAXKXE,
KIPKAXX:VPTEL:SPIS:LKYHY:DMVAE:GXGXR, GIPEPXX:VPTKM:SPIS:LKYHY:NMVAE:SXAXR,
SIPKAXX:VPTEL:SPIS:LKYHY:EMVAE:GXGXR, HVTKPTX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH,
YVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH, TVPKPXX:VPTQL:SPIS:LKYHY:NMVAE:AXGXH,
AVPKAXX:VPTKL:SPIS:LKYHY:NMVAE:AXGXH, KASKAXX:VPTKL:SPIS:LKYHY:GMVAE:EXGXR,
GSAGPXX:VPTKM:SPIS:LKYHY:GMVAE:RXGXS, AAPASXX:VPTRL:SPIS:LKYHY:DMVAE:AXGXR,
STPPTXX:VPTRL:SPIS:LKYHY:DMVAE:SXGXR, HVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH,
RVPSTXX:VPTKT:SPIS:LKYHY:MIVAE:XGXL, ASAAPXX:VPTAL:SPIS:LKYHY:MIVAE:XKXS,
ASASPXX:VPTDL:SPIS:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS:LKYHY:MVVAE:XKXS,
NDEGLEX:VPTEE:SPIS:LKYHY:FLVAE:KXEXR, NDEGLEX:VPTGQ:SPIS:LKYHY:LEVAE:QXEXR,
SSVKXQP:VPTHH:SPIS:LKYHY:RLVAE:LEXAXA, RNVQXRP:VPTQL:SPIS:LKYHY:TLVAE:LAXKXE,
KIPKAXX:VPTEL:SPIS:LKYHY:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIS:LKYHY:NMTVE:SXAXR,
SIPKAXX:VPTEL:SPIS:LKYHY:EMVVE:GXGXR, HVTKPTX:APTKL:SPIS:LKYHY:NMVVR:SXGXH,
YVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS:LKYHY:NMVVR:AXGXH,
AVPKAXX:APTKL:SPIS:LKYHY:NMVVK:AXGXH, KASKAXX:VPTKL:SPIS:LKYHY:GMAVS:EXGXR,
GSAGPXX:TPTKM:SPIS:LKYHY:GMVVD:RXGXS, AAPASXX:VPARL:SPIS:LKYHY:DMVVE:AXGXR,
STPPTXX:VPTRL:SPIS:LKYHY:DMVVE:SXGXR, HVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH,
RVPSTXX:APVKT:SPIS:LKYHY:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS:LKYHY:MIVRS:XKXS,
ASASPXX:VSQDL:SPIS:LKYHY:MIVKS:XKXS, ASASPXX:VPQDL:SPIS:LKYHY:MVVKS:XKXS,
NDEGLEX:VPTEE:SPIS:LKYHY:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS:LKYHY:LEEHS:QXEXR,
SSVKXQP:SRVHH:SPIS:LKYHY:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS:LKYHY:TLEDH:LAXKXE,

KIPKAXX:VPTEL:EPIS:KFKYE:DMAVS:GXGXR, GIPEPXX:VPTKM:EPIS:KFKYE:NMAVS:SXAXR,
SIPKAXX:VPTEL:EPIS:KFKYE:EMAVS:GXGXR, HVTKPTX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH,
YVPKPXX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH, TVPKPXX:VPTQL:EPIS:KFKYE:NMAVS:AXGXH,
AVPKAXX:VPTKL:EPIS:KFKYE:NMAVS:AXGXH, KVGKAXX:VPTKL:EPIS:KFKYE:EGMSAVS:XGXR,
GSAGPXX:VPTKM:EPIS:KFKYE:GMAVS:RXGXS, AAPASXX:VPTRL:EPIS:KFKYE:DMAVS:AXGXR,
STPPTXX:VPTRL:EPIS:KFKYE:DMAVS:SXGXR, HVPKPXX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH,
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ASASPXX:VPTDL:EPIS:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS:KFKYE:MVAVS:XKXS,
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SSVKXQP:VPTHH:EPIS:KFKYE:RLAVS:LEXAXA, RNVQXRP:VPTQL:EPIS:KFKYE:TLAVS:LAXKXE,
KIPKAXX:VPTEL:EPIS:KFKYE:DMVVE:GXGXR, GIPEPXX:VPEKM:EPIS:KFKYE:NMTVE:SXAXR,
SIPKAXX:VPTEL:EPIS:KFKYE:EMVVE:GXGXR, HVTKPTX:APTKL:EPIS:KFKYE:NMVVR:SXGXH,
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SSVKXQP:SRVHH:EPIS:KFKYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPIS:KFKYE:TLEDH:LAXKXE,
KIPKAXX:TPTEL:SPIN:YGKIP:DMVVD:GXGXR, GIPEPXX:TPTKM:SPIN:YGKIP:NMVVD:SXAXR,
SIPKAXX:TPTEL:SPIN:YGKIP:EMVVD:GXGXR, HVTKPTX:TPTKL:SPIN:YGKIP:NMVVD:SXGXH,
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SSVKXQP:TPTHH:SPIN:YGKIP:RLVVD:LEXAXA, RNVQXRP:TPTQL:SPIN:YGKIP:TLVVD:LAXKXE,
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YVPKPXX:VPTKL:SNIT:IGEMS:NMQHN:SXGXH, TVPKPXX:VPTQL:SNIT:IGEMS:NMQHN:AXGXH,
AVPKAXX:VPTKL:SNIT:IGEMS:NMQHN:AXGXH, KVGKAXX:VPTKL:SNIT:IGEMS:EGMSQHN:XGXR,
KASKAXX:VPTKL:SNIT:IGEMS:GMQHN:EXGXR, GSAGPXX:VPTKM:SNIT:IGEMS:GMQHN:RXGXS,
AAPASXX:VPTRL:SNIT:IGEMS:DMQHN:AXGXR, STPPTXX:VPTRL:SNIT:IGEMS:DMQHN:SXGXR,
HVPKPXX:VPTKL:SNIT:IGEMS:NMQHN:SXGXH, RVPSTXX:VPTKT:SNIT:IGEMS:MIQHN:XGXL,
ASAAPXX:VPTAL:SNIT:IGEMS:MIQHN:XKXS, ASASPXX:VPTDL:SNIT:IGEMS:MIQHN:XKXS,
ASASPXX:VPTDL:SNIT:IGEMS:MVQHN:XKXS, NDEGLEX:VPTGQ:SNIT:IGEMS:LEQHN:QXEXR,
NDEGLEX:VPTEE:SNIT:IGEMS:FLQHN:KXEXR, SSVKXQP:VPTHH:SNIT:IGEMS:RLQHN:LEXAXA,
RNVQXRP:VPTQL:SNIT:IGEMS:TLQHN:LAXKXE, KIPKAXX:VPTEL:SNIT:IGEMS:DMVVE:GXGXR,
GIPEPXX:VPEKM:SNIT:IGEMS:NMTVE:SXAXR, SIPKAXX:VPTEL:SNIT:IGEMS:EMVVE:GXGXR,
HVTKPTX:APTKL:SNIT:IGEMS:NMVVR:SXGXH, YVPKPXX:APTKL:SNIT:IGEMS:NMVVR:SXGXH,
TVPKPXX:APTQL:SNIT:IGEMS:NMVVR:AXGXH, AVPKAXX:APTKL:SNIT:IGEMS:NMVVK:AXGXH,
KVGKAXX:VPTKL:SNIT:IGEMS:EGMSVAE:XGXR, KASKAXX:VPTKL:SNIT:IGEMS:GMAVS:EXGXR,
GSAGPXX:TPTKM:SNIT:IGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT:IGEMS:DMVVE:AXGXR,
STPPTXX:VPTRL:SNIT:IGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT:IGEMS:NMVVR:SXGXH,
RVPSTXX:APVKT:SNIT:IGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT:IGEMS:MIVRS:XKXS,
ASASPXX:VSQDL:SNIT:IGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT:IGEMS:MVVKS:XKXS,
NDEGLEX:VPTGQ:SNIT:IGEMS:LEEHS:QXEXR, SSVKXQP:SRVHH:SNIT:IGEMS:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SNIT:IGEMS:TLEDH:LAXKXE, KIPKAXX:VPTEL:SNIT:LGEMS:DMEHS:GXGXR,
GIPEPXX:VPTKM:SNIT:LGEMS:NMEHS:SXAXR, SIPKAXX:VPTEL:SNIT:LGEMS:EMEHS:GXGXR,
HVTKPTX:VPTKL:SNIT:LGEMS:NMEHS:SXGXH, YVPKPXX:VPTKL:SNIT:LGEMS:NMEHS:SXGXH,
TVPKPXX:VPTQL:SNIT:LGEMS:NMEHS:AXGXH, AVPKAXX:VPTKL:SNIT:LGEMS:NMEHS:AXGXH,
KVGKAXX:VPTKL:SNIT:LGEMS:EGMSEHS:XGXR, KASKAXX:VPTKL:SNIT:LGEMS:GMEHS:EXGXR,
GSAGPXX:VPTKM:SNIT:LGEMS:GMEHS:RXGXS, AAPASXX:VPTRL:SNIT:LGEMS:DMEHS:AXGXR,
STPPTXX:VPTRL:SNIT:LGEMS:DMEHS:SXGXR, HVPKPXX:VPTKL:SNIT:LGEMS:NMEHS:SXGXH,
RVPSTXX:VPTKT:SNIT:LGEMS:MIEHS:XGXL, ASAAPXX:VPTAL:SNIT:LGEMS:MIEHS:XKXS,

ASASPXX:VPTDL:SNIT:LGEMS:MIEHS:XKXS,
NDEGLEX:VPTEE:SNIT:LGEMS:FLEHS:KXEXR,
RNVQXRP:VPTQL:SNIT:LGEMS:TLEHS:LAXKXE,
GIPEPXX:VPEKM:SNIT:LGEMS:NMTVE:SXAXR,
HVTKPTX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
TVPKPXX:APTQL:SNIT:LGEMS:NMVVR:AXGXH,
KVGKAXX:VPTKL:SNIT:LGEMS:EGMSVAE:XGXR,
GSAGPXX:TPTKM:SNIT:LGEMS:GMVVD:RXGXS,
STPPTXX:VPTRL:SNIT:LGEMS:DMVVE:SXGXR,
RVPSTXX:APVKT:SNIT:LGEMS:MIVEE:XGXL,
ASASPXX:VSQDL:SNIT:LGEMS:MIVKS:XKXS,
NDEGLEX:VPTEE:SNIT:LGEMS:FLQHN:KXEXR,
RNVQXRP:TQVQL:SNIT:LGEMS:TLEDH:LAXKXE,
KIPKAXX:VPTEL:SNIT:LGEMS:DMVVE:GXGXR,
SIPKAXX:VPTEL:SNIT:LGEMS:EMVVE:GXGXR,
YVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
AVPKAXX:APTKL:SNIT:LGEMS:NMVVK:AXGXH,
KASKAXX:VPTKL:SNIT:LGEMS:GMAVS:EXGXR,
AAPASXX:VPARL:SNIT:LGEMS:DMVVE:AXGXR,
HVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
ASAAPXX:VPQAL:SNIT:LGEMS:MIVRS:XKXS,
ASASPXX:VPQDL:SNIT:LGEMS:MVVKS:XKXS,
NDEGLEX:VPTEE:SNIT:LGEMS:MVEHS:XKXS,
SSVKXQP:VPTHH:SNIT:LGEMS:RLEHS:LEXAXA,
KIPKAXX:VPTEL:SNIT:LGEMS:DMVVE:GXGXR,
SIPKAXX:VPTEL:SNIT:LGEMS:EMVVE:GXGXR,
YVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
AVPKAXX:APTKL:SNIT:LGEMS:NMVVK:AXGXH,
KASKAXX:VPTKL:SNIT:LGEMS:GMAVS:EXGXR,
AAPASXX:VPARL:SNIT:LGEMS:DMVVE:AXGXR,
HVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
ASAAPXX:VPQAL:SNIT:LGEMS:MIVRS:XKXS,
ASASPXX:VPQDL:SNIT:LGEMS:MVVKS:XKXS,
NDEGLEX:VPTGQ:RSVK:KEVQV:LEEHS:QXEXR,
KIPKAXX:TQVEL:RPVQ:KKATV:DMEDH:GXGXR,
SIPKAXX:TQVEL:RPVQ:KKATV:EMEDH:GXGXR,
YVPKPXX:TQVKL:RPVQ:KKATV:NMEDH:SXGXH,
AVPKAXX:TQVKL:RPVQ:KKATV:NMEDH:AXGXH,
KVGKAXX:TQVKL:RPVQ:KKATV:EGMSEDH:XGXR,
KASKAXX:TQVKL:RPVQ:KKATV:GMEDH:EXGXR,
AAPASXX:TQVRL:RPVQ:KKATV:DMEDH:AXGXR,
HVPKPXX:TQVKL:RPVQ:KKATV:NMEDH:SXGXH,
ASAAPXX:TQVAL:RPVQ:KKATV:MIEDH:XKXS,

ASASPXX:VPTDL:SNIT:LGEMS:MVEHS:XKXS,
SSVKXQP:VPTHH:SNIT:LGEMS:RLEHS:LEXAXA,
KIPKAXX:VPTEL:SNIT:LGEMS:DMVVE:GXGXR,
SIPKAXX:VPTEL:SNIT:LGEMS:EMVVE:GXGXR,
YVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
AVPKAXX:APTKL:SNIT:LGEMS:NMVVK:AXGXH,
KASKAXX:VPTKL:SNIT:LGEMS:GMAVS:EXGXR,
AAPASXX:VPARL:SNIT:LGEMS:DMVVE:AXGXR,
HVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
ASAAPXX:VPQAL:SNIT:LGEMS:MIVRS:XKXS,
ASASPXX:VPQDL:SNIT:LGEMS:MVVKS:XKXS,
SSVKXQP:SRVHH:SNIT:LGEMS:RLEEH:LEXAXA,
KIPKAXX:SRVEL:RSVK:KEVQV:DMEEH:GXGXR,
SIPKAXX:SRVEL:RSVK:KEVQV:EMEEH:GXGXR,
YVPKPXX:SRVKL:RSVK:KEVQV:NMEEH:SXGXH,
AVPKAXX:SRVKL:RSVK:KEVQV:NMEEH:AXGXH,
GSAGPXX:SRVKM:RSVK:KEVQV:GMEEH:RXGXS,
STPPTXX:SRVRL:RSVK:KEVQV:DMEEH:SXGXR,
RVPSTXX:SRVKT:RSVK:KEVQV:MIEEH:XGXL,
ASASPXX:SRVDL:RSVK:KEVQV:MIEEH:XKXS,
NDEGLEX:SRVEE:RSVK:KEVQV:FLEEH:KXEXR,
RNVQXRP:SRVQL:RSVK:KEVQV:TLEEH:LAXKXE,
GIPEPXX:VPEKM:RSVK:KEVQV:NMTVE:SXAXR,
HVTKPTX:APTKL:RSVK:KEVQV:NMVVR:SXGXH,
TVPKPXX:APTQL:RSVK:KEVQV:NMVVR:AXGXH,
KVGKAXX:VPTKL:RSVK:KEVQV:EGMSVAE:XGXR,
GSAGPXX:TPTKM:RSVK:KEVQV:GMVVD:RXGXS,
STPPTXX:VPTRL:RSVK:KEVQV:DMVVE:SXGXR,
RVPSTXX:APVKT:RSVK:KEVQV:MIVEE:XGXL,
ASASPXX:VSQDL:RSVK:KEVQV:MIVKS:XKXS,
NDEGLEX:VPTEE:RSVK:KEVQV:FLQHN:KXEXR,
RNVQXRP:TQVQL:RSVK:KEVQV:TLEDH:LAXKXE,
GIPEPXX:TQVKM:RPVQ:KKATV:NMEDH:SXAXR,
HVTKPTX:TQVKL:RPVQ:KKATV:NMEDH:SXGXH,
TVPKPXX:TQVQL:RPVQ:KKATV:NMEDH:AXGXH,
GSAGPXX:TQVKM:RPVQ:KKATV:GMEDH:RXGXS,
STPPTXX:TQVRL:RPVQ:KKATV:DMEDH:SXGXR,
RVPSTXX:TQVKT:RPVQ:KKATV:MIEDH:XGXL,
ASASPXX:TQVDL:RPVQ:KKATV:MIEDH:XKXS,

ASASPXX:TQVDL:RPVQ:KKATV:MVEDH:XKXS, NDEGLEX:TQVEE:RPVQ:KKATV:FLEDH:KXEXR, NDEGLEX:TQVGQ:RPVQ:KKATV:LEEDH:QXEXR, SSVKXQP:TQVHH:RPVQ:KKATV:RLEDH:LEXAXA, KIPKAXX:VPTEL:RPVQ:KKATV:DMVVE:GXGXR, GIPEPXX:VPEKM:RPVQ:KKATV:NMTVE:SXAXR, SIPKAXX:VPTEL:RPVQ:KKATV:EMVVE:GXGXR, HVTKPTX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, YVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, TVPKPXX:APTQL:RPVQ:KKATV:NMVVR:AXGXH, AVPKAXX:APTKL:RPVQ:KKATV:NMVVK:AXGXH, KVGKAXX:VPTKL:RPVQ:KKATV:EGMSVAE:XGXR, KASKAXX:VPTKL:RPVQ:KKATV:GMAVS:EXGXR, GSAGPXX:TPTKM:RPVQ:KKATV:GMVVD:RXGXS, AAPASXX:VPARL:RPVQ:KKATV:DMVVE:AXGXR, STPPTXX:VPTRL:RPVQ:KKATV:DMVVE:SXGXR, HVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, RVPSTXX:APVKT:RPVQ:KKATV:MIVEE:XGXL, ASAAPXX:VPQAL:RPVQ:KKATV:MIVRS:XKXS, ASASPXX:VSQDL:RPVQ:KKATV:MIVKS:XKXS, ASASPXX:VPQDL:RPVQ:KKATV:MVVKS:XKXS, NDEGLEX:VPTEE:RPVQ:KKATV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RPVQ:KKATV:LEEHS:QXEXR and SSVKXQP:SRVHH:RPVQ:KKATV:RLEEH:LEXAXA. More particularly, the hexaplet PEP7:PEP5:PEP1:PEP2:PEP6:PEP8 is selected from the group consisting of GIPEPXX:VPTKM:SAIS:LKNYQ:NMVVE:SXAXR, HVTKPTX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, YVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, TVPKPXX:VPTQL:SAIS:LKNYQ:NMVVE:AXGXH, AVPKAXX:VPTKL:SAIS:LKNYQ:NMVVE:AXGXH, KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVVE:XGXR, KASKAXX:VPTKL:SAIS:LKNYQ:GMVVE:EXGXR, GSAGPXX:VPTKM:SAIS:LKNYQ:GMVVE:RXGXS, AAPASXX:VPTRL:SAIS:LKNYQ:DMVVE:AXGXR, STPPTXX:VPTRL:SAIS:LKNYQ:DMVVE:SXGXR, HVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, RVPSTXX:VPTKT:SAIS:LKNYQ:MIVVE:XGXL, ASAAPXX:VPTAL:SAIS:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS:LKNYQ:MVVVE:XKXS, GIPEPXX:VPEKM:SAIS:LKNYQ:NMTVE:SXAXR, HVTKPTX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, YVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, TVPKPXX:APTQL:SAIS:LKNYQ:NMVVR:AXGXH, AVPKAXX:APTKL:SAIS:LKNYQ:NMVVK:AXGXH, KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVAE:XGXR, KASKAXX:VPTKL:SAIS:LKNYQ:GMAVS:EXGXR, GSAGPXX:TPTKM:SAIS:LKNYQ:GMVVD:RXGXS, AAPASXX:VPARL:SAIS:LKNYQ:DMVVE:AXGXR, HVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, RVPSTXX:APVKT:SAIS:LKNYQ:MIVEE:XGXL, ASAAPXX:VPQAL:SAIS:LKNYQ:MIVRS:XKXS, ASASPXX:VSQDL:SAIS:LKNYQ:MIVKS:XKXS, ASASPXX:VPQDL:SAIS:LKNYQ:MVVKS:XKXS, NDEGLEX:VPTEE:SAIS:LKNYQ:FLQHN:KXEXR, NDEGLEX:VPTGQ:SAIS:LKNYQ:LEEHS:QXEXR, SSVKXQP:SRVHH:SAIS:LKNYQ:RLEEH:LEXAXA, RNVQXRP:TQVQL:SAIS:LKNYQ:TLEDH:LAXKXE, KIPKAXX:VPEEL:SSLS:LKVYP:DMTVE:GXGXR, SIPKAXX:VPEEL:SSLS:LKVYP:EMTVE:GXGXR, HVTKPTX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, YVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, TVPKPXX:VPEQL:SSLS:LKVYP:NMTVE:AXGXH, AVPKAXX:VPEKL:SSLS:LKVYP:NMTVE:AXGXH, KVGKAXX:VPEKL:SSLS:LKVYP:EGMSTVE:XGXR, KASKAXX:VPEKL:SSLS:LKVYP:GMTVE:EXGXR, GSAGPXX:VPEKM:SSLS:LKVYP:GMTVE:RXGXS, AAPASXX:VPERL:SSLS:LKVYP:DMTVE:AXGXR, STPPTXX:VPERL:SSLS:LKVYP:DMTVE:SXGXR, HVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, RVPSTXX:VPEKT:SSLS:LKVYP:MITVE:XGXL, ASAAPXX:VPEAL:SSLS:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS:LKVYP:MVTVE:XKXS, KIPKAXX:VPTEL:SSLS:LKVYP:DMVVE:GXGXR, SIPKAXX:VPTEL:SSLS:LKVYP:EMVVE:GXGXR, HVTKPTX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, YVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, TVPKPXX:APTQL:SSLS:LKVYP:NMVVR:AXGXH, AVPKAXX:APTKL:SSLS:LKVYP:NMVVK:AXGXH, KVGKAXX:VPTKL:SSLS:LKVYP:EGMSVAE:XGXR,

KASKAXX:VPTKL:SSLS:LKVYP:GMAVS:EXGXR, GSAGPXX:TPTKM:SSLS:LKVYP:GMVVD:RXGXS,
AAPASXX:VPARL:SSLS:LKVYP:DMVVE:AXGXR, STPPTXX:VPTRL:SSLS:LKVYP:DMVVE:SXGXR,
HVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, RVPSTXX:APVKT:SSLS:LKVYP:MIVEE:XGXL,
ASAAPXX:VPQAL:SSLS:LKVYP:MIVRS:XKXS, ASASPXX:VSQDL:SSLS:LKVYP:MIVKS:XKXS,
ASASPXX:VPQDL:SSLS:LKVYP:MVVKS:XKXS, NDEGLEX:VPTEE:SSLS:LKVYP:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SSLS:LKVYP:LEEHS:QXEXR, SSVKXQP:SRVHH:SSLS:LKVYP:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SSLS:LKVYP:TLEDH:LAXKXE, KIPKAXX:APTEL:NAIS:LKKYR:DMVVR:GXGXR,
GIPEPXX:APTKM:NAIS:LKKYR:NMVVR:SXAXR, SIPKAXX:APTEL:NAIS:LKKYR:EMVVR:GXGXR,
AVPKAXX:APTKL:NAIS:LKKYR:NMVVR:AXGXH, KVGKAXX:APTKL:NAIS:LKKYR:EGMSVVR:XGXR,
KASKAXX:APTKL:NAIS:LKKYR:GMVVR:EXGXR, GSAGPXX:APTKM:NAIS:LKKYR:GMVVR:RXGXS,
AAPASXX:APTRL:NAIS:LKKYR:DMVVR:AXGXR, STPPTXX:APTRL:NAIS:LKKYR:DMVVR:SXGXR,
RVPSTXX:APTKT:NAIS:LKKYR:MIVVR:XGXL, ASAAPXX:APTAL:NAIS:LKKYR:MIVVR:XKXS,
ASASPXX:APTDL:NAIS:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS:LKKYR:MVVVR:XKXS,
KIPKAXX:VPTEL:NAIS:LKKYR:DMVVE:GXGXR, GIPEPXX:VPEKM:NAIS:LKKYR:NMTVE:SXAXR,
SIPKAXX:VPTEL:NAIS:LKKYR:EMVVE:GXGXR, AVPKAXX:APTKL:NAIS:LKKYR:NMVVK:AXGXH,
KVGKAXX:VPTKL:NAIS:LKKYR:EGMSVAE:XGXR, KASKAXX:VPTKL:NAIS:LKKYR:GMAVS:EXGXR,
GSAGPXX:TPTKM:NAIS:LKKYR:GMVVD:RXGXS, AAPASXX:VPARL:NAIS:LKKYR:DMVVE:AXGXR,
STPPTXX:VPTRL:NAIS:LKKYR:DMVVE:SXGXR, RVPSTXX:APVKT:NAIS:LKKYR:MIVEE:XGXL,
ASAAPXX:VPQAL:NAIS:LKKYR:MIVRS:XKXS, ASASPXX:VSQDL:NAIS:LKKYR:MIVKS:XKXS,
ASASPXX:VPQDL:NAIS:LKKYR:MVVKS:XKXS, NDEGLEX:VPTEE:NAIS:LKKYR:FLQHN:KXEXR,
NDEGLEX:VPTGQ:NAIS:LKKYR:LEEHS:QXEXR, SSVKXQP:SRVHH:NAIS:LKKYR:RLEEH:LEXAXA,
RNVQXRP:TQVQL:NAIS:LKKYR:TLEDH:LAXKXE, KIPKAXX:APTEL:SATS:LRKHR:DMVVK:GXGXR,
GIPEPXX:APTKM:SATS:LRKHR:NMVVK:SXAXR, SIPKAXX:APTEL:SATS:LRKHR:EMVVK:GXGXR,
HVTKPTX:APTKL:SATS:LRKHR:NMVVK:SXGXH, YVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH,
TVPKPXX:APTQL:SATS:LRKHR:NMVVK:AXGXH, KVGKAXX:APTKL:SATS:LRKHR:EGMSVVK:XGXR,
KASKAXX:APTKL:SATS:LRKHR:GMVVK:EXGXR, GSAGPXX:APTKM:SATS:LRKHR:GMVVK:RXGXS,
AAPASXX:APTRL:SATS:LRKHR:DMVVK:AXGXR, STPPTXX:APTRL:SATS:LRKHR:DMVVK:SXGXR,
HVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH, RVPSTXX:APTKT:SATS:LRKHR:MIVVK:XGXL,
ASAAPXX:APTAL:SATS:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS:LRKHR:MIVVK:XKXS,
ASASPXX:APTDL:SATS:LRKHR:MVVVK:XKXS, KIPKAXX:VPTEL:SATS:LRKHR:DMVVE:GXGXR,
GIPEPXX:VPEKM:SATS:LRKHR:NMTVE:SXAXR, SIPKAXX:VPTEL:SATS:LRKHR:EMVVE:GXGXR,
HVTKPTX:APTKL:SATS:LRKHR:NMVVR:SXGXH, YVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH,
TVPKPXX:APTQL:SATS:LRKHR:NMVVR:AXGXH, KVGKAXX:VPTKL:SATS:LRKHR:EGMSVAE:XGXR,
KASKAXX:VPTKL:SATS:LRKHR:GMAVS:EXGXR, GSAGPXX:TPTKM:SATS:LRKHR:GMVVD:RXGXS,
AAPASXX:VPARL:SATS:LRKHR:DMVVE:AXGXR, STPPTXX:VPTRL:SATS:LRKHR:DMVVE:SXGXR,
HVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH, RVPSTXX:APVKT:SATS:LRKHR:MIVEE:XGXL,
ASAAPXX:VPQAL:SATS:LRKHR:MIVRS:XKXS, ASASPXX:VSQDL:SATS:LRKHR:MIVKS:XKXS,
ASASPXX:VPQDL:SATS:LRKHR:MVVKS:XKXS, NDEGLEX:VPTEE:SATS:LRKHR:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SATS:LRKHR:LEEHS:QXEXR, SSVKXQP:SRVHH:SATS:LRKHR:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SATS:LRKHR:TLEDH:LAXKXE, KIPKAXX:VPTEL:SPIS:LKYHY:DMVAE:GXGXR,
GIPEPXX:VPTKM:SPIS:LKYHY:NMVAE:SXAXR, SIPKAXX:VPTEL:SPIS:LKYHY:EMVAE:GXGXR,
HVTKPTX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH, YVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH,

TVPKPXX:VPTQL:SPIS:LKYHY:NMVAE:AXGXH, AVPKAXX:VPTKL:SPIS:LKYHY:NMVAE:AXGXH,
KASKAXX:VPTKL:SPIS:LKYHY:GMVAE:EXGXR, GSAGPXX:VPTKM:SPIS:LKYHY:GMVAE:RXGXS,
AAPASXX:VPTRL:SPIS:LKYHY:DMVAE:AXGXR, STPPTXX:VPTRL:SPIS:LKYHY:DMVAE:SXGXR,
HVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH, RVPSTXX:VPTKT:SPIS:LKYHY:MIVAE:XGXL,
ASAAPXX:VPTAL:SPIS:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS:LKYHY:MIVAE:XKXS,
ASASPXX:VPTDL:SPIS:LKYHY:MVVAE:XKXS, KIPKAXX:VPTEL:SPIS:LKYHY:DMVVE:GXGXR,
GIPEPXX:VPEKM:SPIS:LKYHY:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIS:LKYHY:EMVVE:GXGXR,
HVTKPTX:APTKL:SPIS:LKYHY:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH,
TVPKPXX:APTQL:SPIS:LKYHY:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS:LKYHY:NMVVK:AXGXH,
KASKAXX:VPTKL:SPIS:LKYHY:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS:LKYHY:GMVVD:RXGXS,
AAPASXX:VPARL:SPIS:LKYHY:DMVVE:AXGXR, STPPTXX:VPTRL:SPIS:LKYHY:DMVVE:SXGXR,
HVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS:LKYHY:MIVEE:XGXL,
ASAAPXX:VPQAL:SPIS:LKYHY:MIVRS:XKXS, ASASPXX:VSQDL:SPIS:LKYHY:MIVKS:XKXS,
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KASKAXX:APVKL:KPLS:DHHKD:GMVEE:EXGXR, GSAGPXX:APVKM:KPLS:DHHKD:GMVEE:RXGXS,
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GSAGPXX:TPTKM:SNIT:LGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT:LGEMS:DMVVE:AXGXR,
STPPTXX:VPTRL:SNIT:LGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,
RVPSTXX:APVKT:SNIT:LGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT:LGEMS:MIVRS:XKXS,
ASASPXX:VSQDL:SNIT:LGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT:LGEMS:MVVKS:XKXS,
NDEGLEX:VPTEE:SNIT:LGEMS:FLQHN:KXEXR, SSVKXQP:SRVHH:SNIT:LGEMS:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SNIT:LGEMS:TLEDH:LAXKXE, RNVQXRP:SRVQL:RSVK:KEVQV:TLEEH:LAXKXE,
KIPKAXX:VPTEL:RSVK:KEVQV:DMVVE:GXGXR, GIPEPXX:VPEKM:RSVK:KEVQV:NMTVE:SXAXR,
SIPKAXX:VPTEL:RSVK:KEVQV:EMVVE:GXGXR, HVTKPTX:APTKL:RSVK:KEVQV:NMVVR:SXGXH,
YVPKPXX:APTKL:RSVK:KEVQV:NMVVR:SXGXH, TVPKPXX:APTQL:RSVK:KEVQV:NMVVR:AXGXH,
AVPKAXX:APTKL:RSVK:KEVQV:NMVVK:AXGXH, KVGKAXX:VPTKL:RSVK:KEVQV:EGMSVAE:XGXR,
KASKAXX:VPTKL:RSVK:KEVQV:GMAVS:EXGXR, GSAGPXX:TPTKM:RSVK:KEVQV:GMVVD:RXGXS,
AAPASXX:VPARL:RSVK:KEVQV:DMVVE:AXGXR, STPPTXX:VPTRL:RSVK:KEVQV:DMVVE:SXGXR,
HVPKPXX:APTKL:RSVK:KEVQV:NMVVR:SXGXH, RVPSTXX:APVKT:RSVK:KEVQV:MIVEE:XGXL,
ASAAPXX:VPQAL:RSVK:KEVQV:MIVRS:XKXS, ASASPXX:VSQDL:RSVK:KEVQV:MIVKS:XKXS,

ASASPXX:VPQDL:RSVK:KEVQV:MVVKS:XKXS, NDEGLEX:VPTEE:RSVK:KEVQV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RSVK:KEVQV:LEEHS:QXEXR, RNVQXRP:TQVQL:RSVK:KEVQV:TLEDH:LAXKXE, SSVKXQP:TQVHH:RPVQ:KKATV:RLEDH:LEXAXA, KIPKAXX:VPTEL:RPVQ:KKATV:DMVVE:GXGXR, GIPEPXX:VPEKM:RPVQ:KKATV:NMTVE:SXAXR, SIPKAXX:VPTEL:RPVQ:KKATV:EMVVE:GXGXR, HVTKPTX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, YVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, TVPKPXX:APTQL:RPVQ:KKATV:NMVVR:AXGXH, AVPKAXX:APTKL:RPVQ:KKATV:NMVVK:AXGXH, KVGKAXX:VPTKL:RPVQ:KKATV:EGMSVAE:XGXR, KASKAXX:VPTKL:RPVQ:KKATV:GMAVS:EXGXR, GSAGPXX:TPTKM:RPVQ:KKATV:GMVVD:RXGXS, AAPASXX:VPARL:RPVQ:KKATV:DMVVE:AXGXR, STPPTXX:VPTRL:RPVQ:KKATV:DMVVE:SXGXR, HVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH, RVPSTXX:APVKT:RPVQ:KKATV:MIVEE:XGXL, ASAAPXX:VPQAL:RPVQ:KKATV:MIVRS:XKXS, ASASPXX:VSQDL:RPVQ:KKATV:MIVKS:XKXS, ASASPXX:VPQDL:RPVQ:KKATV:MVVKS:XKXS, NDEGLEX:VPTEE:RPVQ:KKATV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RPVQ:KKATV:LEEHS:QXEXR and SSVKXQP:SRVHH:RPVQ:KKATV:RLEEH:LEXAXA.

In particular, in certain embodiments, the hexaplet PEP7:PEP5:PEP12:PEP2:PEP6:PEP8 is selected from the group consisting of GIPEPXX:VPTKM:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:SXAXR, SIPKAXX:VPTEL:SAIS-AA^{17}-LYL:LKNYQ:EMVVE:GXGXR, HVTKPTX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:SXGXH, YVPKPXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:SXGXH, TVPKPXX:VPTQL:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:AXGXH, AVPKAXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:AXGXH, KVGKAXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:EGMSVVE:XGXR, KASKAXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:GMVVE:EXGXR, GSAGPXX:VPTKM:SAIS-AA^{17}-LYL:LKNYQ:GMVVE:RXGXS, AAPASXX:VPTRL:SAIS-AA^{17}-LYL:LKNYQ:DMVVE:AXGXR, STPPTXX:VPTRL:SAIS-AA^{17}-LYL:LKNYQ:DMVVE:SXGXR, HVPKPXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVE:SXGXH, RVPSTXX:VPTKT:SAIS-AA^{17}-LYL:LKNYQ:MIVVE:XGXL, ASAAPXX:VPTAL:SAIS-AA^{17}-LYL:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS-AA^{17}-LYL:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS-AA^{17}-LYL:LKNYQ:MVVVE:XKXS, NDEGLEX:VPTEE:SAIS-AA^{17}-LYL:LKNYQ:FLVVE:KXEXR, NDEGLEX:VPTGQ:SAIS-AA^{17}-LYL:LKNYQ:LEVVE:QXEXR, SSVKXQP:VPTHH:SAIS-AA^{17}-LYL:LKNYQ:RLVVE:LEXAXA, RNVQXRP:VPTQL:SAIS-AA^{17}-LYL:LKNYQ:TLVVE:LAXKXE, GIPEPXX:VPEKM:SAIS-AA^{17}-LYL:LKNYQ:NMTVE:SXAXR, HVTKPTX:APTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVR:SXGXH, YVPKPXX:APTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVR:SXGXH, TVPKPXX:APTQL:SAIS-AA^{17}-LYL:LKNYQ:NMVVR:AXGXH, AVPKAXX:APTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVK:AXGXH, KVGKAXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:EGMSVAE:XGXR, KASKAXX:VPTKL:SAIS-AA^{17}-LYL:LKNYQ:GMAVS:EXGXR, GSAGPXX:TPTKM:SAIS-AA^{17}-LYL:LKNYQ:GMVVD:RXGXS, AAPASXX:VPARL:SAIS-AA^{17}-LYL:LKNYQ:DMVVE:AXGXR, HVPKPXX:APTKL:SAIS-AA^{17}-LYL:LKNYQ:NMVVR:SXGXH, RVPSTXX:APVKT:SAIS-AA^{17}-LYL:LKNYQ:MIVEE:XGXL, ASAAPXX:VPQAL:SAIS-AA^{17}-LYL:LKNYQ:MIVRS:XKXS, ASASPXX:VSQDL:SAIS-AA^{17}-LYL:LKNYQ:MIVKS:XKXS, ASASPXX:VPQDL:SAIS-AA^{17}-LYL:LKNYQ:MVVKS:XKXS, NDEGLEX:VPTEE:SAIS-AA^{17}-LYL:LKNYQ:FLQHN:KXEXR, NDEGLEX:VPTGQ:SAIS-AA^{17}-LYL:LKNYQ:LEEHS:QXEXR, SSVKXQP:SRVHH:SAIS-AA^{17}-LYL:LKNYQ:RLEEH:LEXAXA, RNVQXRP:TQVQL:SAIS-AA^{17}-LYL:LKNYQ:TLEDH:LAXKXE, KIPKAXX:VPEEL:SSLS-AA^{17}-LFF:LKVYP:DMTVE:GXGXR, SIPKAXX:VPEEL:SSLS-AA^{17}-LFF:LKVYP:EMTVE:GXGXR,

HVTKPTX:VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE:SXGXH, YVPKPXX:VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE:SXGXH, TVPKPXX:VPEQL:SSLS-AA[17]-LFF:LKVYP:NMTVE:AXGXH, AVPKAXX:VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE:AXGXH, KVGKAXX:VPEKL:SSLS-AA[17]-LFF:LKVYP:EGMSTVE:XGXR, KASKAXX:VPEKL:SSLS-AA[17]-LFF:LKVYP:GMTVE:EXGXR, GSAGPXX:VPEKM:SSLS-AA[17]-LFF:LKVYP:GMTVE:RXGXS, AAPASXX:VPERL:SSLS-AA[17]-LFF:LKVYP:DMTVE:AXGXR, STPPTXX:VPERL:SSLS-AA[17]-LFF:LKVYP:DMTVE:SXGXR, HVPKPXX:VPEKL:SSLS-AA[17]-LFF:LKVYP:NMTVE:SXGXH, RVPSTXX:VPEKT:SSLS-AA[17]-LFF:LKVYP:MITVE:XGXL, ASAAPXX:VPEAL:SSLS-AA[17]-LFF:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS-AA[17]-LFF:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS-AA[17]-LFF:LKVYP:MVTVE:XKXS, NDEGLEX:VPEEE:SSLS-AA[17]-LFF:LKVYP:FLTVE:KXEXR, NDEGLEX:VPEGQ:SSLS-AA[17]-LFF:LKVYP:LETVE:QXEXR, SSVKXQP:VPEHH:SSLS-AA[17]-LFF:LKVYP:RLTVE:LEXAXA, RNVQXRP:VPEQL:SSLS-AA[17]-LFF:LKVYP:TLTVE:LAXKXE, KIPKAXX:VPTEL:SSLS-AA[17]-LFF:LKVYP:DMVVE:GXGXR, SIPKAXX:VPTEL:SSLS-AA[17]-LFF:LKVYP:EMVVE:GXGXR, HVTKPTX:APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVR:SXGXH, YVPKPXX:APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVR:SXGXH, TVPKPXX:APTQL:SSLS-AA[17]-LFF:LKVYP:NMVVR:AXGXH, AVPKAXX:APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVK:AXGXH, KVGKAXX:VPTKL:SSLS-AA[17]-LFF:LKVYP:EGMSVAE:XGXR, KASKAXX:VPTKL:SSLS-AA[17]-LFF:LKVYP:GMAVS:EXGXR, GSAGPXX:TPTKM:SSLS-AA[17]-LFF:LKVYP:GMVVD:RXGXS, AAPASXX:VPARL:SSLS-AA[17]-LFF:LKVYP:DMVVE:AXGXR, STPPTXX:VPTRL:SSLS-AA[17]-LFF:LKVYP:DMVVE:SXGXR, HVPKPXX:APTKL:SSLS-AA[17]-LFF:LKVYP:NMVVR:SXGXH, RVPSTXX:APVKT:SSLS-AA[17]-LFF:LKVYP:MIVEE:XGXL, ASAAPXX:VPQAL:SSLS-AA[17]-LFF:LKVYP:MIVRS:XKXS, ASASPXX:VSQDL:SSLS-AA[17]-LFF:LKVYP:MIVKS:XKXS, ASASPXX:VPQDL:SSLS-AA[17]-LFF:LKVYP:MVVKS:XKXS, NDEGLEX:VPTEE:SSLS-AA[17]-LFF:LKVYP:FLQHN:KXEXR, NDEGLEX:VPTGQ:SSLS-AA[17]-LFF:LKVYP:LEEHS:QXEXR, SSVKXQP:SRVHH:SSLS-AA[17]-LFF:LKVYP:RLEEH:LEXAXA, RNVQXRP:TQVQL:SSLS-AA[17]-LFF:LKVYP:TLEDH:LAXKXE, KIPKAXX:VPTEL:SAIS-AA[17]-LYL:LKNYQ:DMVVE:GXGXR, KIPKAXX:APTEL:NAIS-AA[17]-LYF:LKKYR:DMVVR:GXGXR, GIPEPXX:APTKM:NAIS-AA[17]-LYF:LKKYR:NMVVR:SXAXR, SIPKAXX:APTEL:NAIS-AA[17]-LYF:LKKYR:EMVVR:GXGXR, YVPKPXX:APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR:SXGXH, TVPKPXX:APTQL:NAIS-AA[17]-LYF:LKKYR:NMVVR:AXGXH, AVPKAXX:APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR:AXGXH, KVGKAXX:APTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVVR:XGXR, KASKAXX:APTKL:NAIS-AA[17]-LYF:LKKYR:GMVVR:EXGXR, GSAGPXX:APTKM:NAIS-AA[17]-LYF:LKKYR:GMVVR:RXGXS, AAPASXX:APTRL:NAIS-AA[17]-LYF:LKKYR:DMVVR:AXGXR, STPPTXX:APTRL:NAIS-AA[17]-LYF:LKKYR:DMVVR:SXGXR, HVPKPXX:APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR:SXGXH, RVPSTXX:APTKT:NAIS-AA[17]-LYF:LKKYR:MIVVR:XGXL, ASAAPXX:APTAL:NAIS-AA[17]-LYF:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS-AA[17]-LYF:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS-AA[17]-LYF:LKKYR:MVVVR:XKXS, NDEGLEX:APTEE:NAIS-AA[17]-LYF:LKKYR:FLVVR:KXEXR, NDEGLEX:APTGQ:NAIS-AA[17]-LYF:LKKYR:LEVVR:QXEXR, SSVKXQP:APTHH:NAIS-AA[17]-LYF:LKKYR:RLVVR:LEXAXA, RNVQXRP:APTQL:NAIS-AA[17]-LYF:LKKYR:TLVVR:LAXKXE, KIPKAXX:VPTEL:NAIS-AA[17]-LYF:LKKYR:DMVVE:GXGXR, GIPEPXX:VPEKM:NAIS-AA[17]-LYF:LKKYR:NMTVE:SXAXR, SIPKAXX:VPTEL:NAIS-AA[17]-LYF:LKKYR:EMVVE:GXGXR, AVPKAXX:APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVK:AXGXH,

KVGKAXX:VPTKL:NAIS-AA[17]-LYF:LKKYR:EGMSVAE:XGXR, KASKAXX:VPTKL:NAIS-AA[17]-LYF:LKKYR:GMAVS:EXGXR, GSAGPXX:TPTKM:NAIS-AA[17]-LYF:LKKYR:GMVVD:RXGXS, AAPASXX:VPARL:NAIS-AA[17]-LYF:LKKYR:DMVVE:AXGXR, STPPTXX:VPTRL:NAIS-AA[17]-LYF:LKKYR:DMVVE:SXGXR, RVPSTXX:APVKT:NAIS-AA[17]-LYF:LKKYR:MIVEE:XGXL, ASAAPXX:VPQAL:NAIS-AA[17]-LYF:LKKYR:MIVRS:XKXS, ASASPXX:VSQDL:NAIS-AA[17]-LYF:LKKYR:MIVKS:XKXS, ASASPXX:VPQDL:NAIS-AA[17]-LYF:LKKYR:MVVKS:XKXS, NDEGLEX:VPTEE:NAIS-AA[17]-LYF:LKKYR:FLQHN:KXEXR, NDEGLEX:VPTGQ:NAIS-AA[17]-LYF:LKKYR:LEEHS:QXEXR, SSVKXQP:SRVHH:NAIS-AA[17]-LYF:LKKYR:RLEEH:LEXAXA, RNVQXRP:TQVQL:NAIS-AA[17]-LYF:LKKYR:TLEDH:LAXKXE, HVTKPTX:APTKL:NAIS-AA[17]-LYF:LKKYR:NMVVR:SXGXH, KIPKAXX:APTEL:SATS-AA[17]-LYY:LRKHR:DMVVK:GXGXR, GIPEPXX:APTKM:SATS-AA[17]-LYY:LRKHR:NMVVK:SXAXR, SIPKAXX:APTEL:SATS-AA[17]-LYY:LRKHR:EMVVK:GXGXR, HVTKPTX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVK:SXGXH, YVPKPXX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVK:SXGXH, TVPKPXX:APTQL:SATS-AA[17]-LYY:LRKHR:NMVVK:AXGXH, KVGKAXX:APTKL:SATS-AA[17]-LYY:LRKHR:EGMSVVK:XGXR, KASKAXX:APTKL:SATS-AA[17]-LYY:LRKHR:GMVVK:EXGXR, GSAGPXX:APTKM:SATS-AA[17]-LYY:LRKHR:GMVVK:RXGXS, AAPASXX:APTRL:SATS-AA[17]-LYY:LRKHR:DMVVK:AXGXR, STPPTXX:APTRL:SATS-AA[17]-LYY:LRKHR:DMVVK:SXGXR, HVPKPXX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVK:SXGXH, RVPSTXX:APTKT:SATS-AA[17]-LYY:LRKHR:MIVVK:XGXL, ASAAPXX:APTAL:SATS-AA[17]-LYY:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS-AA[17]-LYY:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS-AA[17]-LYY:LRKHR:MVVVK:XKXS, NDEGLEX:APTEE:SATS-AA[17]-LYY:LRKHR:FLVVK:KXEXR, NDEGLEX:APTGQ:SATS-AA[17]-LYY:LRKHR:LEVVK:QXEXR, SSVKXQP:APTHH:SATS-AA[17]-LYY:LRKHR:RLVVK:LEXAXA, RNVQXRP:APTQL:SATS-AA[17]-LYY:LRKHR:TLVVK:LAXKXE, KIPKAXX:VPTEL:SATS-AA[17]-LYY:LRKHR:DMVVE:GXGXR, GIPEPXX:VPEKM:SATS-AA[17]-LYY:LRKHR:NMTVE:SXAXR, SIPKAXX:VPTEL:SATS-AA[17]-LYY:LRKHR:EMVVE:GXGXR, HVTKPTX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVR:SXGXH, YVPKPXX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVR:SXGXH, TVPKPXX:APTQL:SATS-AA[17]-LYY:LRKHR:NMVVR:AXGXH, KVGKAXX:VPTKL:SATS-AA[17]-LYY:LRKHR:EGMSVAE:XGXR, KASKAXX:VPTKL:SATS-AA[17]-LYY:LRKHR:GMAVS:EXGXR, GSAGPXX:TPTKM:SATS-AA[17]-LYY:LRKHR:GMVVD:RXGXS, AAPASXX:VPARL:SATS-AA[17]-LYY:LRKHR:DMVVE:AXGXR, STPPTXX:VPTRL:SATS-AA[17]-LYY:LRKHR:DMVVE:SXGXR, HVPKPXX:APTKL:SATS-AA[17]-LYY:LRKHR:NMVVR:SXGXH, RVPSTXX:APVKT:SATS-AA[17]-LYY:LRKHR:MIVEE:XGXL, ASAAPXX:VPQAL:SATS-AA[17]-LYY:LRKHR:MIVRS:XKXS, ASASPXX:VSQDL:SATS-AA[17]-LYY:LRKHR:MIVKS:XKXS, ASASPXX:VPQDL:SATS-AA[17]-LYY:LRKHR:MVVKS:XKXS, NDEGLEX:VPTEE:SATS-AA[17]-LYY:LRKHR:FLQHN:KXEXR, NDEGLEX:VPTGQ:SATS-AA[17]-LYY:LRKHR:LEEHS:QXEXR, SSVKXQP:SRVHH:SATS-AA[17]-LYY:LRKHR:RLEEH:LEXAXA, RNVQXRP:TQVQL:SATS-AA[17]-LYY:LRKHR:TLEDH:LAXKXE, KIPKAXX:VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVAE:GXGXR, GIPEPXX:VPTKM:SPIS-AA[17]-LYK:LKYHY:NMVAE:SXAXR, SIPKAXX:VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVAE:GXGXR, HVTKPTX:VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE:SXGXH, YVPKPXX:VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE:SXGXH, TVPKPXX:VPTQL:SPIS-AA[17]-LYK:LKYHY:NMVAE:AXGXH, AVPKAXX:VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE:AXGXH, KASKAXX:VPTKL:SPIS-AA[17]-LYK:LKYHY:GMVAE:EXGXR, GSAGPXX:VPTKM:SPIS-AA[17]-LYK:LKYHY:GMVAE:RXGXS,

AAPASXX:VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAE:AXGXR, STPPTXX:VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVAE:SXGXR, HVPKPXX:VPTKL:SPIS-AA[17]-LYK:LKYHY:NMVAE:SXGXH, RVPSTXX:VPTKT:SPIS-AA[17]-LYK:LKYHY:MIVAE:XGXL, ASAAPXX:VPTAL:SPIS-AA[17]-LYK:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS-AA[17]-LYK:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS-AA[17]-LYK:LKYHY:MVVAE:XKXS, NDEGLEX:VPTEE:SPIS-AA[17]-LYK:LKYHY:FLVAE:KXEXR, NDEGLEX:VPTGQ:SPIS-AA[17]-LYK:LKYHY:LEVAE:QXEXR, SSVKXQP:VPTHH:SPIS-AA[17]-LYK:LKYHY:RLVAE:LEXAXA, RNVQXRP:VPTQL:SPIS-AA[17]-LYK:LKYHY:TLVAE:LAXKXE, KIPKAXX:VPTEL:SPIS-AA[17]-LYK:LKYHY:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIS-AA[17]-LYK:LKYHY:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIS-AA[17]-LYK:LKYHY:EMVVE:GXGXR, HVTKPTX:APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA[17]-LYK:LKYHY:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVK:AXGXH, KASKAXX:VPTKL:SPIS-AA[17]-LYK:LKYHY:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA[17]-LYK:LKYHY:GMVVD:RXGXS, AAPASXX:VPARL:SPIS-AA[17]-LYK:LKYHY:DMVVE:AXGXR, STPPTXX:VPTRL:SPIS-AA[17]-LYK:LKYHY:DMVVE:SXGXR, HVPKPXX:APTKL:SPIS-AA[17]-LYK:LKYHY:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA[17]-LYK:LKYHY:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA[17]-LYK:LKYHY:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA[17]-LYK:LKYHY:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA[17]-LYK:LKYHY:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA[17]-LYK:LKYHY:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA[17]-LYK:LKYHY:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA[17]-LYK:LKYHY:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA[17]-LYK:LKYHY:TLEDH:LAXKXE, KIPKAXX:VPTEL:EPIS-AA[17]-LYL:KFKYE:DMAVS:GXGXR, GIPEPXX:VPTKM:EPIS-AA[17]-LYL:KFKYE:NMAVS:SXAXR, SIPKAXX:VPTEL:EPIS-AA[17]-LYL:KFKYE:EMAVS:GXGXR, HVTKPTX:VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS:SXGXH, YVPKPXX:VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS:SXGXH, TVPKPXX:VPTQL:EPIS-AA[17]-LYL:KFKYE:NMAVS:AXGXH, AVPKAXX:VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS:AXGXH, KVGKAXX:VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSAVS:XGXR, GSAGPXX:VPTKM:EPIS-AA[17]-LYL:KFKYE:GMAVS:RXGXS, AAPASXX:VPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVS:AXGXR, STPPTXX:VPTRL:EPIS-AA[17]-LYL:KFKYE:DMAVS:SXGXR, HVPKPXX:VPTKL:EPIS-AA[17]-LYL:KFKYE:NMAVS:SXGXH, RVPSTXX:VPTKT:EPIS-AA[17]-LYL:KFKYE:MIAVS:XGXL, ASAAPXX:VPTAL:EPIS-AA[17]-LYL:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS-AA[17]-LYL:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS-AA[17]-LYL:KFKYE:MVAVS:XKXS, NDEGLEX:VPTEE:EPIS-AA[17]-LYL:KFKYE:FLAVS:KXEXR, NDEGLEX:VPTGQ:EPIS-AA[17]-LYL:KFKYE:LEAVS:QXEXR, SSVKXQP:VPTHH:EPIS-AA[17]-LYL:KFKYE:RLAVS:LEXAXA, RNVQXRP:VPTQL:EPIS-AA[17]-LYL:KFKYE:TLAVS:LAXKXE, KIPKAXX:VPTEL:EPIS-AA[17]-LYL:KFKYE:DMVVE:GXGXR, GIPEPXX:VPEKM:EPIS-AA[17]-LYL:KFKYE:NMTVE:SXAXR, SIPKAXX:VPTEL:EPIS-AA[17]-LYL:KFKYE:EMVVE:GXGXR, HVTKPTX:APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVR:SXGXH, YVPKPXX:APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVR:SXGXH, TVPKPXX:APTQL:EPIS-AA[17]-LYL:KFKYE:NMVVR:AXGXH, AVPKAXX:APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVK:AXGXH, KVGKAXX:VPTKL:EPIS-AA[17]-LYL:KFKYE:EGMSVAE:XGXR, GSAGPXX:TPTKM:EPIS-AA[17]-LYL:KFKYE:GMVVD:RXGXS, AAPASXX:VPARL:EPIS-AA[17]-LYL:KFKYE:DMVVE:AXGXR, STPPTXX:VPTRL:EPIS-AA[17]-LYL:KFKYE:DMVVE:SXGXR, HVPKPXX:APTKL:EPIS-AA[17]-LYL:KFKYE:NMVVR:SXGXH,

RVPSTXX:APVKT:EPIS-AA[17]-LYL:KFKYE:MIVEE:XGXL, ASAAPXX:VPQAL:EPIS-AA[17]-LYL:KFKYE:MIVRS:XKXS, ASASPXX:VSQDL:EPIS-AA[17]-LYL:KFKYE:MIVKS:XKXS, ASASPXX:VPQDL:EPIS-AA[17]-LYL:KFKYE:MVVKS:XKXS, NDEGLEX:VPTEE:EPIS-AA[17]-LYL:KFKYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPIS-AA[17]-LYL:KFKYE:LEEHS:QXEXR, SSVKXQP:SRVHH:EPIS-AA[17]-LYL:KFKYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPIS-AA[17]-LYL:KFKYE:TLEDH:LAXKXE, KIPKAXX:TPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVD:GXGXR, GIPEPXX:TPTKM:SPIN-AA[17]-LYF:YGKIP:NMVVD:SXAXR, SIPKAXX:TPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVD:GXGXR, HVTKPTX:TPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVD:SXGXH, YVPKPXX:TPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVD:SXGXH, TVPKPXX:TPTQL:SPIN-AA[17]-LYF:YGKIP:NMVVD:AXGXH, AVPKAXX:TPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVVD:XGXR, KVGKAXX:TPTKL:SPIN-AA[17]-LYF:YGKIP:GMVVD:EXGXR, KASKAXX:TPTKL:SPIN-AA[17]-LYF:YGKIP:DMVVD:AXGXR, AAPASXX:TPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVD:SXGXR, STPPTXX:TPTRL:SPIN-AA[17]-LYF:YGKIP:NMVVD:SXGXH, HVPKPXX:TPTKL:SPIN-AA[17]-LYF:YGKIP:NMVVD:SXGXH, RVPSTXX:TPTKT:SPIN-AA[17]-LYF:YGKIP:MIVVD:XGXL, ASAAPXX:TPTAL:SPIN-AA[17]-LYF:YGKIP:MIVVD:XKXS, ASASPXX:TPTDL:SPIN-AA[17]-LYF:YGKIP:MIVVD:XKXS, ASASPXX:TPTDL:SPIN-AA[17]-LYF:YGKIP:MVVVD:XKXS, NDEGLEX:TPTEE:SPIN-AA[17]-LYF:YGKIP:FLVVD:KXEXR, NDEGLEX:TPTGQ:SPIN-AA[17]-LYF:YGKIP:LEVVD:QXEXR, SSVKXQP:TPTHH:SPIN-AA[17]-LYF:YGKIP:RLVVD:LEXAXA, RNVQXRP:TPTQL:SPIN-AA[17]-LYF:YGKIP:TLVVD:LAXKXE, KIPKAXX:VPTEL:SPIN-AA[17]-LYF:YGKIP:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIN-AA[17]-LYF:YGKIP:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIN-AA[17]-LYF:YGKIP:EMVVE:GXGXR, HVTKPTX:APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVR:SXGXH, YVPKPXX:APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVR:SXGXH, TVPKPXX:APTQL:SPIN-AA[17]-LYF:YGKIP:NMVVR:AXGXH, AVPKAXX:APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIN-AA[17]-LYF:YGKIP:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIN-AA[17]-LYF:YGKIP:GMAVS:EXGXR, AAPASXX:VPARL:SPIN-AA[17]-LYF:YGKIP:DMVVE:AXGXR, STPPTXX:VPTRL:SPIN-AA[17]-LYF:YGKIP:DMVVE:SXGXR, HVPKPXX:APTKL:SPIN-AA[17]-LYF:YGKIP:NMVVR:SXGXH, RVPSTXX:APVKT:SPIN-AA[17]-LYF:YGKIP:MIVEE:XGXL, ASAAPXX:VPQAL:SPIN-AA[17]-LYF:YGKIP:MIVRS:XKXS, ASASPXX:VSQDL:SPIN-AA[17]-LYF:YGKIP:MIVKS:XKXS, ASASPXX:VPQDL:SPIN-AA[17]-LYF:YGKIP:MVVKS:XKXS, NDEGLEX:VPTEE:SPIN-AA[17]-LYF:YGKIP:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIN-AA[17]-LYF:YGKIP:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIN-AA[17]-LYF:YGKIP:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIN-AA[17]-LYF:YGKIP:TLEDH:LAXKXE, KIPKAXX:VPAEL:SPIS-AA[17]-LYI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPAKM:SPIS-AA[17]-LYI:YKQYE:NMVVE:SXAXR, SIPKAXX:VPAEL:SPIS-AA[17]-LYI:YKQYE:EMVVE:GXGXR, HVTKPTX:VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE:SXGXH, YVPKPXX:VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE:SXGXH, TVPKPXX:VPAQL:SPIS-AA[17]-LYI:YKQYE:NMVVE:AXGXH, AVPKAXX:VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE:AXGXH, KVGKAXX:VPAKL:SPIS-AA[17]-LYI:YKQYE:EGMSVVE:XGXR, KASKAXX:VPAKL:SPIS-AA[17]-LYI:YKQYE:GMVVE:EXGXR, GSAGPXX:VPAKM:SPIS-AA[17]-LYI:YKQYE:GMVVE:RXGXS, STPPTXX:VPARL:SPIS-AA[17]-LYI:YKQYE:DMVVE:SXGXR, HVPKPXX:VPAKL:SPIS-AA[17]-LYI:YKQYE:NMVVE:SXGXH, RVPSTXX:VPAKT:SPIS-AA[17]-LYI:YKQYE:MIVVE:XGXL, ASAAPXX:VPAAL:SPIS-AA[17]-LYI:YKQYE:MIVVE:XKXS, ASASPXX:VPADL:SPIS-AA[17]-LYI:YKQYE:MIVVE:XKXS,

ASASPXX:VPADL:SPIS-AA[17]-LYI:YKQYE:MVVVE:XKXS, NDEGLEX:VPAEE:SPIS-AA[17]-LYI:YKQYE:FLVVE:KXEXR, NDEGLEX:VPAGQ:SPIS-AA[17]-LYI:YKQYE:LEVVE:QXEXR, SSVKXQP:VPAHH:SPIS-AA[17]-LYI:YKQYE:RLVVE:LEXAXA, RNVQXRP:VPAQL:SPIS-AA[17]-LYI:YKQYE:TLVVE:LAXKXE, KIPKAXX:VPTEL:SPIS-AA[17]-LYI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIS-AA[17]-LYI:YKQYE:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIS-AA[17]-LYI:YKQYE:EMVVE:GXGXR, HVTKPTX:APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA[17]-LYI:YKQYE:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIS-AA[17]-LYI:YKQYE:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIS-AA[17]-LYI:YKQYE:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA[17]-LYI:YKQYE:GMVVD:RXGXS, STPPTXX:VPTRL:SPIS-AA[17]-LYI:YKQYE:DMVVE:SXGXR, HVPKPXX:APTKL:SPIS-AA[17]-LYI:YKQYE:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA[17]-LYI:YKQYE:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA[17]-LYI:YKQYE:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA[17]-LYI:YKQYE:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA[17]-LYI:YKQYE:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA[17]-LYI:YKQYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA[17]-LYI:YKQYE:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA[17]-LYI:YKQYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA[17]-LYI:YKQYE:TLEDH:LAXKXE, KIPKAXX:VPTEL:SPIS-AA[17]-LFI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPTKM:SPIS-AA[17]-LFI:YKQYE:NMVVE:SXAXR, SIPKAXX:VPTEL:SPIS-AA[17]-LFI:YKQYE:EMVVE:GXGXR, HVTKPTX:VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE:SXGXH, YVPKPXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE:SXGXH, TVPKPXX:VPTQL:SPIS-AA[17]-LFI:YKQYE:NMVVE:AXGXH, AVPKAXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE:AXGXH, KVGKAXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVVE:XGXR, KASKAXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:GMVVE:EXGXR, GSAGPXX:VPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVE:RXGXS, AAPASXX:VPTRL:SPIS-AA[17]-LFI:YKQYE:DMVVE:AXGXR, HVPKPXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:NMVVE:SXGXH, RVPSTXX:VPTKT:SPIS-AA[17]-LFI:YKQYE:MIVVE:XGXL, ASAAPXX:VPTAL:SPIS-AA[17]-LFI:YKQYE:MIVVE:XKXS, ASASPXX:VPTDL:SPIS-AA[17]-LFI:YKQYE:MIVVE:XKXS, ASASPXX:VPTDL:SPIS-AA[17]-LFI:YKQYE:MVVVE:XKXS, NDEGLEX:VPTEE:SPIS-AA[17]-LFI:YKQYE:FLVVE:KXEXR, NDEGLEX:VPTGQ:SPIS-AA[17]-LFI:YKQYE:LEVVE:QXEXR, SSVKXQP:VPTHH:SPIS-AA[17]-LFI:YKQYE:RLVVE:LEXAXA, RNVQXRP:VPTQL:SPIS-AA[17]-LFI:YKQYE:TLVVE:LAXKXE, GIPEPXX:VPEKM:SPIS-AA[17]-LFI:YKQYE:NMTVE:SXAXR, HVTKPTX:APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA[17]-LFI:YKQYE:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIS-AA[17]-LFI:YKQYE:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA[17]-LFI:YKQYE:GMVVD:RXGXS, AAPASXX:VPARL:SPIS-AA[17]-LFI:YKQYE:DMVVE:AXGXR, HVPKPXX:APTKL:SPIS-AA[17]-LFI:YKQYE:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA[17]-LFI:YKQYE:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA[17]-LFI:YKQYE:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA[17]-LFI:YKQYE:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA[17]-LFI:YKQYE:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA[17]-LFI:YKQYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA[17]-LFI:YKQYE:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA[17]-LFI:YKQYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA[17]-LFI:YKQYE:TLEDH:LAXKXE,

KIPKAXX:APVEL:KPLS-AA[17]-LYV:DHHKD:DMVEE:GXGXR, GIPEPXX:APVKM:KPLS-AA[17]-LYV:DHHKD:NMVEE:SXAXR, SIPKAXX:APVEL:KPLS-AA[17]-LYV:DHHKD:EMVEE:GXGXR, HVTKPTX:APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE:SXGXH, YVPKPXX:APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE:SXGXH, TVPKPXX:APVQL:KPLS-AA[17]-LYV:DHHKD:NMVEE:AXGXH, AVPKAXX:APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE:AXGXH, KVGKAXX:APVKL:KPLS-AA[17]-LYV:DHHKD:EGMSVEE:XGXR, KASKAXX:APVKL:KPLS-AA[17]-LYV:DHHKD:GMVEE:EXGXR, GSAGPXX:APVKM:KPLS-AA[17]-LYV:DHHKD:GMVEE:RXGXS, AAPASXX:APVRL:KPLS-AA[17]-LYV:DHHKD:DMVEE:AXGXR, STPPTXX:APVRL:KPLS-AA[17]-LYV:DHHKD:DMVEE:SXGXR, HVPKPXX:APVKL:KPLS-AA[17]-LYV:DHHKD:NMVEE:SXGXH, ASAAPXX:APVAL:KPLS-AA[17]-LYV:DHHKD:MIVEE:XKXS, ASASPXX:APVDL:KPLS-AA[17]-LYV:DHHKD:MIVEE:XKXS, ASASPXX:APVDL:KPLS-AA[17]-LYV:DHHKD:MVVEE:XKXS, NDEGLEX:APVEE:KPLS-AA[17]-LYV:DHHKD:FLVEE:KXEXR, NDEGLEX:APVGQ:KPLS-AA[17]-LYV:DHHKD:LEVEE:QXEXR, SSVKXQP:APVHH:KPLS-AA[17]-LYV:DHHKD:RLVEE:LEXAXA, RNVQXRP:APVQL:KPLS-AA[17]-LYV:DHHKD:TLVEE:LAXKXE, KIPKAXX:VPTEL:KPLS-AA[17]-LYV:DHHKD:DMVVE:GXGXR, GIPEPXX:VPEKM:KPLS-AA[17]-LYV:DHHKD:NMTVE:SXAXR, SIPKAXX:VPTEL:KPLS-AA[17]-LYV:DHHKD:EMVVE:GXGXR, HVTKPTX:APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVR:SXGXH, YVPKPXX:APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVR:SXGXH, TVPKPXX:APTQL:KPLS-AA[17]-LYV:DHHKD:NMVVR:AXGXH, AVPKAXX:APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVK:AXGXH, KVGKAXX:VPTKL:KPLS-AA[17]-LYV:DHHKD:EGMSVAE:XGXR, KASKAXX:VPTKL:KPLS-AA[17]-LYV:DHHKD:GMAVS:EXGXR, GSAGPXX:TPTKM:KPLS-AA[17]-LYV:DHHKD:GMVVD:RXGXS, AAPASXX:VPARL:KPLS-AA[17]-LYV:DHHKD:DMVVE:AXGXR, STPPTXX:VPTRL:KPLS-AA[17]-LYV:DHHKD:DMVVE:SXGXR, HVPKPXX:APTKL:KPLS-AA[17]-LYV:DHHKD:NMVVR:SXGXH, ASAAPXX:VPQAL:KPLS-AA[17]-LYV:DHHKD:MIVRS:XKXS, ASASPXX:VSQDL:KPLS-AA[17]-LYV:DHHKD:MIVKS:XKXS, ASASPXX:VPQDL:KPLS-AA[17]-LYV:DHHKD:MVVKS:XKXS, NDEGLEX:VPTEE:KPLS-AA[17]-LYV:DHHKD:FLQHN:KXEXR, NDEGLEX:VPTGQ:KPLS-AA[17]-LYV:DHHKD:LEEHS:QXEXR, SSVKXQP:SRVHH:KPLS-AA[17]-LYV:DHHKD:RLEEH:LEXAXA, RNVQXRP:TQVQL:KPLS-AA[17]-LYV:DHHKD:TLEDH:LAXKXE, KIPKAXX:VPQEL:EPLP-AA[17]-VYY:EQLSN:DMVRS:GXGXR, GIPEPXX:VPQKM:EPLP-AA[17]-VYY:EQLSN:NMVRS:SXAXR, SIPKAXX:VPQEL:EPLP-AA[17]-VYY:EQLSN:EMVRS:GXGXR, HVTKPTX:VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS:SXGXH, YVPKPXX:VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS:SXGXH, TVPKPXX:VPQQL:EPLP-AA[17]-VYY:EQLSN:NMVRS:AXGXH, AVPKAXX:VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS:AXGXH, KVGKAXX:VPQKL:EPLP-AA[17]-VYY:EQLSN:EGMSVRS:XGXR, KASKAXX:VPQKL:EPLP-AA[17]-VYY:EQLSN:GMVRS:EXGXR, GSAGPXX:VPQKM:EPLP-AA[17]-VYY:EQLSN:GMVRS:RXGXS, AAPASXX:VPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRS:AXGXR, STPPTXX:VPQRL:EPLP-AA[17]-VYY:EQLSN:DMVRS:SXGXR, HVPKPXX:VPQKL:EPLP-AA[17]-VYY:EQLSN:NMVRS:SXGXH, RVPSTXX:VPQKT:EPLP-AA[17]-VYY:EQLSN:MIVRS:XGXL, ASASPXX:VPQDL:EPLP-AA[17]-VYY:EQLSN:MIVRS:XKXS, ASASPXX:VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVRS:XKXS, NDEGLEX:VPQEE:EPLP-AA[17]-VYY:EQLSN:FLVRS:KXEXR, NDEGLEX:VPQGQ:EPLP-AA[17]-VYY:EQLSN:LEVRS:QXEXR, SSVKXQP:VPQHH:EPLP-AA[17]-VYY:EQLSN:RLVRS:LEXAXA, RNVQXRP:VPQQL:EPLP-AA[17]-VYY:EQLSN:TLVRS:LAXKXE, KIPKAXX:VPTEL:EPLP-AA[17]-VYY:EQLSN:DMVVE:GXGXR, GIPEPXX:VPEKM:EPLP-AA[17]-VYY:EQLSN:NMTVE:SXAXR, SIPKAXX:VPTEL:EPLP-AA[17]-VYY:EQLSN:EMVVE:GXGXR,

HVTKPTX:APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVR:SXGXH, YVPKPXX:APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVR:SXGXH, TVPKPXX:APTQL:EPLP-AA[17]-VYY:EQLSN:NMVVR:AXGXH, AVPKAXX:APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVK:AXGXH, KVGKAXX:VPTKL:EPLP-AA[17]-VYY:EQLSN:EGMSVAE:XGXR, KASKAXX:VPTKL:EPLP-AA[17]-VYY:EQLSN:GMAVS:EXGXR, GSAGPXX:TPTKM:EPLP-AA[17]-VYY:EQLSN:GMVVD:RXGXS, AAPASXX:VPARL:EPLP-AA[17]-VYY:EQLSN:DMVVE:AXGXR, STPPTXX:VPTRL:EPLP-AA[17]-VYY:EQLSN:DMVVE:SXGXR, HVPKPXX:APTKL:EPLP-AA[17]-VYY:EQLSN:NMVVR:SXGXH, RVPSTXX:APVKT:EPLP-AA[17]-VYY:EQLSN:MIVEE:XGXL, ASASPXX:VSQDL:EPLP-AA[17]-VYY:EQLSN:MIVKS:XKXS, ASASPXX:VPQDL:EPLP-AA[17]-VYY:EQLSN:MVVKS:XKXS, NDEGLEX:VPTEE:EPLP-AA[17]-VYY:EQLSN:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPLP-AA[17]-VYY:EQLSN:LEEHS:QXEXR, SSVKXQP:SRVHH:EPLP-AA[17]-VYY:EQLSN:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPLP-AA[17]-VYY:EQLSN:TLEDH:LAXKXE, KIPKAXX:VSQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS:GXGXR, GIPEPXX:VSQKM:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXAXR, SIPKAXX:VSQEL:EPLT-AA[17]-LYY:EQLSN:EMVKS:GXGXR, HVTKPTX:VSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, YVPKPXX:VSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, TVPKPXX:VSQQL:EPLT-AA[17]-LYY:EQLSN:NMVKS:AXGXH, AVPKAXX:VSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:AXGXH, KVGKAXX:VSQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKS:XGXR, KASKAXX:VSQKL:EPLT-AA[17]-LYY:EQLSN:GMVKS:EXGXR, GSAGPXX:VSQKM:EPLT-AA[17]-LYY:EQLSN:GMVKS:RXGXS, AAPASXX:VSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS:AXGXR, STPPTXX:VSQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS:SXGXR, HVPKPXX:VSQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, RVPSTXX:VSQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS:XGXL, ASAAPXX:VSQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS:XKXS, ASASPXX:VSQDL:EPLT-AA[17]-LYY:EQLSN:MVVKS:XKXS, NDEGLEX:VSQEE:EPLT-AA[17]-LYY:EQLSN:FLVKS:KXEXR, NDEGLEX:VSQGQ:EPLT-AA[17]-LYY:EQLSN:LEVKS:QXEXR, SSVKXQP:VSQHH:EPLT-AA[17]-LYY:EQLSN:RLVKS:LEXAXA, RNVQXRP:VSQQL:EPLT-AA[17]-LYY:EQLSN:TLVKS:LAXKXE, KIPKAXX:VPTEL:EPLT-AA[17]-LYY:EQLSN:DMVVE:GXGXR, GIPEPXX:VPEKM:EPLT-AA[17]-LYY:EQLSN:NMTVE:SXAXR, SIPKAXX:VPTEL:EPLT-AA[17]-LYY:EQLSN:EMVVE:GXGXR, HVTKPTX:APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVR:SXGXH, YVPKPXX:APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVR:SXGXH, TVPKPXX:APTQL:EPLT-AA[17]-LYY:EQLSN:NMVVR:AXGXH, AVPKAXX:APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVK:AXGXH, KVGKAXX:VPTKL:EPLT-AA[17]-LYY:EQLSN:EGMSVAE:XGXR, KASKAXX:VPTKL:EPLT-AA[17]-LYY:EQLSN:GMAVS:EXGXR, GSAGPXX:TPTKM:EPLT-AA[17]-LYY:EQLSN:GMVVD:RXGXS, AAPASXX:VPARL:EPLT-AA[17]-LYY:EQLSN:DMVVE:AXGXR, STPPTXX:VPTRL:EPLT-AA[17]-LYY:EQLSN:DMVVE:SXGXR, HVPKPXX:APTKL:EPLT-AA[17]-LYY:EQLSN:NMVVR:SXGXH, RVPSTXX:APVKT:EPLT-AA[17]-LYY:EQLSN:MIVEE:XGXL, ASAAPXX:VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVRS:XKXS, ASASPXX:VPQDL:EPLT-AA[17]-LYY:EQLSN:MVVKS:XKXS, NDEGLEX:VPTEE:EPLT-AA[17]-LYY:EQLSN:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPLT-AA[17]-LYY:EQLSN:LEEHS:QXEXR, SSVKXQP:SRVHH:EPLT-AA[17]-LYY:EQLSN:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPLT-AA[17]-LYY:EQLSN:TLEDH:LAXKXE, KIPKAXX:VPQEL:EPLT-AA[17]-LYY:EQLSN:DMVKS:GXGXR, GIPEPXX:VPQKM:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXAXR, SIPKAXX:VPQEL:EPLT-AA[17]-LYY:EQLSN:EMVKS:GXGXR, HVTKPTX:VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, YVPKPXX:VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, TVPKPXX:VPQQL:EPLT-AA[17]-LYY:EQLSN:NMVKS:AXGXH,

AVPKAXX:VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:AXGXH, KVGKAXX:VPQKL:EPLT-AA[17]-LYY:EQLSN:EGMSVKS:XGXR, KASKAXX:VPQKL:EPLT-AA[17]-LYY:EQLSN:GMVKS:EXGXR, GSAGPXX:VPQKM:EPLT-AA[17]-LYY:EQLSN:GMVKS:RXGXS, AAPASXX:VPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS:AXGXR, STPPTXX:VPQRL:EPLT-AA[17]-LYY:EQLSN:DMVKS:SXGXR, HVPKPXX:VPQKL:EPLT-AA[17]-LYY:EQLSN:NMVKS:SXGXH, RVPSTXX:VPQKT:EPLT-AA[17]-LYY:EQLSN:MIVKS:XGXL, ASAAPXX:VPQAL:EPLT-AA[17]-LYY:EQLSN:MIVKS:XKXS, ASASPXX:VPQDL:EPLT-AA[17]-LYY:EQLSN:MIVKS:XKXS, NDEGLEX:VPQEE:EPLT-AA[17]-LYY:EQLSN:FLVKS:KXEXR, NDEGLEX:VPQGQ:EPLT-AA[17]-LYY:EQLSN:LEVKS:QXEXR, SSVKXQP:VPQHH:EPLT-AA[17]-LYY:EQLSN:RLVKS:LEXAXA, RNVQXRP:VPQQL:EPLT-AA[17]-LYY:EQLSN:TLVKS:LAXKXE, ASASPXX:VSQDL:EPLT-AA[17]-LYY:EQLSN:MIVKS:XKXS, KIPKAXX:VPTEL:SNIT-AA[17]-QIM:IGEMS:DMQHN:GXGXR, GIPEPXX:VPTKM:SNIT-AA[17]-QIM:IGEMS:NMQHN:SXAXR, SIPKAXX:VPTEL:SNIT-AA[17]-QIM:IGEMS:EMQHN:GXGXR, HVTKPTX:VPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHN:SXGXH, YVPKPXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHN:SXGXH, TVPKPXX:VPTQL:SNIT-AA[17]-QIM:IGEMS:NMQHN:AXGXH, AVPKAXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHN:AXGXH, KVGKAXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSQHN:XGXR, KASKAXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:GMQHN:EXGXR, GSAGPXX:VPTKM:SNIT-AA[17]-QIM:IGEMS:GMQHN:RXGXS, AAPASXX:VPTRL:SNIT-AA[17]-QIM:IGEMS:DMQHN:AXGXR, STPPTXX:VPTRL:SNIT-AA[17]-QIM:IGEMS:DMQHN:SXGXR, HVPKPXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:NMQHN:SXGXH, RVPSTXX:VPTKT:SNIT-AA[17]-QIM:IGEMS:MIQHN:XGXL, ASAAPXX:VPTAL:SNIT-AA[17]-QIM:IGEMS:MIQHN:XKXS, ASASPXX:VPTDL:SNIT-AA[17]-QIM:IGEMS:MIQHN:XKXS, ASASPXX:VPTDL:SNIT-AA[17]-QIM:IGEMS:MVQHN:XKXS, NDEGLEX:VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEQHN:QXEXR, NDEGLEX:VPTEE:SNIT-AA[17]-QIM:IGEMS:FLQHN:KXEXR, SSVKXQP:VPTHH:SNIT-AA[17]-QIM:IGEMS:RLQHN:LEXAXA, RNVQXRP:VPTQL:SNIT-AA[17]-QIM:IGEMS:TLQHN:LAXKXE, KIPKAXX:VPTEL:SNIT-AA[17]-QIM:IGEMS:DMVVE:GXGXR, GIPEPXX:VPEKM:SNIT-AA[17]-QIM:IGEMS:NMTVE:SXAXR, SIPKAXX:VPTEL:SNIT-AA[17]-QIM:IGEMS:EMVVE:GXGXR, HVTKPTX:APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVR:SXGXH, YVPKPXX:APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVR:SXGXH, TVPKPXX:APTQL:SNIT-AA[17]-QIM:IGEMS:NMVVR:AXGXH, AVPKAXX:APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVK:AXGXH, KVGKAXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:EGMSVAE:XGXR, KASKAXX:VPTKL:SNIT-AA[17]-QIM:IGEMS:GMAVS:EXGXR, GSAGPXX:TPTKM:SNIT-AA[17]-QIM:IGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT-AA[17]-QIM:IGEMS:DMVVE:AXGXR, STPPTXX:VPTRL:SNIT-AA[17]-QIM:IGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT-AA[17]-QIM:IGEMS:NMVVR:SXGXH, RVPSTXX:APVKT:SNIT-AA[17]-QIM:IGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT-AA[17]-QIM:IGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT-AA[17]-QIM:IGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT-AA[17]-QIM:IGEMS:MVVKS:XKXS, NDEGLEX:VPTGQ:SNIT-AA[17]-QIM:IGEMS:LEEHS:QXEXR, SSVKXQP:SRVHH:SNIT-AA[17]-QIM:IGEMS:RLEEH:LEXAXA, RNVQXRP:TQVQL:SNIT-AA[17]-QIM:IGEMS:TLEDH:LAXKXE, KIPKAXX:VPTEL:SNIT-AA[17]-QIM:LGEMS:DMEHS:GXGXR, GIPEPXX:VPTKM:SNIT-AA[17]-QIM:LGEMS:NMEHS:SXAXR, SIPKAXX:VPTEL:SNIT-AA[17]-QIM:LGEMS:EMEHS:GXGXR, HVTKPTX:VPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHS:SXGXH, YVPKPXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHS:SXGXH, TVPKPXX:VPTQL:SNIT-AA[17]-QIM:LGEMS:NMEHS:AXGXH, AVPKAXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHS:AXGXH,

KVGKAXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSEHS:XGXR, KASKAXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:GMEHS:EXGXR, GSAGPXX:VPTKM:SNIT-AA[17]-QIM:LGEMS:GMEHS:RXGXS, AAPASXX:VPTRL:SNIT-AA[17]-QIM:LGEMS:DMEHS:AXGXR, STPPTXX:VPTRL:SNIT-AA[17]-QIM:LGEMS:DMEHS:SXGXR, HVPKPXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:NMEHS:SXGXH, RVPSTXX:VPTKT:SNIT-AA[17]-QIM:LGEMS:MIEHS:XGXL, ASAAPXX:VPTAL:SNIT-AA[17]-QIM:LGEMS:MIEHS:XKXS, ASASPXX:VPTDL:SNIT-AA[17]-QIM:LGEMS:MIEHS:XKXS, ASASPXX:VPTDL:SNIT-AA[17]-QIM:LGEMS:MVEHS:XKXS, NDEGLEX:VPTEE:SNIT-AA[17]-QIM:LGEMS:FLEHS:KXEXR, SSVKXQP:VPTHH:SNIT-AA[17]-QIM:LGEMS:RLEHS:LEXAXA, RNVQXRP:VPTQL:SNIT-AA[17]-QIM:LGEMS:TLEHS:LAXKXE, KIPKAXX:VPTEL:SNIT-AA[17]-QIM:LGEMS:DMVVE:GXGXR, GIPEPXX:VPEKM:SNIT-AA[17]-QIM:LGEMS:NMTVE:SXAXR, SIPKAXX:VPTEL:SNIT-AA[17]-QIM:LGEMS:EMVVE:GXGXR, HVTKPTX:APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVR:SXGXH, YVPKPXX:APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVR:SXGXH, TVPKPXX:APTQL:SNIT-AA[17]-QIM:LGEMS:NMVVR:AXGXH, AVPKAXX:APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVK:AXGXH, KVGKAXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:EGMSVAE:XGXR, KASKAXX:VPTKL:SNIT-AA[17]-QIM:LGEMS:GMAVS:EXGXR, GSAGPXX:TPTKM:SNIT-AA[17]-QIM:LGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT-AA[17]-QIM:LGEMS:DMVVE:AXGXR, STPPTXX:VPTRL:SNIT-AA[17]-QIM:LGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT-AA[17]-QIM:LGEMS:NMVVR:SXGXH, RVPSTXX:APVKT:SNIT-AA[17]-QIM:LGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT-AA[17]-QIM:LGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT-AA[17]-QIM:LGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT-AA[17]-QIM:LGEMS:MVVKS:XKXS, NDEGLEX:VPTEE:SNIT-AA[17]-QIM:LGEMS:FLQHN:KXEXR, SSVKXQP:SRVHH:SNIT-AA[17]-QIM:LGEMS:RLEEH:LEXAXA, RNVQXRP:TQVQL:SNIT-AA[17]-QIM:LGEMS:TLEDH:LAXKXE, KIPKAXX:SRVEL:RSVK-AA[17]-AKV:KEVQV:DMEEH:GXGXR, GIPEPXX:SRVKM:RSVK-AA[17]-AKV:KEVQV:NMEEH:SXAXR, SIPKAXX:SRVEL:RSVK-AA[17]-AKV:KEVQV:EMEEH:GXGXR, HVTKPTX:SRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEH:SXGXH, YVPKPXX:SRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEH:SXGXH, TVPKPXX:SRVQL:RSVK-AA[17]-AKV:KEVQV:NMEEH:AXGXH, AVPKAXX:SRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEH:AXGXH, KVGKAXX:SRVKL:RSVK-AA[17]-AKV:KEVQV:EGMSEEH:XGXR, KASKAXX:SRVKL:RSVK-AA[17]-AKV:KEVQV:GMEEH:EXGXR, GSAGPXX:SRVKM:RSVK-AA[17]-AKV:KEVQV:GMEEH:RXGXS, AAPASXX:SRVRL:RSVK-AA[17]-AKV:KEVQV:DMEEH:AXGXR, STPPTXX:SRVRL:RSVK-AA[17]-AKV:KEVQV:DMEEH:SXGXR, HVPKPXX:SRVKL:RSVK-AA[17]-AKV:KEVQV:NMEEH:SXGXH, RVPSTXX:SRVKT:RSVK-AA[17]-AKV:KEVQV:MIEEH:XGXL, ASAAPXX:SRVAL:RSVK-AA[17]-AKV:KEVQV:MIEEH:XKXS, ASASPXX:SRVDL:RSVK-AA[17]-AKV:KEVQV:MIEEH:XKXS, ASASPXX:SRVDL:RSVK-AA[17]-AKV:KEVQV:MVEEH:XKXS, NDEGLEX:SRVEE:RSVK-AA[17]-AKV:KEVQV:FLEEH:KXEXR, NDEGLEX:SRVGQ:RSVK-AA[17]-AKV:KEVQV:LEEEH:QXEXR, RNVQXRP:SRVQL:RSVK-AA[17]-AKV:KEVQV:TLEEH:LAXKXE, KIPKAXX:VPTEL:RSVK-AA[17]-AKV:KEVQV:DMVVE:GXGXR, GIPEPXX:VPEKM:RSVK-AA[17]-AKV:KEVQV:NMTVE:SXAXR, SIPKAXX:VPTEL:RSVK-AA[17]-AKV:KEVQV:EMVVE:GXGXR, HVTKPTX:APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVR:SXGXH, YVPKPXX:APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVR:SXGXH, TVPKPXX:APTQL:RSVK-AA[17]-AKV:KEVQV:NMVVR:AXGXH, AVPKAXX:APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVK:AXGXH, KVGKAXX:VPTKL:RSVK-AA[17]-AKV:KEVQV:EGMSVAE:XGXR, KASKAXX:VPTKL:RSVK-AA[17]-AKV:KEVQV:GMAVS:EXGXR, GSAGPXX:TPTKM:RSVK-AA[17]-AKV:KEVQV:GMVVD:RXGXS,

AAPASXX:VPARL:RSVK-AA[17]-AKV:KEVQV:DMVVE:AXGXR, STPPTXX:VPTRL:RSVK-AA[17]-AKV:KEVQV:DMVVE:SXGXR, HVPKPXX:APTKL:RSVK-AA[17]-AKV:KEVQV:NMVVR:SXGXH, RVPSTXX:APVKT:RSVK-AA[17]-AKV:KEVQV:MIVEE:XGXL, ASAAPXX:VPQAL:RSVK-AA[17]-AKV:KEVQV:MIVRS:XKXS, ASASPXX:VSQDL:RSVK-AA[17]-AKV:KEVQV:MIVKS:XKXS, ASASPXX:VPQDL:RSVK-AA[17]-AKV:KEVQV:MVVKS:XKXS, NDEGLEX:VPTEE:RSVK-AA[17]-AKV:KEVQV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RSVK-AA[17]-AKV:KEVQV:LEEHS:QXEXR, RNVQXRP:TQVQL:RSVK-AA[17]-AKV:KEVQV:TLEDH:LAXKXE, KIPKAXX:TQVEL:RPVQ-AA[17]-RKI:KKATV:DMEDH:GXGXR, GIPEPXX:TQVKM:RPVQ-AA[17]-RKI:KKATV:NMEDH:SXAXR, SIPKAXX:TQVEL:RPVQ-AA[17]-RKI:KKATV:EMEDH:GXGXR, HVTKPTX:TQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDH:SXGXH, YVPKPXX:TQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDH:SXGXH, TVPKPXX:TQVQL:RPVQ-AA[17]-RKI:KKATV:NMEDH:AXGXH, AVPKAXX:TQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDH:AXGXH, KVGKAXX:TQVKL:RPVQ-AA[17]-RKI:KKATV:EGMSEDH:XGXR, KASKAXX:TQVKL:RPVQ-AA[17]-RKI:KKATV:GMEDH:EXGXR, GSAGPXX:TQVKM:RPVQ-AA[17]-RKI:KKATV:GMEDH:RXGXS, AAPASXX:TQVRL:RPVQ-AA[17]-RKI:KKATV:DMEDH:AXGXR, STPPTXX:TQVRL:RPVQ-AA[17]-RKI:KKATV:DMEDH:SXGXR, HVPKPXX:TQVKL:RPVQ-AA[17]-RKI:KKATV:NMEDH:SXGXH, RVPSTXX:TQVKT:RPVQ-AA[17]-RKI:KKATV:MIEDH:XGXL, ASAAPXX:TQVAL:RPVQ-AA[17]-RKI:KKATV:MIEDH:XKXS, ASASPXX:TQVDL:RPVQ-AA[17]-RKI:KKATV:MIEDH:XKXS, ASASPXX:TQVDL:RPVQ-AA[17]-RKI:KKATV:MVEDH:XKXS, NDEGLEX:TQVEE:RPVQ-AA[17]-RKI:KKATV:FLEDH:KXEXR, NDEGLEX:TQVGQ:RPVQ-AA[17]-RKI:KKATV:LEEDH:QXEXR, SSVKXQP:TQVHH:RPVQ-AA[17]-RKI:KKATV:RLEDH:LEXAXA, KIPKAXX:VPTEL:RPVQ-AA[17]-RKI:KKATV:DMVVE:GXGXR, GIPEPXX:VPEKM:RPVQ-AA[17]-RKI:KKATV:NMTVE:SXAXR, SIPKAXX:VPTEL:RPVQ-AA[17]-RKI:KKATV:EMVVE:GXGXR, HVTKPTX:APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVR:SXGXH, YVPKPXX:APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVR:SXGXH, TVPKPXX:APTQL:RPVQ-AA[17]-RKI:KKATV:NMVVR:AXGXH, AVPKAXX:APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVK:AXGXH, KVGKAXX:VPTKL:RPVQ-AA[17]-RKI:KKATV:EGMSVAE:XGXR, KASKAXX:VPTKL:RPVQ-AA[17]-RKI:KKATV:GMAVS:EXGXR, GSAGPXX:TPTKM:RPVQ-AA[17]-RKI:KKATV:GMVVD:RXGXS, AAPASXX:VPARL:RPVQ-AA[17]-RKI:KKATV:DMVVE:AXGXR, STPPTXX:VPTRL:RPVQ-AA[17]-RKI:KKATV:DMVVE:SXGXR, HVPKPXX:APTKL:RPVQ-AA[17]-RKI:KKATV:NMVVR:SXGXH, RVPSTXX:APVKT:RPVQ-AA[17]-RKI:KKATV:MIVEE:XGXL, ASAAPXX:VPQAL:RPVQ-AA[17]-RKI:KKATV:MIVRS:XKXS, ASASPXX:VSQDL:RPVQ-AA[17]-RKI:KKATV:MIVKS:XKXS, ASASPXX:VPQDL:RPVQ-AA[17]-RKI:KKATV:MVVKS:XKXS, NDEGLEX:VPTEE:RPVQ-AA[17]-RKI:KKATV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RPVQ-AA[17]-RKI:KKATV:LEEHS:QXEXR and SSVKXQP:SRVHH:RPVQ-AA[17]-RKI:KKATV:RLEEH:LEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T). More particularly, the hexaplet PEP7:PEP5:PEP12:PEP2:PEP6:PEP8 is selected from the group consisting of GIPEPXX:VPTKM:SAIS-AA17-LYL:LKNYQ:NMVVE:SXAXR, HVTKPTX:VPTKL:SAIS-AA17-LYL:LKNYQ:NMVVE:SXGXH, YVPKPXX:VPTKL:SAIS-AA17-LYL:LKNYQ:NMVVE:SXGXH, TVPKPXX:VPTQL:SAIS-AA17-LYL:LKNYQ:NMVVE:AXGXH, AVPKAXX:VPTKL:SAIS-AA17-LYL:LKNYQ:NMVVE:AXGXH, KVGKAXX:VPTKL:SAIS-AA17-LYL:LKNYQ:EGMSVVE:XGXR, KASKAXX:VPTKL:SAIS-AA17-LYL:LKNYQ:GMVVE:EXGXR, GSAGPXX:VPTKM:SAIS-AA17-LYL:LKNYQ:GMVVE:RXGXS, AAPASXX:VPTRL:SAIS-AA17-LYL:LKNYQ:DMVVE:AXGXR,

STPPTXX:VPTRL:SAIS-AA17-LYL:LKNYQ:DMVVE:SXGXR, HVPKPXX:VPTKL:SAIS-AA17-LYL:LKNYQ:NMVVE:SXGXH, RVPSTXX:VPTKT:SAIS-AA17-LYL:LKNYQ:MIVVE:XGXL, ASAAPXX:VPTAL:SAIS-AA17-LYL:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS-AA17-LYL:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS-AA17-LYL:LKNYQ:MVVVE:XKXS, GIPEPXX:VPEKM:SAIS-AA17-LYL:LKNYQ:NMTVE:SXAXR, HVTKPTX:APTKL:SAIS-AA17-LYL:LKNYQ:NMVVR:SXGXH, YVPKPXX:APTKL:SAIS-AA17-LYL:LKNYQ:NMVVR:SXGXH, TVPKPXX:APTQL:SAIS-AA17-LYL:LKNYQ:NMVVR:AXGXH, AVPKAXX:APTKL:SAIS-AA17-LYL:LKNYQ:NMVVK:AXGXH, KVGKAXX:VPTKL:SAIS-AA17-LYL:LKNYQ:EGMSVAE:XGXR, KASKAXX:VPTKL:SAIS-AA17-LYL:LKNYQ:GMAVS:EXGXR, GSAGPXX:TPTKM:SAIS-AA17-LYL:LKNYQ:GMVVD:RXGXS, AAPASXX:VPARL:SAIS-AA17-LYL:LKNYQ:DMVVE:AXGXR, HVPKPXX:APTKL:SAIS-AA17-LYL:LKNYQ:NMVVR:SXGXH, RVPSTXX:APVKT:SAIS-AA17-LYL:LKNYQ:MIVEE:XGXL, ASAAPXX:VPQAL:SAIS-AA17-LYL:LKNYQ:MIVRS:XKXS, ASASPXX:VSQDL:SAIS-AA17-LYL:LKNYQ:MIVKS:XKXS, ASASPXX:VPQDL:SAIS-AA17-LYL:LKNYQ:MVVKS:XKXS, NDEGLEX:VPTEE:SAIS-AA17-LYL:LKNYQ:FLQHN:KXEXR, NDEGLEX:VPTGQ:SAIS-AA17-LYL:LKNYQ:LEEHS:QXEXR, SSVKXQP:SRVHH:SAIS-AA17-LYL:LKNYQ:RLEEH:LEXAXA, RNVQXRP:TQVQL:SAIS-AA17-LYL:LKNYQ:TLEDH:LAXKXE, KIPKAXX:VPEEL:SSLS-AA17-LFF:LKVYP:DMTVE:GXGXR, SIPKAXX:VPEEL:SSLS-AA17-LFF:LKVYP:EMTVE:GXGXR, HVTKPTX:VPEKL:SSLS-AA17-LFF:LKVYP:NMTVE:SXGXH, YVPKPXX:VPEKL:SSLS-AA17-LFF:LKVYP:NMTVE:SXGXH, TVPKPXX:VPEQL:SSLS-AA17-LFF:LKVYP:NMTVE:AXGXH, AVPKAXX:VPEKL:SSLS-AA17-LFF:LKVYP:NMTVE:AXGXH, KVGKAXX:VPEKL:SSLS-AA17-LFF:LKVYP:EGMSTVE:XGXR, KASKAXX:VPEKL:SSLS-AA17-LFF:LKVYP:GMTVE:EXGXR, GSAGPXX:VPEKM:SSLS-AA17-LFF:LKVYP:GMTVE:RXGXS, AAPASXX:VPERL:SSLS-AA17-LFF:LKVYP:DMTVE:AXGXR, STPPTXX:VPERL:SSLS-AA17-LFF:LKVYP:DMTVE:SXGXR, HVPKPXX:VPEKL:SSLS-AA17-LFF:LKVYP:NMTVE:SXGXH, RVPSTXX:VPEKT:SSLS-AA17-LFF:LKVYP:MITVE:XGXL, ASAAPXX:VPEAL:SSLS-AA17-LFF:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS-AA17-LFF:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS-AA17-LFF:LKVYP:MVTVE:XKXS, KIPKAXX:VPTEL:SSLS-AA17-LFF:LKVYP:DMVVE:GXGXR, SIPKAXX:VPTEL:SSLS-AA17-LFF:LKVYP:EMVVE:GXGXR, HVTKPTX:APTKL:SSLS-AA17-LFF:LKVYP:NMVVR:SXGXH, YVPKPXX:APTKL:SSLS-AA17-LFF:LKVYP:NMVVR:SXGXH, TVPKPXX:APTQL:SSLS-AA17-LFF:LKVYP:NMVVR:AXGXH, AVPKAXX:APTKL:SSLS-AA17-LFF:LKVYP:NMVVK:AXGXH, KVGKAXX:VPTKL:SSLS-AA17-LFF:LKVYP:EGMSVAE:XGXR, KASKAXX:VPTKL:SSLS-AA17-LFF:LKVYP:GMAVS:EXGXR, GSAGPXX:TPTKM:SSLS-AA17-LFF:LKVYP:GMVVD:RXGXS, AAPASXX:VPARL:SSLS-AA17-LFF:LKVYP:DMVVE:AXGXR, STPPTXX:VPTRL:SSLS-AA17-LFF:LKVYP:DMVVE:SXGXR, HVPKPXX:APTKL:SSLS-AA17-LFF:LKVYP:NMVVR:SXGXH, RVPSTXX:APVKT:SSLS-AA17-LFF:LKVYP:MIVEE:XGXL, ASAAPXX:VPQAL:SSLS-AA17-LFF:LKVYP:MIVRS:XKXS, ASASPXX:VSQDL:SSLS-AA17-LFF:LKVYP:MIVKS:XKXS, ASASPXX:VPQDL:SSLS-AA17-LFF:LKVYP:MVVKS:XKXS, NDEGLEX:VPTEE:SSLS-AA17-LFF:LKVYP:FLQHN:KXEXR, NDEGLEX:VPTGQ:SSLS-AA17-LFF:LKVYP:LEEHS:QXEXR, SSVKXQP:SRVHH:SSLS-AA17-LFF:LKVYP:RLEEH:LEXAXA, RNVQXRP:TQVQL:SSLS-AA17-LFF:LKVYP:TLEDH:LAXKXE, KIPKAXX:APTEL:NAIS-AA17-LYF:LKKYR:DMVVR:GXGXR, GIPEPXX:APTKM:NAIS-AA17-LYF:LKKYR:NMVVR:SXAXR, SIPKAXX:APTEL:NAIS-AA17-LYF:LKKYR:EMVVR:GXGXR,

AVPKAXX:APTKL:NAIS-AA17-LYF:LKKYR:NMVVR:AXGXH, KVGKAXX:APTKL:NAIS-AA17-LYF:LKKYR:EGMSVVR:XGXR, KASKAXX:APTKL:NAIS-AA17-LYF:LKKYR:GMVVR:EXGXR, GSAGPXX:APTKM:NAIS-AA17-LYF:LKKYR:GMVVR:RXGXS, AAPASXX:APTRL:NAIS-AA17-LYF:LKKYR:DMVVR:AXGXR, STPPTXX:APTRL:NAIS-AA17-LYF:LKKYR:DMVVR:SXGXR, RVPSTXX:APTKT:NAIS-AA17-LYF:LKKYR:MIVVR:XGXL, ASAAPXX:APTAL:NAIS-AA17-LYF:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS-AA17-LYF:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS-AA17-LYF:LKKYR:MVVVR:XKXS, KIPKAXX:VPTEL:NAIS-AA17-LYF:LKKYR:DMVVE:GXGXR, GIPEPXX:VPEKM:NAIS-AA17-LYF:LKKYR:NMTVE:SXAXR, SIPKAXX:VPTEL:NAIS-AA17-LYF:LKKYR:EMVVE:GXGXR, AVPKAXX:APTKL:NAIS-AA17-LYF:LKKYR:NMVVK:AXGXH, KVGKAXX:VPTKL:NAIS-AA17-LYF:LKKYR:EGMSVAE:XGXR, KASKAXX:VPTKL:NAIS-AA17-LYF:LKKYR:GMAVS:EXGXR, GSAGPXX:TPTKM:NAIS-AA17-LYF:LKKYR:GMVVD:RXGXS, AAPASXX:VPARL:NAIS-AA17-LYF:LKKYR:DMVVE:AXGXR, STPPTXX:VPTRL:NAIS-AA17-LYF:LKKYR:DMVVE:SXGXR, RVPSTXX:APVKT:NAIS-AA17-LYF:LKKYR:MIVEE:XGXL, ASAAPXX:VPQAL:NAIS-AA17-LYF:LKKYR:MIVRS:XKXS, ASASPXX:VSQDL:NAIS-AA17-LYF:LKKYR:MIVKS:XKXS, ASASPXX:VPQDL:NAIS-AA17-LYF:LKKYR:MVVKS:XKXS, NDEGLEX:VPTEE:NAIS-AA17-LYF:LKKYR:FLQHN:KXEXR, NDEGLEX:VPTGQ:NAIS-AA17-LYF:LKKYR:LEEHS:QXEXR, SSVKXQP:SRVHH:NAIS-AA17-LYF:LKKYR:RLEEH:LEXAXA, RNVQXRP:TQVQL:NAIS-AA17-LYF:LKKYR:TLEDH:LAXKXE, KIPKAXX:APTEL:SATS-AA17-LYY:LRKHR:DMVVK:GXGXR, GIPEPXX:APTKM:SATS-AA17-LYY:LRKHR:NMVVK:SXAXR, SIPKAXX:APTEL:SATS-AA17-LYY:LRKHR:EMVVK:GXGXR, HVTKPTX:APTKL:SATS-AA17-LYY:LRKHR:NMVVK:SXGXH, YVPKPXX:APTKL:SATS-AA17-LYY:LRKHR:NMVVK:SXGXH, TVPKPXX:APTQL:SATS-AA17-LYY:LRKHR:NMVVK:AXGXH, KVGKAXX:APTKL:SATS-AA17-LYY:LRKHR:EGMSVVK:XGXR, KASKAXX:APTKL:SATS-AA17-LYY:LRKHR:GMVVK:EXGXR, GSAGPXX:APTKM:SATS-AA17-LYY:LRKHR:GMVVK:RXGXS, AAPASXX:APTRL:SATS-AA17-LYY:LRKHR:DMVVK:AXGXR, STPPTXX:APTRL:SATS-AA17-LYY:LRKHR:DMVVK:SXGXR, HVPKPXX:APTKL:SATS-AA17-LYY:LRKHR:NMVVK:SXGXH, RVPSTXX:APTKT:SATS-AA17-LYY:LRKHR:MIVVK:XGXL, ASAAPXX:APTAL:SATS-AA17-LYY:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS-AA17-LYY:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS-AA17-LYY:LRKHR:MVVVK:XKXS, KIPKAXX:VPTEL:SATS-AA17-LYY:LRKHR:DMVVE:GXGXR, GIPEPXX:VPEKM:SATS-AA17-LYY:LRKHR:NMTVE:SXAXR, SIPKAXX:VPTEL:SATS-AA17-LYY:LRKHR:EMVVE:GXGXR, HVTKPTX:APTKL:SATS-AA17-LYY:LRKHR:NMVVR:SXGXH, YVPKPXX:APTKL:SATS-AA17-LYY:LRKHR:NMVVR:SXGXH, TVPKPXX:APTQL:SATS-AA17-LYY:LRKHR:NMVVR:AXGXH, KVGKAXX:VPTKL:SATS-AA17-LYY:LRKHR:EGMSVAE:XGXR, KASKAXX:VPTKL:SATS-AA17-LYY:LRKHR:GMAVS:EXGXR, GSAGPXX:TPTKM:SATS-AA17-LYY:LRKHR:GMVVD:RXGXS, AAPASXX:VPARL:SATS-AA17-LYY:LRKHR:DMVVE:AXGXR, STPPTXX:VPTRL:SATS-AA17-LYY:LRKHR:DMVVE:SXGXR, HVPKPXX:APTKL:SATS-AA17-LYY:LRKHR:NMVVR:SXGXH, RVPSTXX:APVKT:SATS-AA17-LYY:LRKHR:MIVEE:XGXL, ASAAPXX:VPQAL:SATS-AA17-LYY:LRKHR:MIVRS:XKXS, ASASPXX:VSQDL:SATS-AA17-LYY:LRKHR:MIVKS:XKXS, ASASPXX:VPQDL:SATS-AA17-LYY:LRKHR:MVVKS:XKXS, NDEGLEX:VPTEE:SATS-AA17-LYY:LRKHR:FLQHN:KXEXR, NDEGLEX:VPTGQ:SATS-AA17-LYY:LRKHR:LEEHS:QXEXR, SSVKXQP:SRVHH:SATS-AA17-LYY:LRKHR:RLEEH:LEXAXA, RNVQXRP:TQVQL:SATS-AA17-LYY:LRKHR:TLEDH:LAXKXE,

KIPKAXX:VPTEL:SPIS-AA17-LYK:LKYHY:DMVAE:GXGXR, GIPEPXX:VPTKM:SPIS-AA17-LYK:LKYHY:NMVAE:SXAXR, SIPKAXX:VPTEL:SPIS-AA17-LYK:LKYHY:EMVAE:GXGXR, HVTKPTX:VPTKL:SPIS-AA17-LYK:LKYHY:NMVAE:SXGXH, YVPKPXX:VPTKL:SPIS-AA17-LYK:LKYHY:NMVAE:SXGXH, TVPKPXX:VPTQL:SPIS-AA17-LYK:LKYHY:NMVAE:AXGXH, AVPKAXX:VPTKL:SPIS-AA17-LYK:LKYHY:NMVAE:AXGXH, KASKAXX:VPTKL:SPIS-AA17-LYK:LKYHY:GMVAE:EXGXR, GSAGPXX:VPTKM:SPIS-AA17-LYK:LKYHY:GMVAE:RXGXS, AAPASXX:VPTRL:SPIS-AA17-LYK:LKYHY:DMVAE:AXGXR, STPPTXX:VPTRL:SPIS-AA17-LYK:LKYHY:DMVAE:SXGXR, HVPKPXX:VPTKL:SPIS-AA17-LYK:LKYHY:NMVAE:SXGXH, RVPSTXX:VPTKT:SPIS-AA17-LYK:LKYHY:MIVAE:XGXL, ASAAPXX:VPTAL:SPIS-AA17-LYK:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS-AA17-LYK:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS-AA17-LYK:LKYHY:MVVAE:XKXS, KIPKAXX:VPTEL:SPIS-AA17-LYK:LKYHY:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIS-AA17-LYK:LKYHY:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIS-AA17-LYK:LKYHY:EMVVE:GXGXR, HVTKPTX:APTKL:SPIS-AA17-LYK:LKYHY:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA17-LYK:LKYHY:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA17-LYK:LKYHY:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA17-LYK:LKYHY:NMVVK:AXGXH, KASKAXX:VPTKL:SPIS-AA17-LYK:LKYHY:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA17-LYK:LKYHY:GMVVD:RXGXS, AAPASXX:VPARL:SPIS-AA17-LYK:LKYHY:DMVVE:AXGXR, STPPTXX:VPTRL:SPIS-AA17-LYK:LKYHY:DMVVE:SXGXR, HVPKPXX:APTKL:SPIS-AA17-LYK:LKYHY:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA17-LYK:LKYHY:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA17-LYK:LKYHY:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA17-LYK:LKYHY:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA17-LYK:LKYHY:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA17-LYK:LKYHY:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA17-LYK:LKYHY:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA17-LYK:LKYHY:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA17-LYK:LKYHY:TLEDH:LAXKXE, KIPKAXX:VPTEL:EPIS-AA17-LYL:KFKYE:DMAVS:GXGXR, GIPEPXX:VPTKM:EPIS-AA17-LYL:KFKYE:NMAVS:SXAXR, SIPKAXX:VPTEL:EPIS-AA17-LYL:KFKYE:EMAVS:GXGXR, HVTKPTX:VPTKL:EPIS-AA17-LYL:KFKYE:NMAVS:SXGXH, YVPKPXX:VPTKL:EPIS-AA17-LYL:KFKYE:NMAVS:SXGXH, TVPKPXX:VPTQL:EPIS-AA17-LYL:KFKYE:NMAVS:AXGXH, AVPKAXX:VPTKL:EPIS-AA17-LYL:KFKYE:NMAVS:AXGXH, KVGKAXX:VPTKL:EPIS-AA17-LYL:KFKYE:EGMSAVS:XGXR, GSAGPXX:VPTKM:EPIS-AA17-LYL:KFKYE:GMAVS:RXGXS, AAPASXX:VPTRL:EPIS-AA17-LYL:KFKYE:DMAVS:AXGXR, STPPTXX:VPTRL:EPIS-AA17-LYL:KFKYE:DMAVS:SXGXR, HVPKPXX:VPTKL:EPIS-AA17-LYL:KFKYE:NMAVS:SXGXH, RVPSTXX:VPTKT:EPIS-AA17-LYL:KFKYE:MIAVS:XGXL, ASAAPXX:VPTAL:EPIS-AA17-LYL:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS-AA17-LYL:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS-AA17-LYL:KFKYE:MVAVS:XKXS, KIPKAXX:VPTEL:EPIS-AA17-LYL:KFKYE:DMVVE:GXGXR, GIPEPXX:VPEKM:EPIS-AA17-LYL:KFKYE:NMTVE:SXAXR, SIPKAXX:VPTEL:EPIS-AA17-LYL:KFKYE:EMVVE:GXGXR, HVTKPTX:APTKL:EPIS-AA17-LYL:KFKYE:NMVVR:SXGXH, YVPKPXX:APTKL:EPIS-AA17-LYL:KFKYE:NMVVR:SXGXH, TVPKPXX:APTQL:EPIS-AA17-LYL:KFKYE:NMVVR:AXGXH, AVPKAXX:APTKL:EPIS-AA17-LYL:KFKYE:NMVVK:AXGXH, KVGKAXX:VPTKL:EPIS-AA17-LYL:KFKYE:EGMSVAE:XGXR, GSAGPXX:TPTKM:EPIS-AA17-LYL:KFKYE:GMVVD:RXGXS, AAPASXX:VPARL:EPIS-AA17-LYL:KFKYE:DMVVE:AXGXR, STPPTXX:VPTRL:EPIS-AA17-LYL:KFKYE:DMVVE:SXGXR,

HVPKPXX:APTKL:EPIS-AA17-LYL:KFKYE:NMVVR:SXGXH, RVPSTXX:APVKT:EPIS-AA17-LYL:KFKYE:MIVEE:XGXL, ASAAPXX:VPQAL:EPIS-AA17-LYL:KFKYE:MIVRS:XKXS, ASASPXX:VSQDL:EPIS-AA17-LYL:KFKYE:MIVKS:XKXS, ASASPXX:VPQDL:EPIS-AA17-LYL:KFKYE:MVVKS:XKXS, NDEGLEX:VPTEE:EPIS-AA17-LYL:KFKYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPIS-AA17-LYL:KFKYE:LEEHS:QXEXR, SSVKXQP:SRVHH:EPIS-AA17-LYL:KFKYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPIS-AA17-LYL:KFKYE:TLEDH:LAXKXE, KIPKAXX:TPTEL:SPIN-AA17-LYF:YGKIP:DMVVD:GXGXR, GIPEPXX:TPTKM:SPIN-AA17-LYF:YGKIP:NMVVD:SXAXR, SIPKAXX:TPTEL:SPIN-AA17-LYF:YGKIP:EMVVD:GXGXR, HVTKPTX:TPTKL:SPIN-AA17-LYF:YGKIP:NMVVD:SXGXH, YVPKPXX:TPTKL:SPIN-AA17-LYF:YGKIP:NMVVD:SXGXH, TVPKPXX:TPTQL:SPIN-AA17-LYF:YGKIP:NMVVD:AXGXH, AVPKAXX:TPTKL:SPIN-AA17-LYF:YGKIP:NMVVD:AXGXH, KVGKAXX:TPTKL:SPIN-AA17-LYF:YGKIP:EGMSVVD:XGXR, KASKAXX:TPTKL:SPIN-AA17-LYF:YGKIP:GMVVD:EXGXR, AAPASXX:TPTRL:SPIN-AA17-LYF:YGKIP:DMVVD:AXGXR, STPPTXX:TPTRL:SPIN-AA17-LYF:YGKIP:DMVVD:SXGXR, HVPKPXX:TPTKL:SPIN-AA17-LYF:YGKIP:NMVVD:SXGXH, RVPSTXX:TPTKT:SPIN-AA17-LYF:YGKIP:MIVVD:XGXL, ASAAPXX:TPTAL:SPIN-AA17-LYF:YGKIP:MIVVD:XKXS, ASASPXX:TPTDL:SPIN-AA17-LYF:YGKIP:MIVVD:XKXS, ASASPXX:TPTDL:SPIN-AA17-LYF:YGKIP:MVVVD:XKXS, KIPKAXX:VPTEL:SPIN-AA17-LYF:YGKIP:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIN-AA17-LYF:YGKIP:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIN-AA17-LYF:YGKIP:EMVVE:GXGXR, HVTKPTX:APTKL:SPIN-AA17-LYF:YGKIP:NMVVR:SXGXH, YVPKPXX:APTKL:SPIN-AA17-LYF:YGKIP:NMVVR:SXGXH, TVPKPXX:APTQL:SPIN-AA17-LYF:YGKIP:NMVVR:AXGXH, AVPKAXX:APTKL:SPIN-AA17-LYF:YGKIP:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIN-AA17-LYF:YGKIP:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIN-AA17-LYF:YGKIP:GMAVS:EXGXR, AAPASXX:VPARL:SPIN-AA17-LYF:YGKIP:DMVVE:AXGXR, STPPTXX:VPTRL:SPIN-AA17-LYF:YGKIP:DMVVE:SXGXR, HVPKPXX:APTKL:SPIN-AA17-LYF:YGKIP:NMVVR:SXGXH, RVPSTXX:APVKT:SPIN-AA17-LYF:YGKIP:MIVEE:XGXL, ASAAPXX:VPQAL:SPIN-AA17-LYF:YGKIP:MIVRS:XKXS, ASASPXX:VSQDL:SPIN-AA17-LYF:YGKIP:MIVKS:XKXS, ASASPXX:VPQDL:SPIN-AA17-LYF:YGKIP:MVVKS:XKXS, NDEGLEX:VPTEE:SPIN-AA17-LYF:YGKIP:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIN-AA17-LYF:YGKIP:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIN-AA17-LYF:YGKIP:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIN-AA17-LYF:YGKIP:TLEDH:LAXKXE, KIPKAXX:VPAEL:SPIS-AA17-LYI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPAKM:SPIS-AA17-LYI:YKQYE:NMVVE:SXAXR, SIPKAXX:VPAEL:SPIS-AA17-LYI:YKQYE:EMVVE:GXGXR, HVTKPTX:VPAKL:SPIS-AA17-LYI:YKQYE:NMVVE:SXGXH, YVPKPXX:VPAKL:SPIS-AA17-LYI:YKQYE:NMVVE:SXGXH, TVPKPXX:VPAQL:SPIS-AA17-LYI:YKQYE:NMVVE:AXGXH, AVPKAXX:VPAKL:SPIS-AA17-LYI:YKQYE:NMVVE:AXGXH, KVGKAXX:VPAKL:SPIS-AA17-LYI:YKQYE:EGMSVVE:XGXR, KASKAXX:VPAKL:SPIS-AA17-LYI:YKQYE:GMVVE:EXGXR, GSAGPXX:VPAKM:SPIS-AA17-LYI:YKQYE:GMVVE:RXGXS, STPPTXX:VPARL:SPIS-AA17-LYI:YKQYE:DMVVE:SXGXR, HVPKPXX:VPAKL:SPIS-AA17-LYI:YKQYE:NMVVE:SXGXH, RVPSTXX:VPAKT:SPIS-AA17-LYI:YKQYE:MIVVE:XGXL, ASAAPXX:VPAAL:SPIS-AA17-LYI:YKQYE:MIVVE:XKXS, ASASPXX:VPADL:SPIS-AA17-LYI:YKQYE:MIVVE:XKXS, ASASPXX:VPADL:SPIS-AA17-LYI:YKQYE:MVVVE:XKXS, KIPKAXX:VPTEL:SPIS-AA17-LYI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPEKM:SPIS-AA17-LYI:YKQYE:NMTVE:SXAXR,

SIPKAXX:VPTEL:SPIS-AA17-LYI:YKQYE:EMVVE:GXGXR, HVTKPTX:APTKL:SPIS-AA17-LYI:YKQYE:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA17-LYI:YKQYE:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA17-LYI:YKQYE:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA17-LYI:YKQYE:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIS-AA17-LYI:YKQYE:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIS-AA17-LYI:YKQYE:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA17-LYI:YKQYE:GMVVD:RXGXS, STPPTXX:VPTRL:SPIS-AA17-LYI:YKQYE:DMVVE:SXGXR, HVPKPXX:APTKL:SPIS-AA17-LYI:YKQYE:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA17-LYI:YKQYE:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA17-LYI:YKQYE:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA17-LYI:YKQYE:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA17-LYI:YKQYE:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA17-LYI:YKQYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA17-LYI:YKQYE:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA17-LYI:YKQYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA17-LYI:YKQYE:TLEDH:LAXKXE, KIPKAXX:VPTEL:SPIS-AA17-LFI:YKQYE:DMVVE:GXGXR, GIPEPXX:VPTKM:SPIS-AA17-LFI:YKQYE:NMVVE:SXAXR, SIPKAXX:VPTEL:SPIS-AA17-LFI:YKQYE:EMVVE:GXGXR, HVTKPTX:VPTKL:SPIS-AA17-LFI:YKQYE:NMVVE:SXGXH, YVPKPXX:VPTKL:SPIS-AA17-LFI:YKQYE:NMVVE:SXGXH, TVPKPXX:VPTQL:SPIS-AA17-LFI:YKQYE:NMVVE:AXGXH, AVPKAXX:VPTKL:SPIS-AA17-LFI:YKQYE:NMVVE:AXGXH, KVGKAXX:VPTKL:SPIS-AA17-LFI:YKQYE:EGMSVVE:XGXR, KASKAXX:VPTKL:SPIS-AA17-LFI:YKQYE:GMVVE:EXGXR, GSAGPXX:VPTKM:SPIS-AA17-LFI:YKQYE:GMVVE:RXGXS, AAPASXX:VPTRL:SPIS-AA17-LFI:YKQYE:DMVVE:AXGXR, HVPKPXX:VPTKL:SPIS-AA17-LFI:YKQYE:NMVVE:SXGXH, RVPSTXX:VPTKT:SPIS-AA17-LFI:YKQYE:MIVVE:XGXL, ASAAPXX:VPTAL:SPIS-AA17-LFI:YKQYE:MIVVE:XKXS, ASASPXX:VPTDL:SPIS-AA17-LFI:YKQYE:MIVVE:XKXS, ASASPXX:VPTDL:SPIS-AA17-LFI:YKQYE:MVVVE:XKXS, GIPEPXX:VPEKM:SPIS-AA17-LFI:YKQYE:NMTVE:SXAXR, HVTKPTX:APTKL:SPIS-AA17-LFI:YKQYE:NMVVR:SXGXH, YVPKPXX:APTKL:SPIS-AA17-LFI:YKQYE:NMVVR:SXGXH, TVPKPXX:APTQL:SPIS-AA17-LFI:YKQYE:NMVVR:AXGXH, AVPKAXX:APTKL:SPIS-AA17-LFI:YKQYE:NMVVK:AXGXH, KVGKAXX:VPTKL:SPIS-AA17-LFI:YKQYE:EGMSVAE:XGXR, KASKAXX:VPTKL:SPIS-AA17-LFI:YKQYE:GMAVS:EXGXR, GSAGPXX:TPTKM:SPIS-AA17-LFI:YKQYE:GMVVD:RXGXS, AAPASXX:VPARL:SPIS-AA17-LFI:YKQYE:DMVVE:AXGXR, HVPKPXX:APTKL:SPIS-AA17-LFI:YKQYE:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS-AA17-LFI:YKQYE:MIVEE:XGXL, ASAAPXX:VPQAL:SPIS-AA17-LFI:YKQYE:MIVRS:XKXS, ASASPXX:VSQDL:SPIS-AA17-LFI:YKQYE:MIVKS:XKXS, ASASPXX:VPQDL:SPIS-AA17-LFI:YKQYE:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS-AA17-LFI:YKQYE:FLQHN:KXEXR, NDEGLEX:VPTGQ:SPIS-AA17-LFI:YKQYE:LEEHS:QXEXR, SSVKXQP:SRVHH:SPIS-AA17-LFI:YKQYE:RLEEH:LEXAXA, RNVQXRP:TQVQL:SPIS-AA17-LFI:YKQYE:TLEDH:LAXKXE, KIPKAXX:APVEL:KPLS-AA17-LYV:DHHKD:DMVEE:GXGXR, GIPEPXX:APVKM:KPLS-AA17-LYV:DHHKD:NMVEE:SXAXR, SIPKAXX:APVEL:KPLS-AA17-LYV:DHHKD:EMVEE:GXGXR, HVTKPTX:APVKL:KPLS-AA17-LYV:DHHKD:NMVEE:SXGXH, YVPKPXX:APVKL:KPLS-AA17-LYV:DHHKD:NMVEE:SXGXH, TVPKPXX:APVQL:KPLS-AA17-LYV:DHHKD:NMVEE:AXGXH, AVPKAXX:APVKL:KPLS-AA17-LYV:DHHKD:NMVEE:AXGXH, KVGKAXX:APVKL:KPLS-AA17-LYV:DHHKD:EGMSVEE:XGXR, KASKAXX:APVKL:KPLS-AA17-LYV:DHHKD:GMVEE:EXGXR, GSAGPXX:APVKM:KPLS-AA17-LYV:DHHKD:GMVEE:RXGXS, AAPASXX:APVRL:KPLS-AA17-LYV:DHHKD:DMVEE:AXGXR,

STPPTXX:APVRL:KPLS-AA17-LYV:DHHKD:DMVEE:SXGXR, HVPKPXX:APVKL:KPLS-AA17-LYV:DHHKD:NMVEE:SXGXH, ASAAPXX:APVAL:KPLS-AA17-LYV:DHHKD:MIVEE:XKXS, ASASPXX:APVDL:KPLS-AA17-LYV:DHHKD:MIVEE:XKXS, ASASPXX:APVDL:KPLS-AA17-LYV:DHHKD:MVVEE:XKXS, KIPKAXX:VPTEL:KPLS-AA17-LYV:DHHKD:DMVVE:GXGXR, GIPEPXX:VPEKM:KPLS-AA17-LYV:DHHKD:NMTVE:SXAXR, SIPKAXX:VPTEL:KPLS-AA17-LYV:DHHKD:EMVVE:GXGXR, HVTKPTX:APTKL:KPLS-AA17-LYV:DHHKD:NMVVR:SXGXH, YVPKPXX:APTKL:KPLS-AA17-LYV:DHHKD:NMVVR:SXGXH, TVPKPXX:APTQL:KPLS-AA17-LYV:DHHKD:NMVVR:AXGXH, AVPKAXX:APTKL:KPLS-AA17-LYV:DHHKD:NMVVK:AXGXH, KVGKAXX:VPTKL:KPLS-AA17-LYV:DHHKD:EGMSVAE:XGXR, KASKAXX:VPTKL:KPLS-AA17-LYV:DHHKD:GMAVS:EXGXR, GSAGPXX:TPTKM:KPLS-AA17-LYV:DHHKD:GMVVD:RXGXS, AAPASXX:VPARL:KPLS-AA17-LYV:DHHKD:DMVVE:AXGXR, STPPTXX:VPTRL:KPLS-AA17-LYV:DHHKD:DMVVE:SXGXR, HVPKPXX:APTKL:KPLS-AA17-LYV:DHHKD:NMVVR:SXGXH, ASAAPXX:VPQAL:KPLS-AA17-LYV:DHHKD:MIVRS:XKXS, ASASPXX:VSQDL:KPLS-AA17-LYV:DHHKD:MIVKS:XKXS, ASASPXX:VPQDL:KPLS-AA17-LYV:DHHKD:MVVKS:XKXS, NDEGLEX:VPTEE:KPLS-AA17-LYV:DHHKD:FLQHN:KXEXR, NDEGLEX:VPTGQ:KPLS-AA17-LYV:DHHKD:LEEHS:QXEXR, SSVKXQP:SRVHH:KPLS-AA17-LYV:DHHKD:RLEEH:LEXAXA, RNVQXRP:TQVQL:KPLS-AA17-LYV:DHHKD:TLEDH:LAXKXE, KIPKAXX:VPQEL:EPLP-AA17-VYY:EQLSN:DMVRS:GXGXR, GIPEPXX:VPQKM:EPLP-AA17-VYY:EQLSN:NMVRS:SXAXR, SIPKAXX:VPQEL:EPLP-AA17-VYY:EQLSN:EMVRS:GXGXR, HVTKPTX:VPQKL:EPLP-AA17-VYY:EQLSN:NMVRS:SXGXH, YVPKPXX:VPQKL:EPLP-AA17-VYY:EQLSN:NMVRS:SXGXH, TVPKPXX:VPQQL:EPLP-AA17-VYY:EQLSN:NMVRS:AXGXH, AVPKAXX:VPQKL:EPLP-AA17-VYY:EQLSN:EGMSVRS:XGXR, KASKAXX:VPQKL:EPLP-AA17-VYY:EQLSN:GMVRS:EXGXR, GSAGPXX:VPQKM:EPLP-AA17-VYY:EQLSN:GMVRS:RXGXS, AAPASXX:VPQRL:EPLP-AA17-VYY:EQLSN:DMVRS:AXGXR, STPPTXX:VPQRL:EPLP-AA17-VYY:EQLSN:DMVRS:SXGXR, HVPKPXX:VPQKL:EPLP-AA17-VYY:EQLSN:NMVRS:SXGXH, RVPSTXX:VPQKT:EPLP-AA17-VYY:EQLSN:MIVRS:XGXL, ASASPXX:VPQDL:EPLP-AA17-VYY:EQLSN:MIVRS:XKXS, ASASPXX:VPQDL:EPLP-AA17-VYY:EQLSN:MVVRS:XKXS, KIPKAXX:VPTEL:EPLP-AA17-VYY:EQLSN:DMVVE:GXGXR, GIPEPXX:VPEKM:EPLP-AA17-VYY:EQLSN:NMTVE:SXAXR, SIPKAXX:VPTEL:EPLP-AA17-VYY:EQLSN:EMVVE:GXGXR, HVTKPTX:APTKL:EPLP-AA17-VYY:EQLSN:NMVVR:SXGXH, YVPKPXX:APTKL:EPLP-AA17-VYY:EQLSN:NMVVR:SXGXH, TVPKPXX:APTQL:EPLP-AA17-VYY:EQLSN:NMVVR:AXGXH, AVPKAXX:APTKL:EPLP-AA17-VYY:EQLSN:NMVVK:AXGXH, KVGKAXX:VPTKL:EPLP-AA17-VYY:EQLSN:EGMSVAE:XGXR, KASKAXX:VPTKL:EPLP-AA17-VYY:EQLSN:GMAVS:EXGXR, GSAGPXX:TPTKM:EPLP-AA17-VYY:EQLSN:GMVVD:RXGXS, AAPASXX:VPARL:EPLP-AA17-VYY:EQLSN:DMVVE:AXGXR, STPPTXX:VPTRL:EPLP-AA17-VYY:EQLSN:DMVVE:SXGXR, HVPKPXX:APTKL:EPLP-AA17-VYY:EQLSN:NMVVR:SXGXH, RVPSTXX:APVKT:EPLP-AA17-VYY:EQLSN:MIVEE:XGXL, ASASPXX:VSQDL:EPLP-AA17-VYY:EQLSN:MIVKS:XKXS, ASASPXX:VPQDL:EPLP-AA17-VYY:EQLSN:MVVKS:XKXS, NDEGLEX:VPTEE:EPLP-AA17-VYY:EQLSN:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPLP-AA17-VYY:EQLSN:LEEHS:QXEXR, SSVKXQP:SRVHH:EPLP-AA17-VYY:EQLSN:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPLP-AA17-VYY:EQLSN:TLEDH:LAXKXE, KIPKAXX:VSQEL:EPLT-AA17-LYY:EQLSN:DMVKS:GXGXR, GIPEPXX:VSQKM:EPLT-AA17-LYY:EQLSN:NMVKS:SXAXR,

SIPKAXX:VSQEL:EPLT-AA17-LYY:EQLSN:EMVKS:GXGXR, HVTKPTX:VSQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, YVPKPXX:VSQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, TVPKPXX:VSQQL:EPLT-AA17-LYY:EQLSN:NMVKS:AXGXH, AVPKAXX:VSQKL:EPLT-AA17-LYY:EQLSN:NMVKS:AXGXH, KVGKAXX:VSQKL:EPLT-AA17-LYY:EQLSN:EGMSVKS:XGXR, KASKAXX:VSQKL:EPLT-AA17-LYY:EQLSN:GMVKS:EXGXR, GSAGPXX:VSQKM:EPLT-AA17-LYY:EQLSN:GMVKS:RXGXS, AAPASXX:VSQRL:EPLT-AA17-LYY:EQLSN:DMVKS:AXGXR, STPPTXX:VSQRL:EPLT-AA17-LYY:EQLSN:DMVKS:SXGXR, HVPKPXX:VSQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, RVPSTXX:VSQKT:EPLT-AA17-LYY:EQLSN:MIVKS:XGXL, ASAAPXX:VSQAL:EPLT-AA17-LYY:EQLSN:MIVKS:XKXS, ASASPXX:VSQDL:EPLT-AA17-LYY:EQLSN:MVVKS:XKXS, KIPKAXX:VPTEL:EPLT-AA17-LYY:EQLSN:DMVVE:GXGXR, GIPEPXX:VPEKM:EPLT-AA17-LYY:EQLSN:NMTVE:SXAXR, SIPKAXX:VPTEL:EPLT-AA17-LYY:EQLSN:EMVVE:GXGXR, HVTKPTX:APTKL:EPLT-AA17-LYY:EQLSN:NMVVR:SXGXH, YVPKPXX:APTKL:EPLT-AA17-LYY:EQLSN:NMVVR:SXGXH, TVPKPXX:APTQL:EPLT-AA17-LYY:EQLSN:NMVVR:AXGXH, AVPKAXX:APTKL:EPLT-AA17-LYY:EQLSN:NMVVK:AXGXH, KVGKAXX:VPTKL:EPLT-AA17-LYY:EQLSN:EGMSVAE:XGXR, KASKAXX:VPTKL:EPLT-AA17-LYY:EQLSN:GMAVS:EXGXR, GSAGPXX:TPTKM:EPLT-AA17-LYY:EQLSN:GMVVD:RXGXS, AAPASXX:VPARL:EPLT-AA17-LYY:EQLSN:DMVVE:AXGXR, STPPTXX:VPTRL:EPLT-AA17-LYY:EQLSN:DMVVE:SXGXR, HVPKPXX:APTKL:EPLT-AA17-LYY:EQLSN:NMVVR:SXGXH, RVPSTXX:APVKT:EPLT-AA17-LYY:EQLSN:MIVEE:XGXL, ASAAPXX:VPQAL:EPLT-AA17-LYY:EQLSN:MIVRS:XKXS, NDEGLEX:VPTEE:EPLT-AA17-LYY:EQLSN:FLQHN:KXEXR, NDEGLEX:VPTGQ:EPLT-AA17-LYY:EQLSN:LEEHS:QXEXR, SSVKXQP:SRVHH:EPLT-AA17-LYY:EQLSN:RLEEH:LEXAXA, RNVQXRP:TQVQL:EPLT-AA17-LYY:EQLSN:TLEDH:LAXKXE, KIPKAXX:VPQEL:EPLT-AA17-LYY:EQLSN:DMVKS:GXGXR, GIPEPXX:VPQKM:EPLT-AA17-LYY:EQLSN:NMVKS:SXAXR, SIPKAXX:VPQEL:EPLT-AA17-LYY:EQLSN:EMVKS:GXGXR, HVTKPTX:VPQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, YVPKPXX:VPQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, TVPKPXX:VPQQL:EPLT-AA17-LYY:EQLSN:NMVKS:AXGXH, AVPKAXX:VPQKL:EPLT-AA17-LYY:EQLSN:NMVKS:AXGXH, KVGKAXX:VPQKL:EPLT-AA17-LYY:EQLSN:EGMSVKS:XGXR, KASKAXX:VPQKL:EPLT-AA17-LYY:EQLSN:GMVKS:EXGXR, GSAGPXX:VPQKM:EPLT-AA17-LYY:EQLSN:GMVKS:RXGXS, AAPASXX:VPQRL:EPLT-AA17-LYY:EQLSN:DMVKS:AXGXR, STPPTXX:VPQRL:EPLT-AA17-LYY:EQLSN:DMVKS:SXGXR, HVPKPXX:VPQKL:EPLT-AA17-LYY:EQLSN:NMVKS:SXGXH, RVPSTXX:VPQKT:EPLT-AA17-LYY:EQLSN:MIVKS:XGXL, ASAAPXX:VPQAL:EPLT-AA17-LYY:EQLSN:MIVKS:XKXS, ASASPXX:VPQDL:EPLT-AA17-LYY:EQLSN:MIVKS:XKXS, NDEGLEX:VPTGQ:SNIT-AA17-QIM:IGEMS:LEQHN:QXEXR, KIPKAXX:VPTEL:SNIT-AA17-QIM:IGEMS:DMVVE:GXGXR, GIPEPXX:VPEKM:SNIT-AA17-QIM:IGEMS:NMTVE:SXAXR, SIPKAXX:VPTEL:SNIT-AA17-QIM:IGEMS:EMVVE:GXGXR, HVTKPTX:APTKL:SNIT-AA17-QIM:IGEMS:NMVVR:SXGXH, YVPKPXX:APTKL:SNIT-AA17-QIM:IGEMS:NMVVR:SXGXH, TVPKPXX:APTQL:SNIT-AA17-QIM:IGEMS:NMVVR:AXGXH, AVPKAXX:APTKL:SNIT-AA17-QIM:IGEMS:NMVVK:AXGXH, KVGKAXX:VPTKL:SNIT-AA17-QIM:IGEMS:EGMSVAE:XGXR, KASKAXX:VPTKL:SNIT-AA17-QIM:IGEMS:GMAVS:EXGXR, GSAGPXX:TPTKM:SNIT-AA17-QIM:IGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT-AA17-QIM:IGEMS:DMVVE:AXGXR, STPPTXX:VPTRL:SNIT-AA17-QIM:IGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT-AA17-QIM:IGEMS:NMVVR:SXGXH,

RVPSTXX:APVKT:SNIT-AA17-QIM:IGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT-AA17-QIM:IGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT-AA17-QIM:IGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT-AA17-QIM:IGEMS:MVVKS:XKXS, NDEGLEX:VPTGQ:SNIT-AA17-QIM:IGEMS:LEEHS:QXEXR, SSVKXQP:SRVHH:SNIT-AA17-QIM:IGEMS:RLEEH:LEXAXA, RNVQXRP:TQVQL:SNIT-AA17-QIM:IGEMS:TLEDH:LAXKXE, NDEGLEX:VPTEE:SNIT-AA17-QIM:LGEMS:FLEHS:KXEXR, KIPKAXX:VPTEL:SNIT-AA17-QIM:LGEMS:DMVVE:GXGXR, GIPEPXX:VPEKM:SNIT-AA17-QIM:LGEMS:NMTVE:SXAXR, SIPKAXX:VPTEL:SNIT-AA17-QIM:LGEMS:EMVVE:GXGXR, HVTKPTX:APTKL:SNIT-AA17-QIM:LGEMS:NMVVR:SXGXH, YVPKPXX:APTKL:SNIT-AA17-QIM:LGEMS:NMVVR:SXGXH, TVPKPXX:APTQL:SNIT-AA17-QIM:LGEMS:NMVVR:AXGXH, AVPKAXX:APTKL:SNIT-AA17-QIM:LGEMS:NMVVK:AXGXH, KVGKAXX:VPTKL:SNIT-AA17-QIM:LGEMS:EGMSVAE:XGXR, KASKAXX:VPTKL:SNIT-AA17-QIM:LGEMS:GMAVS:EXGXR, GSAGPXX:TPTKM:SNIT-AA17-QIM:LGEMS:GMVVD:RXGXS, AAPASXX:VPARL:SNIT-AA17-QIM:LGEMS:DMVVE:AXGXR, STPPTXX:VPTRL:SNIT-AA17-QIM:LGEMS:DMVVE:SXGXR, HVPKPXX:APTKL:SNIT-AA17-QIM:LGEMS:NMVVR:SXGXH, RVPSTXX:APVKT:SNIT-AA17-QIM:LGEMS:MIVEE:XGXL, ASAAPXX:VPQAL:SNIT-AA17-QIM:LGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT-AA17-QIM:LGEMS:MIVKS:XKXS, ASASPXX:VPQDL:SNIT-AA17-QIM:LGEMS:MVVKS:XKXS, NDEGLEX:VPTEE:SNIT-AA17-QIM:LGEMS:FLQHN:KXEXR, SSVKXQP:SRVHH:SNIT-AA17-QIM:LGEMS:RLEEH:LEXAXA, RNVQXRP:TQVQL:SNIT-AA17-QIM:LGEMS:TLEDH:LAXKXE, RNVQXRP:SRVQL:RSVK-AA17-AKV:KEVQV:TLEEH:LAXKXE, KIPKAXX:VPTEL:RSVK-AA17-AKV:KEVQV:DMVVE:GXGXR, GIPEPXX:VPEKM:RSVK-AA17-AKV:KEVQV:NMTVE:SXAXR, SIPKAXX:VPTEL:RSVK-AA17-AKV:KEVQV:EMVVE:GXGXR, HVTKPTX:APTKL:RSVK-AA17-AKV:KEVQV:NMVVR:SXGXH, YVPKPXX:APTKL:RSVK-AA17-AKV:KEVQV:NMVVR:SXGXH, TVPKPXX:APTQL:RSVK-AA17-AKV:KEVQV:NMVVR:AXGXH, AVPKAXX:APTKL:RSVK-AA17-AKV:KEVQV:NMVVK:AXGXH, KVGKAXX:VPTKL:RSVK-AA17-AKV:KEVQV:EGMSVAE:XGXR, KASKAXX:VPTKL:RSVK-AA17-AKV:KEVQV:GMAVS:EXGXR, GSAGPXX:TPTKM:RSVK-AA17-AKV:KEVQV:GMVVD:RXGXS, AAPASXX:VPARL:RSVK-AA17-AKV:KEVQV:DMVVE:AXGXR, STPPTXX:VPTRL:RSVK-AA17-AKV:KEVQV:DMVVE:SXGXR, HVPKPXX:APTKL:RSVK-AA17-AKV:KEVQV:NMVVR:SXGXH, RVPSTXX:APVKT:RSVK-AA17-AKV:KEVQV:MIVEE:XGXL, ASAAPXX:VPQAL:RSVK-AA17-AKV:KEVQV:MIVRS:XKXS, ASASPXX:VSQDL:RSVK-AA17-AKV:KEVQV:MIVKS:XKXS, ASASPXX:VPQDL:RSVK-AA17-AKV:KEVQV:MVVKS:XKXS, NDEGLEX:VPTEE:RSVK-AA17-AKV:KEVQV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RSVK-AA17-AKV:KEVQV:LEEHS:QXEXR, RNVQXRP:TQVQL:RSVK-AA17-AKV:KEVQV:TLEDH:LAXKXE, SSVKXQP:TQVHH:RPVQ-AA17-RKI:KKATV:RLEDH:LEXAXA, KIPKAXX:VPTEL:RPVQ-AA17-RKI:KKATV:DMVVE:GXGXR, GIPEPXX:VPEKM:RPVQ-AA17-RKI:KKATV:NMTVE:SXAXR, SIPKAXX:VPTEL:RPVQ-AA17-RKI:KKATV:EMVVE:GXGXR, HVTKPTX:APTKL:RPVQ-AA17-RKI:KKATV:NMVVR:SXGXH, YVPKPXX:APTKL:RPVQ-AA17-RKI:KKATV:NMVVR:SXGXH, TVPKPXX:APTQL:RPVQ-AA17-RKI:KKATV:NMVVR:AXGXH, AVPKAXX:APTKL:RPVQ-AA17-RKI:KKATV:NMVVK:AXGXH, KVGKAXX:VPTKL:RPVQ-AA17-RKI:KKATV:EGMSVAE:XGXR, KASKAXX:VPTKL:RPVQ-AA17-RKI:KKATV:GMAVS:EXGXR, GSAGPXX:TPTKM:RPVQ-AA17-RKI:KKATV:GMVVD:RXGXS, AAPASXX:VPARL:RPVQ-AA17-RKI:KKATV:DMVVE:AXGXR, STPPTXX:VPTRL:RPVQ-AA17-RKI:KKATV:DMVVE:SXGXR, HVPKPXX:APTKL:RPVQ-AA17-RKI:KKATV:NMVVR:SXGXH,

RVPSTXX:APVKT:RPVQ-AA17-RKI:KKATV:MIVEE:XGXL, ASAAPXX:VPQAL:RPVQ-AA17-RKI:KKATV:MIVRS:XKXS, ASASPXX:VSQDL:RPVQ-AA17-RKI:KKATV:MIVKS:XKXS, ASASPXX:VPQDL:RPVQ-AA17-RKI:KKATV:MVVKS:XKXS, NDEGLEX:VPTEE:RPVQ-AA17-RKI:KKATV:FLQHN:KXEXR, NDEGLEX:VPTGQ:RPVQ-AA17-RKI:KKATV:LEEHS:QXEXR and SSVKXQP:SRVHH:RPVQ-AA17-RKI:KKATV:RLEEH:LEXAXA; and wherein AA^{17} is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the heptuplet PEP7:PEP3:PEP1:LINKER:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS:DENKNVV:LKNYQ:VVE:SXAXR,
SIPKAXX:VPT:SAIS:DEYDKVV:LKNYQ:VVE:GXGXR,
HVTKPTX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,
YVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,
TVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:AXGXH,
AVPKAXX:VPT:SAIS:DSSNNVI:LKNYQ:VVE:AXGXH,
KVGKAXX:VPT:SAIS:DDMGVPT:LKNYQ:VVE:XGXR,
KASKAXX:VPT:SAIS:DKGVVTY:LKNYQ:VVE:EXGXR,
GSAGPXX:VPT:SAIS:NDKQQII:LKNYQ:VVE:RXGXS,
AAPASXX:VPT:SAIS:DAANNVV:LKNYQ:VVE:AXGXR,
STPPTXX:VPT:SAIS:DSANNVV:LKNYQ:VVE:SXGXR,
HVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,
RVPSTXX:VPT:SAIS:DNGRVLL:LKNYQ:VVE:XGXL,
ASAAPXX:VPT:SAIS:VGRKPKV:LKNYQ:VVE:XKXS,
ASASPXX:VPT:SAIS:IGKTPKI:LKNYQ:VVE:XKXS,
ASASPXX:VPT:SAIS:VGRTPKV:LKNYQ:VVE:XKXS,
NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:VVE:KXEXR,
NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:VVE:QXEXR,
SSVKXQP:VPT:SAIS:EYVRKKPKL:LKNYQ:VVE:LEXAXA,
RNVQXRP:VPT:SAIS:EIVRKKPIF:LKNYQ:VVE:LAXKXE,
GIPEPXX:VPE:SAIS:DENKNVV:LKNYQ:TVE:SXAXR,
HVTKPTX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,
YVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,
TVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:AXGXH,
AVPKAXX:APT:SAIS:DSSNNVI:LKNYQ:VVK:AXGXH,
KVGKAXX:VPT:SAIS:DDMGVPT:LKNYQ:VAE:XGXR,
KASKAXX:VPT:SAIS:DKGVVTY:LKNYQ:AVS:EXGXR,
GSAGPXX:TPT:SAIS:NDKQQII:LKNYQ:VVD:RXGXS,
AAPASXX:VPA:SAIS:DAANNVV:LKNYQ:VVE:AXGXR,
HVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,
RVPSTXX:APV:SAIS:DNGRVLL:LKNYQ:VEE:XGXL,
ASAAPXX:VPQ:SAIS:VGRKPKV:LKNYQ:VRS:XKXS,
ASASPXX:VSQ:SAIS:IGKTPKI:LKNYQ:VKS:XKXS,

ASASPXX:VPQ:SAIS:VGRTPKV:LKNYQ:VKS:XKXS,

NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:QHN:KXEXR,

NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:EHS:QXEXR,

SSVKXQP:SRV:SAIS:EYVRKKPKL:LKNYQ:EEH:LEXAXA,

RNVQXRP:TQV:SAIS:EIVRKKPIF:LKNYQ:EDH:LAXKXE,

KIPKAXX:VPE:SSLS:DENEKVV:LKVYP:TVE:GXGXR,

SIPKAXX:VPE:SSLS:DEYDKVV:LKVYP:TVE:GXGXR,

HVTKPTX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,

YVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,

TVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:AXGXH,

AVPKAXX:VPE:SSLS:DSSNNVI:LKVYP:TVE:AXGXH,

KVGKAXX:VPE:SSLS:DDMGVPT:LKVYP:TVE:XGXR,

KASKAXX:VPE:SSLS:DKGVVTY:LKVYP:TVE:EXGXR,

GSAGPXX:VPE:SSLS:NDKQQII:LKVYP:TVE:RXGXS,

AAPASXX:VPE:SSLS:DAANNVV:LKVYP:TVE:AXGXR,

STPPTXX:VPE:SSLS:DSANNVV:LKVYP:TVE:SXGXR,

HVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,

RVPSTXX:VPE:SSLS:DNGRVLL:LKVYP:TVE:XGXL,

ASAAPXX:VPE:SSLS:VGRKPKV:LKVYP:TVE:XKXS,

ASASPXX:VPE:SSLS:IGKTPKI:LKVYP:TVE:XKXS,

ASASPXX:VPE:SSLS:VGRTPKV:LKVYP:TVE:XKXS,

NDEGLEX:VPE:SSLS:RIKPHQGQH:LKVYP:TVE:KXEXR,

NDEGLEX:VPE:SSLS:RIKPHQGQH:LKVYP:TVE:QXEXR,

SSVKXQP:VPE:SSLS:EYVRKKPKL:LKVYP:TVE:LEXAXA,

RNVQXRP:VPE:SSLS:EIVRKKPIF:LKVYP:TVE:LAXKXE,

KIPKAXX:VPT:SSLS:DENEKVV:LKVYP:VVE:GXGXR,

SIPKAXX:VPT:SSLS:DEYDKVV:LKVYP:VVE:GXGXR,

HVTKPTX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,

YVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,

TVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:AXGXH,

AVPKAXX:APT:SSLS:DSSNNVI:LKVYP:VVK:AXGXH,

KVGKAXX:VPT:SSLS:DDMGVPT:LKVYP:VAE:XGXR,

KASKAXX:VPT:SSLS:DKGVVTY:LKVYP:AVS:EXGXR,

GSAGPXX:TPT:SSLS:NDKQQII:LKVYP:VVD:RXGXS,

AAPASXX:VPA:SSLS:DAANNVV:LKVYP:VVE:AXGXR,

STPPTXX:VPT:SSLS:DSANNVV:LKVYP:VVE:SXGXR,

HVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,

RVPSTXX:APV:SSLS:DNGRVLL:LKVYP:VEE:XGXL,

ASAAPXX:VPQ:SSLS:VGRKPKV:LKVYP:VRS:XKXS,

ASASPXX:VSQ:SSLS:IGKTPKI:LKVYP:VKS:XKXS,

ASASPXX:VPQ:SSLS:VGRTPKV:LKVYP:VKS:XKXS,

NDEGLEX:VPT:SSLS:RIKPHQGQH:LKVYP:QHN:KXEXR,

NDEGLEX:VPT:SSLS:RIKPHQGQH:LKVYP:EHS:QXEXR,

SSVKXQP:SRV:SSLS:EYVRKKPKL:LKVYP:EEH:LEXAXA,

RNVQXRP:TQV:SSLS:EIVRKKPIF:LKVYP:EDH:LAXKXE,

KIPKAXX:VPT:SAIS:DENEKVV:LKNYQ:VVE:GXGXR,

KIPKAXX:APT:NAIS:DENEKVV:LKKYR:VVR:GXGXR,

GIPEPXX:APT:NAIS:DENKNVV:LKKYR:VVR:SXAXR,

SIPKAXX:APT:NAIS:DEYDKVV:LKKYR:VVR:GXGXR,

YVPKPXX:APT:NAIS:DDSSNVI:LKKYR:VVR:SXGXH,

TVPKPXX:APT:NAIS:DDSSNVI:LKKYR:VVR:AXGXH,

AVPKAXX:APT:NAIS:DSSNNVI:LKKYR:VVR:AXGXH,

KVGKAXX:APT:NAIS:DDMGVPT:LKKYR:VVR:XGXR,

KASKAXX:APT:NAIS:DKGVVTY:LKKYR:VVR:EXGXR,

GSAGPXX:APT:NAIS:NDKQQII:LKKYR:VVR:RXGXS,

AAPASXX:APT:NAIS:DAANNVV:LKKYR:VVR:AXGXR,

STPPTXX:APT:NAIS:DSANNVV:LKKYR:VVR:SXGXR,

HVPKPXX:APT:NAIS:DDSSNVI:LKKYR:VVR:SXGXH,

RVPSTXX:APT:NAIS:DNGRVLL:LKKYR:VVR:XGXL,

ASAAPXX:APT:NAIS:VGRKPKV:LKKYR:VVR:XKXS,

ASASPXX:APT:NAIS:IGKTPKI:LKKYR:VVR:XKXS,

ASASPXX:APT:NAIS:VGRTPKV:LKKYR:VVR:XKXS,

NDEGLEX:APT:NAIS:RIKPHQGQH:LKKYR:VVR:KXEXR,

NDEGLEX:APT:NAIS:RIKPHQGQH:LKKYR:VVR:QXEXR,

SSVKXQP:APT:NAIS:EYVRKKPKL:LKKYR:VVR:LEXAXA,

RNVQXRP:APT:NAIS:EIVRKKPIF:LKKYR:VVR:LAXKXE,

KIPKAXX:VPT:NAIS:DENEKVV:LKKYR:VVE:GXGXR,

GIPEPXX:VPE:NAIS:DENKNVV:LKKYR:TVE:SXAXR,

SIPKAXX:VPT:NAIS:DEYDKVV:LKKYR:VVE:GXGXR,

AVPKAXX:APT:NAIS:DSSNNVI:LKKYR:VVK:AXGXH,

KVGKAXX:VPT:NAIS:DDMGVPT:LKKYR:VAE:XGXR,

KASKAXX:VPT:NAIS:DKGVVTY:LKKYR:AVS:EXGXR,

GSAGPXX:TPT:NAIS:NDKQQII:LKKYR:VVD:RXGXS,

AAPASXX:VPA:NAIS:DAANNVV:LKKYR:VVE:AXGXR,

STPPTXX:VPT:NAIS:DSANNVV:LKKYR:VVE:SXGXR,

RVPSTXX:APV:NAIS:DNGRVLL:LKKYR:VEE:XGXL,

ASAAPXX:VPQ:NAIS:VGRKPKV:LKKYR:VRS:XKXS,

ASASPXX:VSQ:NAIS:IGKTPKI:LKKYR:VKS:XKXS,

ASASPXX:VPQ:NAIS:VGRTPKV:LKKYR:VKS:XKXS,

NDEGLEX:VPT:NAIS:RIKPHQGQH:LKKYR:QHN:KXEXR,

NDEGLEX:VPT:NAIS:RIKPHQGQH:LKKYR:EHS:QXEXR,

SSVKXQP:SRV:NAIS:EYVRKKPKL:LKKYR:EEH:LEXAXA,

RNVQXRP:TQV:NAIS:EIVRKKPIF:LKKYR:EDH:LAXKXE,

HVTKPTX:APT:NAIS:DDSSNVI:LKKYR:VVR:SXGXH,

KIPKAXX:APT:SATS:DENEKVV:LRKHR:VVK:GXGXR,

GIPEPXX:APT:SATS:DENKNVV:LRKHR:VVK:SXAXR,

SIPKAXX:APT:SATS:DEYDKVV:LRKHR:VVK:GXGXR,

HVTKPTX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

YVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

TVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:AXGXH,

KVGKAXX:APT:SATS:DDMGVPT:LRKHR:VVK:XGXR,

KASKAXX:APT:SATS:DKGVVTY:LRKHR:VVK:EXGXR,

GSAGPXX:APT:SATS:NDKQQII:LRKHR:VVK:RXGXS,

AAPASXX:APT:SATS:DAANNVV:LRKHR:VVK:AXGXR,

STPPTXX:APT:SATS:DSANNVV:LRKHR:VVK:SXGXR,

HVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

RVPSTXX:APT:SATS:DNGRVLL:LRKHR:VVK:XGXL,

ASAAPXX:APT:SATS:VGRKPKV:LRKHR:VVK:XKXS,

ASASPXX:APT:SATS:IGKTPKI:LRKHR:VVK:XKXS,

ASASPXX:APT:SATS:VGRTPKV:LRKHR:VVK:XKXS,

NDEGLEX:APT:SATS:RIKPHQGQH:LRKHR:VVK:KXEXR,

NDEGLEX:APT:SATS:RIKPHQGQH:LRKHR:VVK:QXEXR,

SSVKXQP:APT:SATS:EYVRKKPKL:LRKHR:VVK:LEXAXA,

RNVQXRP:APT:SATS:EIVRKKPIF:LRKHR:VVK:LAXKXE,

KIPKAXX:VPT:SATS:DENEKVV:LRKHR:VVE:GXGXR,

GIPEPXX:VPE:SATS:DENKNVV:LRKHR:TVE:SXAXR,

SIPKAXX:VPT:SATS:DEYDKVV:LRKHR:VVE:GXGXR,

HVTKPTX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,

YVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,

TVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:AXGXH,

KVGKAXX:VPT:SATS:DDMGVPT:LRKHR:VAE:XGXR,

KASKAXX:VPT:SATS:DKGVVTY:LRKHR:AVS:EXGXR,

GSAGPXX:TPT:SATS:NDKQQII:LRKHR:VVD:RXGXS,

AAPASXX:VPA:SATS:DAANNVV:LRKHR:VVE:AXGXR,

STPPTXX:VPT:SATS:DSANNVV:LRKHR:VVE:SXGXR,

HVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,

RVPSTXX:APV:SATS:DNGRVLL:LRKHR:VEE:XGXL,

ASAAPXX:VPQ:SATS:VGRKPKV:LRKHR:VRS:XKXS,

ASASPXX:VSQ:SATS:IGKTPKI:LRKHR:VKS:XKXS,

ASASPXX:VPQ:SATS:VGRTPKV:LRKHR:VKS:XKXS,

NDEGLEX:VPT:SATS:RIKPHQGQH:LRKHR:QHN:KXEXR,

NDEGLEX:VPT:SATS:RIKPHQGQH:LRKHR:EHS:QXEXR,

SSVKXQP:SRV:SATS:EYVRKKPKL:LRKHR:EEH:LEXAXA,

RNVQXRP:TQV:SATS:EIVRKKPIF:LRKHR:EDH:LAXKXE,

KIPKAXX:VPT:SPIS:DENEKVV:LKYHY:VAE:GXGXR,

GIPEPXX:VPT:SPIS:DENKNVV:LKYHY:VAE:SXAXR,

SIPKAXX:VPT:SPIS:DEYDKVV:LKYHY:VAE:GXGXR,
HVTKPTX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
YVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
TVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:AXGXH,
AVPKAXX:VPT:SPIS:DSSNNVI:LKYHY:VAE:AXGXH,
KASKAXX:VPT:SPIS:DKGVVTY:LKYHY:VAE:EXGXR,
GSAGPXX:VPT:SPIS:NDKQQII:LKYHY:VAE:RXGXS,
AAPASXX:VPT:SPIS:DAANNVV:LKYHY:VAE:AXGXR,
STPPTXX:VPT:SPIS:DSANNVV:LKYHY:VAE:SXGXR,
HVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
RVPSTXX:VPT:SPIS:DNGRVLL:LKYHY:VAE:XGXL,
ASAAPXX:VPT:SPIS:VGRKPKV:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS:IGKTPKI:LKYHY:VAE:XKXS,
ASASPXX:VPT:SPIS:VGRTPKV:LKYHY:VAE:XKXS,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:VAE:KXEXR,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:VAE:QXEXR,
SSVKXQP:VPT:SPIS:EYVRKKPKL:LKYHY:VAE:LEXAXA,
RNVQXRP:VPT:SPIS:EIVRKKPIF:LKYHY:VAE:LAXKXE,
KIPKAXX:VPT:SPIS:DENEKVV:LKYHY:VVE:GXGXR,
GIPEPXX:VPE:SPIS:DENKNVV:LKYHY:TVE:SXAXR,
SIPKAXX:VPT:SPIS:DEYDKVV:LKYHY:VVE:GXGXR,
HVTKPTX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
YVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
TVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:AXGXH,
AVPKAXX:APT:SPIS:DSSNNVI:LKYHY:VVK:AXGXH,
KASKAXX:VPT:SPIS:DKGVVTY:LKYHY:AVS:EXGXR,
GSAGPXX:TPT:SPIS:NDKQQII:LKYHY:VVD:RXGXS,
AAPASXX:VPA:SPIS:DAANNVV:LKYHY:VVE:AXGXR,
STPPTXX:VPT:SPIS:DSANNVV:LKYHY:VVE:SXGXR,
HVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
RVPSTXX:APV:SPIS:DNGRVLL:LKYHY:VEE:XGXL,
ASAAPXX:VPQ:SPIS:VGRKPKV:LKYHY:VRS:XKXS,
ASASPXX:VSQ:SPIS:IGKTPKI:LKYHY:VKS:XKXS,
ASASPXX:VPQ:SPIS:VGRTPKV:LKYHY:VKS:XKXS,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:QHN:KXEXR,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:EHS:QXEXR,
SSVKXQP:SRV:SPIS:EYVRKKPKL:LKYHY:EEH:LEXAXA,
RNVQXRP:TQV:SPIS:EIVRKKPIF:LKYHY:EDH:LAXKXE,
KIPKAXX:VPT:EPIS:DENEKVV:KFKYE:AVS:GXGXR,
GIPEPXX:VPT:EPIS:DENKNVV:KFKYE:AVS:SXAXR,
SIPKAXX:VPT:EPIS:DEYDKVV:KFKYE:AVS:GXGXR,
HVTKPTX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,
YVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,

TVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:AXGXH,

AVPKAXX:VPT:EPIS:DSSNNVI:KFKYE:AVS:AXGXH,

KVGKAXX:VPT:EPIS:DDMGVPT:KFKYE:AVS:XGXR,

GSAGPXX:VPT:EPIS:NDKQQII:KFKYE:AVS:RXGXS,

AAPASXX:VPT:EPIS:DAANNVV:KFKYE:AVS:AXGXR,

STPPTXX:VPT:EPIS:DSANNVV:KFKYE:AVS:SXGXR,

HVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,

RVPSTXX:VPT:EPIS:DNGRVLL:KFKYE:AVS:XGXL,

ASAAPXX:VPT:EPIS:VGRKPKV:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS:IGKTPKI:KFKYE:AVS:XKXS,

ASASPXX:VPT:EPIS:VGRTPKV:KFKYE:AVS:XKXS,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:AVS:KXEXR,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:AVS:QXEXR,

SSVKXQP:VPT:EPIS:EYVRKKPKL:KFKYE:AVS:LEXAXA,

RNVQXRP:VPT:EPIS:EIVRKKPIF:KFKYE:AVS:LAXKXE,

KIPKAXX:VPT:EPIS:DENEKVV:KFKYE:VVE:GXGXR,

GIPEPXX:VPE:EPIS:DENKNVV:KFKYE:TVE:SXAXR,

SIPKAXX:VPT:EPIS:DEYDKVV:KFKYE:VVE:GXGXR,

HVTKPTX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,

YVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,

TVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:AXGXH,

AVPKAXX:APT:EPIS:DSSNNVI:KFKYE:VVK:AXGXH,

KVGKAXX:VPT:EPIS:DDMGVPT:KFKYE:VAE:XGXR,

GSAGPXX:TPT:EPIS:NDKQQII:KFKYE:VVD:RXGXS,

AAPASXX:VPA:EPIS:DAANNVV:KFKYE:VVE:AXGXR,

STPPTXX:VPT:EPIS:DSANNVV:KFKYE:VVE:SXGXR,

HVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,

RVPSTXX:APV:EPIS:DNGRVLL:KFKYE:VEE:XGXL,

ASAAPXX:VPQ:EPIS:VGRKPKV:KFKYE:VRS:XKXS,

ASASPXX:VSQ:EPIS:IGKTPKI:KFKYE:VKS:XKXS,

ASASPXX:VPQ:EPIS:VGRTPKV:KFKYE:VKS:XKXS,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:QHN:KXEXR,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:EHS:QXEXR,

SSVKXQP:SRV:EPIS:EYVRKKPKL:KFKYE:EEH:LEXAXA,

RNVQXRP:TQV:EPIS:EIVRKKPIF:KFKYE:EDH:LAXKXE,

KIPKAXX:TPT:SPIN:DENEKVV:YGKIP:VVD:GXGXR,

GIPEPXX:TPT:SPIN:DENKNVV:YGKIP:VVD:SXAXR,

SIPKAXX:TPT:SPIN:DEYDKVV:YGKIP:VVD:GXGXR,

HVTKPTX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

YVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

TVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:AXGXH,

AVPKAXX:TPT:SPIN:DSSNNVI:YGKIP:VVD:AXGXH,

KVGKAXX:TPT:SPIN:DDMGVPT:YGKIP:VVD:XGXR,

KASKAXX:TPT:SPIN:DKGVVTY:YGKIP:VVD:EXGXR,

AAPASXX:TPT:SPIN:DAANNVV:YGKIP:VVD:AXGXR,

STPPTXX:TPT:SPIN:DSANNVV:YGKIP:VVD:SXGXR,

HVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

RVPSTXX:TPT:SPIN:DNGRVLL:YGKIP:VVD:XGXL,

ASAAPXX:TPT:SPIN:VGRKPKV:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN:IGKTPKI:YGKIP:VVD:XKXS,

ASASPXX:TPT:SPIN:VGRTPKV:YGKIP:VVD:XKXS,

NDEGLEX:TPT:SPIN:RIKPHQGQH:YGKIP:VVD:KXEXR,

NDEGLEX:TPT:SPIN:RIKPHQGQH:YGKIP:VVD:QXEXR,

SSVKXQP:TPT:SPIN:EYVRKKPKL:YGKIP:VVD:LEXAXA,

RNVQXRP:TPT:SPIN:EIVRKKPIF:YGKIP:VVD:LAXKXE,

KIPKAXX:VPT:SPIN:DENEKVV:YGKIP:VVE:GXGXR,

GIPEPXX:VPE:SPIN:DENKNVV:YGKIP:TVE:SXAXR,

SIPKAXX:VPT:SPIN:DEYDKVV:YGKIP:VVE:GXGXR,

HVTKPTX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

YVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

TVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:AXGXH,

AVPKAXX:APT:SPIN:DSSNNVI:YGKIP:VVK:AXGXH,

KVGKAXX:VPT:SPIN:DDMGVPT:YGKIP:VAE:XGXR,

KASKAXX:VPT:SPIN:DKGVVTY:YGKIP:AVS:EXGXR,

AAPASXX:VPA:SPIN:DAANNVV:YGKIP:VVE:AXGXR,

STPPTXX:VPT:SPIN:DSANNVV:YGKIP:VVE:SXGXR,

HVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

RVPSTXX:APV:SPIN:DNGRVLL:YGKIP:VEE:XGXL,

ASAAPXX:VPQ:SPIN:VGRKPKV:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN:IGKTPKI:YGKIP:VKS:XKXS,

ASASPXX:VPQ:SPIN:VGRTPKV:YGKIP:VKS:XKXS,

NDEGLEX:VPT:SPIN:RIKPHQGQH:YGKIP:QHN:KXEXR,

NDEGLEX:VPT:SPIN:RIKPHQGQH:YGKIP:EHS:QXEXR,

SSVKXQP:SRV:SPIN:EYVRKKPKL:YGKIP:EEH:LEXAXA,

RNVQXRP:TQV:SPIN:EIVRKKPIF:YGKIP:EDH:LAXKXE,

KIPKAXX:VPA:SPIS:DENEKVV:YKQYE:VVE:GXGXR,

GIPEPXX:VPA:SPIS:DENKNVV:YKQYE:VVE:SXAXR,

SIPKAXX:VPA:SPIS:DEYDKVV:YKQYE:VVE:GXGXR,

HVTKPTX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

YVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

TVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:AXGXH,

AVPKAXX:VPA:SPIS:DSSNNVI:YKQYE:VVE:AXGXH,

KVGKAXX:VPA:SPIS:DDMGVPT:YKQYE:VVE:XGXR,

KASKAXX:VPA:SPIS:DKGVVTY:YKQYE:VVE:EXGXR,

GSAGPXX:VPA:SPIS:NDKQQII:YKQYE:VVE:RXGXS,

STPPTXX:VPA:SPIS:DSANNVV:YKQYE:VVE:SXGXR,

HVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

RVPSTXX:VPA:SPIS:DNGRVLL:YKQYE:VVE:XGXL,

ASAAPXX:VPA:SPIS:VGRKPKV:YKQYE:VVE:XKXS,

ASASPXX:VPA:SPIS:IGKTPKI:YKQYE:VVE:XKXS,

ASASPXX:VPA:SPIS:VGRTPKV:YKQYE:VVE:XKXS,

NDEGLEX:VPA:SPIS:RIKPHQGQH:YKQYE:VVE:KXEXR,

NDEGLEX:VPA:SPIS:RIKPHQGQH:YKQYE:VVE:QXEXR,

SSVKXQP:VPA:SPIS:EYVRKKPKL:YKQYE:VVE:LEXAXA,

RNVQXRP:VPA:SPIS:EIVRKKPIF:YKQYE:VVE:LAXKXE,

KIPKAXX:VPT:SPIS:DENEKVV:YKQYE:VVE:GXGXR,

GIPEPXX:VPE:SPIS:DENKNVV:YKQYE:TVE:SXAXR,

SIPKAXX:VPT:SPIS:DEYDKVV:YKQYE:VVE:GXGXR,

HVTKPTX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,

YVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,

TVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:AXGXH,

AVPKAXX:APT:SPIS:DSSNNVI:YKQYE:VVK:AXGXH,

KVGKAXX:VPT:SPIS:DDMGVPT:YKQYE:VAE:XGXR,

KASKAXX:VPT:SPIS:DKGVVTY:YKQYE:AVS:EXGXR,

GSAGPXX:TPT:SPIS:NDKQQII:YKQYE:VVD:RXGXS,

STPPTXX:VPT:SPIS:DSANNVV:YKQYE:VVE:SXGXR,

HVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,

RVPSTXX:APV:SPIS:DNGRVLL:YKQYE:VEE:XGXL,

ASAAPXX:VPQ:SPIS:VGRKPKV:YKQYE:VRS:XKXS,

ASASPXX:VSQ:SPIS:IGKTPKI:YKQYE:VKS:XKXS,

ASASPXX:VPQ:SPIS:VGRTPKV:YKQYE:VKS:XKXS,

NDEGLEX:VPT:SPIS:RIKPHQGQH:YKQYE:QHN:KXEXR,

NDEGLEX:VPT:SPIS:RIKPHQGQH:YKQYE:EHS:QXEXR,

SSVKXQP:SRV:SPIS:EYVRKKPKL:YKQYE:EEH:LEXAXA,

RNVQXRP:TQV:SPIS:EIVRKKPIF:YKQYE:EDH:LAXKXE,

GIPEPXX:VPT:SPIS:DENKNVV:YKQYE:VVE:SXAXR,

HVTKPTX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

YVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

TVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:AXGXH,

AVPKAXX:VPT:SPIS:DSSNNVI:YKQYE:VVE:AXGXH,

KVGKAXX:VPT:SPIS:DDMGVPT:YKQYE:VVE:XGXR,

KASKAXX:VPT:SPIS:DKGVVTY:YKQYE:VVE:EXGXR,

GSAGPXX:VPT:SPIS:NDKQQII:YKQYE:VVE:RXGXS,

AAPASXX:VPT:SPIS:DAANNVV:YKQYE:VVE:AXGXR,

HVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,

RVPSTXX:VPT:SPIS:DNGRVLL:YKQYE:VVE:XGXL,

ASAAPXX:VPT:SPIS:VGRKPKV:YKQYE:VVE:XKXS,

ASASPXX:VPT:SPIS:IGKTPKI:YKQYE:VVE:XKXS,

ASASPXX:VPT:SPIS:VGRTPKV:YKQYE:VVE:XKXS,

NDEGLEX:VPT:SPIS:RIKPHQGQH:YKQYE:VVE:KXEXR,
NDEGLEX:VPT:SPIS:RIKPHQGQH:YKQYE:VVE:QXEXR,
SSVKXQP:VPT:SPIS:EYVRKKPKL:YKQYE:VVE:LEXAXA,
RNVQXRP:VPT:SPIS:EIVRKKPIF:YKQYE:VVE:LAXKXE,
AAPASXX:VPA:SPIS:DAANNVV:YKQYE:VVE:AXGXR,
KIPKAXX:APV:KPLS:DENEKVV:DHHKD:VEE:GXGXR,
GIPEPXX:APV:KPLS:DENKNVV:DHHKD:VEE:SXAXR,
SIPKAXX:APV:KPLS:DEYDKVV:DHHKD:VEE:GXGXR,
HVTKPTX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
YVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
TVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:AXGXH,
AVPKAXX:APV:KPLS:DSSNNVI:DHHKD:VEE:AXGXH,
KVGKAXX:APV:KPLS:DDMGVPT:DHHKD:VEE:XGXR,
KASKAXX:APV:KPLS:DKGVVTY:DHHKD:VEE:EXGXR,
GSAGPXX:APV:KPLS:NDKQQII:DHHKD:VEE:RXGXS,
AAPASXX:APV:KPLS:DAANNVV:DHHKD:VEE:AXGXR,
STPPTXX:APV:KPLS:DSANNVV:DHHKD:VEE:SXGXR,
HVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
ASAAPXX:APV:KPLS:VGRKPKV:DHHKD:VEE:XKXS,
ASASPXX:APV:KPLS:IGKTPKI:DHHKD:VEE:XKXS,
ASASPXX:APV:KPLS:VGRTPKV:DHHKD:VEE:XKXS,
NDEGLEX:APV:KPLS:RIKPHQGQH:DHHKD:VEE:KXEXR,
NDEGLEX:APV:KPLS:RIKPHQGQH:DHHKD:VEE:QXEXR,
SSVKXQP:APV:KPLS:EYVRKKPKL:DHHKD:VEE:LEXAXA,
RNVQXRP:APV:KPLS:EIVRKKPIF:DHHKD:VEE:LAXKXE,
KIPKAXX:VPT:KPLS:DENEKVV:DHHKD:VVE:GXGXR,
GIPEPXX:VPE:KPLS:DENKNVV:DHHKD:TVE:SXAXR,
SIPKAXX:VPT:KPLS:DEYDKVV:DHHKD:VVE:GXGXR,
HVTKPTX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
YVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
TVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:AXGXH,
AVPKAXX:APT:KPLS:DSSNNVI:DHHKD:VVK:AXGXH,
KVGKAXX:VPT:KPLS:DDMGVPT:DHHKD:VAE:XGXR,
KASKAXX:VPT:KPLS:DKGVVTY:DHHKD:AVS:EXGXR,
GSAGPXX:TPT:KPLS:NDKQQII:DHHKD:VVD:RXGXS,
AAPASXX:VPA:KPLS:DAANNVV:DHHKD:VVE:AXGXR,
STPPTXX:VPT:KPLS:DSANNVV:DHHKD:VVE:SXGXR,
HVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
ASAAPXX:VPQ:KPLS:VGRKPKV:DHHKD:VRS:XKXS,
ASASPXX:VSQ:KPLS:IGKTPKI:DHHKD:VKS:XKXS,
ASASPXX:VPQ:KPLS:VGRTPKV:DHHKD:VKS:XKXS,
NDEGLEX:VPT:KPLS:RIKPHQGQH:DHHKD:QHN:KXEXR,

NDEGLEX:VPT:KPLS:RIKPHQGQH:DHHKD:EHS:QXEXR,

SSVKXQP:SRV:KPLS:EYVRKKPKL:DHHKD:EEH:LEXAXA,

RNVQXRP:TQV:KPLS:EIVRKKPIF:DHHKD:EDH:LAXKXE,

KIPKAXX:VPQ:EPLP:DENEKVV:EQLSN:VRS:GXGXR,

GIPEPXX:VPQ:EPLP:DENKNVV:EQLSN:VRS:SXAXR,

SIPKAXX:VPQ:EPLP:DEYDKVV:EQLSN:VRS:GXGXR,

HVTKPTX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

YVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

TVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:AXGXH,

AVPKAXX:VPQ:EPLP:DSSNNVI:EQLSN:VRS:AXGXH,

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AAPASXX:VPQ:EPLP:DAANNVV:EQLSN:VRS:AXGXR,

STPPTXX:VPQ:EPLP:DSANNVV:EQLSN:VRS:SXGXR,

HVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

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ASASPXX:VPQ:EPLP:VGRTPKV:EQLSN:VRS:XKXS,

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NDEGLEX:VPQ:EPLP:RIKPHQGQH:EQLSN:VRS:QXEXR,

SSVKXQP:VPQ:EPLP:EYVRKKPKL:EQLSN:VRS:LEXAXA,

RNVQXRP:VPQ:EPLP:EIVRKKPIF:EQLSN:VRS:LAXKXE,

KIPKAXX:VPT:EPLP:DENEKVV:EQLSN:VVE:GXGXR,

GIPEPXX:VPE:EPLP:DENKNVV:EQLSN:TVE:SXAXR,

SIPKAXX:VPT:EPLP:DEYDKVV:EQLSN:VVE:GXGXR,

HVTKPTX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

YVPKPXX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

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AVPKAXX:APT:EPLP:DSSNNVI:EQLSN:VVK:AXGXH,

KVGKAXX:VPT:EPLP:DDMGVPT:EQLSN:VAE:XGXR,

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GSAGPXX:TPT:EPLP:NDKQQII:EQLSN:VVD:RXGXS,

AAPASXX:VPA:EPLP:DAANNVV:EQLSN:VVE:AXGXR,

STPPTXX:VPT:EPLP:DSANNVV:EQLSN:VVE:SXGXR,

HVPKPXX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

RVPSTXX:APV:EPLP:DNGRVLL:EQLSN:VEE:XGXL,

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SSVKXQP:SRV:EPLP:EYVRKKPKL:EQLSN:EEH:LEXAXA,

RNVQXRP:TQV:EPLP:EIVRKKPIF:EQLSN:EDH:LAXKXE,
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GIPEPXX:VSQ:EPLT:DENKNVV:EQLSN:VKS:SXAXR,
SIPKAXX:VSQ:EPLT:DEYDKVV:EQLSN:VKS:GXGXR,
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GSAGPXX:VSQ:EPLT:NDKQQII:EQLSN:VKS:RXGXS,
AAPASXX:VSQ:EPLT:DAANNVV:EQLSN:VKS:AXGXR,
STPPTXX:VSQ:EPLT:DSANNVV:EQLSN:VKS:SXGXR,
HVPKPXX:VSQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,
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ASAAPXX:VSQ:EPLT:VGRKPKV:EQLSN:VKS:XKXS,
ASASPXX:VSQ:EPLT:VGRTPKV:EQLSN:VKS:XKXS,
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AAPASXX:VPA:EPLT:DAANNVV:EQLSN:VVE:AXGXR,
STPPTXX:VPT:EPLT:DSANNVV:EQLSN:VVE:SXGXR,
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ASASPXX:VPQ:EPLT:VGRTPKV:EQLSN:VKS:XKXS,
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AAPASXX:VPQ:EPLT:DAANNVV:EQLSN:VKS:AXGXR,
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ASASPXX:VPQ:EPLT:IGKTPKI:EQLSN:VKS:XKXS,
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YVPKPXX:VPT:SNIT:DDSSNVI:IGEMS:QHN:SXGXH,
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AVPKAXX:VPT:SNIT:DSSNNVI:IGEMS:QHN:AXGXH,
KVGKAXX:VPT:SNIT:DDMGVPT:IGEMS:QHN:XGXR,
KASKAXX:VPT:SNIT:DKGVVTY:IGEMS:QHN:EXGXR,
GSAGPXX:VPT:SNIT:NDKQQII:IGEMS:QHN:RXGXS,
AAPASXX:VPT:SNIT:DAANNVV:IGEMS:QHN:AXGXR,
STPPTXX:VPT:SNIT:DSANNVV:IGEMS:QHN:SXGXR,
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RVPSTXX:VPT:SNIT:DNGRVLL:IGEMS:QHN:XGXL,
ASAAPXX:VPT:SNIT:VGRKPKV:IGEMS:QHN:XKXS,
ASASPXX:VPT:SNIT:IGKTPKI:IGEMS:QHN:XKXS,
ASASPXX:VPT:SNIT:VGRTPKV:IGEMS:QHN:XKXS,
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NDEGLEX:VPT:SNIT:RIKPHQGQH:IGEMS:QHN:KXEXR,
SSVKXQP:VPT:SNIT:EYVRKKPKL:IGEMS:QHN:LEXAXA,
RNVQXRP:VPT:SNIT:EIVRKKPIF:IGEMS:QHN:LAXKXE,
KIPKAXX:VPT:SNIT:DENEKVV:IGEMS:VVE:GXGXR,

GIPEPXX:VPE:SNIT:DENKNVV:IGEMS:TVE:SXAXR,
SIPKAXX:VPT:SNIT:DEYDKVV:IGEMS:VVE:GXGXR,
HVTKPTX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,
YVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:AXGXH,
AVPKAXX:APT:SNIT:DSSNNVI:IGEMS:VVK:AXGXH,
KVGKAXX:VPT:SNIT:DDMGVPT:IGEMS:VAE:XGXR,
KASKAXX:VPT:SNIT:DKGVVTY:IGEMS:AVS:EXGXR,
GSAGPXX:TPT:SNIT:NDKQQII:IGEMS:VVD:RXGXS,
AAPASXX:VPA:SNIT:DAANNVV:IGEMS:VVE:AXGXR,
STPPTXX:VPT:SNIT:DSANNVV:IGEMS:VVE:SXGXR,
HVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,
RVPSTXX:APV:SNIT:DNGRVLL:IGEMS:VEE:XGXL,
ASAAPXX:VPQ:SNIT:VGRKPKV:IGEMS:VRS:XKXS,
ASASPXX:VSQ:SNIT:IGKTPKI:IGEMS:VKS:XKXS,
ASASPXX:VPQ:SNIT:VGRTPKV:IGEMS:VKS:XKXS,
NDEGLEX:VPT:SNIT:RIKPHQGQH:IGEMS:EHS:QXEXR,
SSVKXQP:SRV:SNIT:EYVRKKPKL:IGEMS:EEH:LEXAXA,
RNVQXRP:TQV:SNIT:EIVRKKPIF:IGEMS:EDH:LAXKXE,
KIPKAXX:VPT:SNIT:DENEKVV:LGEMS:EHS:GXGXR,
GIPEPXX:VPT:SNIT:DENKNVV:LGEMS:EHS:SXAXR,
SIPKAXX:VPT:SNIT:DEYDKVV:LGEMS:EHS:GXGXR,
HVTKPTX:VPT:SNIT:DDSSNVI:LGEMS:EHS:SXGXH,
YVPKPXX:VPT:SNIT:DDSSNVI:LGEMS:EHS:SXGXH,
TVPKPXX:VPT:SNIT:DDSSNVI:LGEMS:EHS:AXGXH,
AVPKAXX:VPT:SNIT:DSSNNVI:LGEMS:EHS:AXGXH,
KVGKAXX:VPT:SNIT:DDMGVPT:LGEMS:EHS:XGXR,
KASKAXX:VPT:SNIT:DKGVVTY:LGEMS:EHS:EXGXR,
GSAGPXX:VPT:SNIT:NDKQQII:LGEMS:EHS:RXGXS,
AAPASXX:VPT:SNIT:DAANNVV:LGEMS:EHS:AXGXR,
STPPTXX:VPT:SNIT:DSANNVV:LGEMS:EHS:SXGXR,
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ASASPXX:VPT:SNIT:VGRTPKV:LGEMS:EHS:XKXS,
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SIPKAXX:VPT:SNIT:DEYDKVV:LGEMS:VVE:GXGXR,

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YVPKPXX:APT:SNIT:DDSSNVI:LGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:DDSSNVI:LGEMS:VVR:AXGXH,
AVPKAXX:APT:SNIT:DSSNNVI:LGEMS:VVK:AXGXH,
KVGKAXX:VPT:SNIT:DDMGVPT:LGEMS:VAE:XGXR,
KASKAXX:VPT:SNIT:DKGVVTY:LGEMS:AVS:EXGXR,
GSAGPXX:TPT:SNIT:NDKQQII:LGEMS:VVD:RXGXS,
AAPASXX:VPA:SNIT:DAANNVV:LGEMS:VVE:AXGXR,
STPPTXX:VPT:SNIT:DSANNVV:LGEMS:VVE:SXGXR,
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GIPEPXX:SRV:RSVK:DENKNVV:KEVQV:EEH:SXAXR,
SIPKAXX:SRV:RSVK:DEYDKVV:KEVQV:EEH:GXGXR,
HVTKPTX:SRV:RSVK:DDSSNVI:KEVQV:EEH:SXGXH,
YVPKPXX:SRV:RSVK:DDSSNVI:KEVQV:EEH:SXGXH,
TVPKPXX:SRV:RSVK:DDSSNVI:KEVQV:EEH:AXGXH,
AVPKAXX:SRV:RSVK:DSSNNVI:KEVQV:EEH:AXGXH,
KVGKAXX:SRV:RSVK:DDMGVPT:KEVQV:EEH:XGXR,
KASKAXX:SRV:RSVK:DKGVVTY:KEVQV:EEH:EXGXR,
GSAGPXX:SRV:RSVK:NDKQQII:KEVQV:EEH:RXGXS,
AAPASXX:SRV:RSVK:DAANNVV:KEVQV:EEH:AXGXR,
STPPTXX:SRV:RSVK:DSANNVV:KEVQV:EEH:SXGXR,
HVPKPXX:SRV:RSVK:DDSSNVI:KEVQV:EEH:SXGXH,
RVPSTXX:SRV:RSVK:DNGRVLL:KEVQV:EEH:XGXL,
ASAAPXX:SRV:RSVK:VGRKPKV:KEVQV:EEH:XKXS,
ASASPXX:SRV:RSVK:IGKTPKI:KEVQV:EEH:XKXS,
ASASPXX:SRV:RSVK:VGRTPKV:KEVQV:EEH:XKXS,
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KIPKAXX:VPT:RSVK:DENEKVV:KEVQV:VVE:GXGXR,
GIPEPXX:VPE:RSVK:DENKNVV:KEVQV:TVE:SXAXR,
SIPKAXX:VPT:RSVK:DEYDKVV:KEVQV:VVE:GXGXR,
HVTKPTX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,
YVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,

TVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:AXGXH,
AVPKAXX:APT:RSVK:DSSNNVI:KEVQV:VVK:AXGXH,
KVGKAXX:VPT:RSVK:DDMGVPT:KEVQV:VAE:XGXR,
KASKAXX:VPT:RSVK:DKGVVTY:KEVQV:AVS:EXGXR,
GSAGPXX:TPT:RSVK:NDKQQII:KEVQV:VVD:RXGXS,
AAPASXX:VPA:RSVK:DAANNVV:KEVQV:VVE:AXGXR,
STPPTXX:VPT:RSVK:DSANNVV:KEVQV:VVE:SXGXR,
HVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,
RVPSTXX:APV:RSVK:DNGRVLL:KEVQV:VEE:XGXL,
ASAAPXX:VPQ:RSVK:VGRKPKV:KEVQV:VRS:XKXS,
ASASPXX:VSQ:RSVK:IGKTPKI:KEVQV:VKS:XKXS,
ASASPXX:VPQ:RSVK:VGRTPKV:KEVQV:VKS:XKXS,
NDEGLEX:VPT:RSVK:RIKPHQGQH:KEVQV:QHN:KXEXR,
NDEGLEX:VPT:RSVK:RIKPHQGQH:KEVQV:EHS:QXEXR,
RNVQXRP:TQV:RSVK:EIVRKKPIF:KEVQV:EDH:LAXKXE,
KIPKAXX:TQV:RPVQ:DENEKVV:KKATV:EDH:GXGXR,
GIPEPXX:TQV:RPVQ:DENKNVV:KKATV:EDH:SXAXR,
SIPKAXX:TQV:RPVQ:DEYDKVV:KKATV:EDH:GXGXR,
HVTKPTX:TQV:RPVQ:DDSSNVI:KKATV:EDH:SXGXH,
YVPKPXX:TQV:RPVQ:DDSSNVI:KKATV:EDH:SXGXH,
TVPKPXX:TQV:RPVQ:DDSSNVI:KKATV:EDH:AXGXH,
AVPKAXX:TQV:RPVQ:DSSNNVI:KKATV:EDH:AXGXH,
KVGKAXX:TQV:RPVQ:DDMGVPT:KKATV:EDH:XGXR,
KASKAXX:TQV:RPVQ:DKGVVTY:KKATV:EDH:EXGXR,
GSAGPXX:TQV:RPVQ:NDKQQII:KKATV:EDH:RXGXS,
AAPASXX:TQV:RPVQ:DAANNVV:KKATV:EDH:AXGXR,
STPPTXX:TQV:RPVQ:DSANNVV:KKATV:EDH:SXGXR,
HVPKPXX:TQV:RPVQ:DDSSNVI:KKATV:EDH:SXGXH,
RVPSTXX:TQV:RPVQ:DNGRVLL:KKATV:EDH:XGXL,
ASAAPXX:TQV:RPVQ:VGRKPKV:KKATV:EDH:XKXS,
ASASPXX:TQV:RPVQ:IGKTPKI:KKATV:EDH:XKXS,
ASASPXX:TQV:RPVQ:VGRTPKV:KKATV:EDH:XKXS,
NDEGLEX:TQV:RPVQ:RIKPHQGQH:KKATV:EDH:KXEXR,
NDEGLEX:TQV:RPVQ:RIKPHQGQH:KKATV:EDH:QXEXR,
SSVKXQP:TQV:RPVQ:EYVRKKPKL:KKATV:EDH:LEXAXA,
KIPKAXX:VPT:RPVQ:DENEKVV:KKATV:VVE:GXGXR,
GIPEPXX:VPE:RPVQ:DENKNVV:KKATV:TVE:SXAXR,
SIPKAXX:VPT:RPVQ:DEYDKVV:KKATV:VVE:GXGXR,
HVTKPTX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,
YVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,
TVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:AXGXH,
AVPKAXX:APT:RPVQ:DSSNNVI:KKATV:VVK:AXGXH,

KVGKAXX:VPT:RPVQ:DDMGVPT:KKATV:VAE:XGXR,

KASKAXX:VPT:RPVQ:DKGVVTY:KKATV:AVS:EXGXR,

GSAGPXX:TPT:RPVQ:NDKQQII:KKATV:VVD:RXGXS,

AAPASXX:VPA:RPVQ:DAANNVV:KKATV:VVE:AXGXR,

STPPTXX:VPT:RPVQ:DSANNVV:KKATV:VVE:SXGXR,

HVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,

RVPSTXX:APV:RPVQ:DNGRVLL:KKATV:VEE:XGXL,

ASAAPXX:VPQ:RPVQ:VGRKPKV:KKATV:VRS:XKXS,

ASASPXX:VSQ:RPVQ:IGKTPKI:KKATV:VKS:XKXS,

ASASPXX:VPQ:RPVQ:VGRTPKV:KKATV:VKS:XKXS,

NDEGLEX:VPT:RPVQ:RIKPHQGQH:KKATV:QHN:KXEXR,

NDEGLEX:VPT:RPVQ:RIKPHQGQH:KKATV:EHS:QXEXR and

SSVKXQP:SRV:RPVQ:EYVRKKPKL:KKATV:EEH:LEXAXA. More particularly, in certain embodiments, the heptuplet PEP7:PEP3:PEP1:LINKER:PEP2:PEP4:PEP8 is selected from the group consisting of

GIPEPXX:VPT:SAIS:DENKNVV:LKNYQ:VVE:SXAXR,

HVTKPTX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,

YVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,

TVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:AXGXH,

AVPKAXX:VPT:SAIS:DSSNNVI:LKNYQ:VVE:AXGXH,

KVGKAXX:VPT:SAIS:DDMGVPT:LKNYQ:VVE:XGXR,

KASKAXX:VPT:SAIS:DKGVVTY:LKNYQ:VVE:EXGXR,

GSAGPXX:VPT:SAIS:NDKQQII:LKNYQ:VVE:RXGXS,

AAPASXX:VPT:SAIS:DAANNVV:LKNYQ:VVE:AXGXR,

STPPTXX:VPT:SAIS:DSANNVV:LKNYQ:VVE:SXGXR,

HVPKPXX:VPT:SAIS:DDSSNVI:LKNYQ:VVE:SXGXH,

RVPSTXX:VPT:SAIS:DNGRVLL:LKNYQ:VVE:XGXL,

ASAAPXX:VPT:SAIS:VGRKPKV:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS:IGKTPKI:LKNYQ:VVE:XKXS,

ASASPXX:VPT:SAIS:VGRTPKV:LKNYQ:VVE:XKXS,

GIPEPXX:VPE:SAIS:DENKNVV:LKNYQ:TVE:SXAXR,

HVTKPTX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,

YVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,

TVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:AXGXH,

AVPKAXX:APT:SAIS:DSSNNVI:LKNYQ:VVK:AXGXH,

KVGKAXX:VPT:SAIS:DDMGVPT:LKNYQ:VAE:XGXR,

KASKAXX:VPT:SAIS:DKGVVTY:LKNYQ:AVS:EXGXR,

GSAGPXX:TPT:SAIS:NDKQQII:LKNYQ:VVD:RXGXS,

AAPASXX:VPA:SAIS:DAANNVV:LKNYQ:VVE:AXGXR,

HVPKPXX:APT:SAIS:DDSSNVI:LKNYQ:VVR:SXGXH,

RVPSTXX:APV:SAIS:DNGRVLL:LKNYQ:VEE:XGXL,

ASAAPXX:VPQ:SAIS:VGRKPKV:LKNYQ:VRS:XKXS,

ASASPXX:VSQ:SAIS:IGKTPKI:LKNYQ:VKS:XKXS,

ASASPXX:VPQ:SAIS:VGRTPKV:LKNYQ:VKS:XKXS,

NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:QHN:KXEXR,
NDEGLEX:VPT:SAIS:RIKPHQGQH:LKNYQ:EHS:QXEXR,
SSVKXQP:SRV:SAIS:EYVRKKPKL:LKNYQ:EEH:LEXAXA,
RNVQXRP:TQV:SAIS:EIVRKKPIF:LKNYQ:EDH:LAXKXE,
KIPKAXX:VPE:SSLS:DENEKVV:LKVYP:TVE:GXGXR,
SIPKAXX:VPE:SSLS:DEYDKVV:LKVYP:TVE:GXGXR,
HVTKPTX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,
YVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,
TVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:AXGXH,
AVPKAXX:VPE:SSLS:DSSNNVI:LKVYP:TVE:AXGXH,
KVGKAXX:VPE:SSLS:DDMGVPT:LKVYP:TVE:XGXR,
KASKAXX:VPE:SSLS:DKGVVTY:LKVYP:TVE:EXGXR,
GSAGPXX:VPE:SSLS:NDKQQII:LKVYP:TVE:RXGXS,
AAPASXX:VPE:SSLS:DAANNVV:LKVYP:TVE:AXGXR,
STPPTXX:VPE:SSLS:DSANNVV:LKVYP:TVE:SXGXR,
HVPKPXX:VPE:SSLS:DDSSNVI:LKVYP:TVE:SXGXH,
RVPSTXX:VPE:SSLS:DNGRVLL:LKVYP:TVE:XGXL,
ASAAPXX:VPE:SSLS:VGRKPKV:LKVYP:TVE:XKXS,
ASASPXX:VPE:SSLS:IGKTPKI:LKVYP:TVE:XKXS,
ASASPXX:VPE:SSLS:VGRTPKV:LKVYP:TVE:XKXS,
KIPKAXX:VPT:SSLS:DENEKVV:LKVYP:VVE:GXGXR,
SIPKAXX:VPT:SSLS:DEYDKVV:LKVYP:VVE:GXGXR,
HVTKPTX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,
YVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,
TVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:AXGXH,
AVPKAXX:APT:SSLS:DSSNNVI:LKVYP:VVK:AXGXH,
KVGKAXX:VPT:SSLS:DDMGVPT:LKVYP:VAE:XGXR,
KASKAXX:VPT:SSLS:DKGVVTY:LKVYP:AVS:EXGXR,
GSAGPXX:TPT:SSLS:NDKQQII:LKVYP:VVD:RXGXS,
AAPASXX:VPA:SSLS:DAANNVV:LKVYP:VVE:AXGXR,
STPPTXX:VPT:SSLS:DSANNVV:LKVYP:VVE:SXGXR,
HVPKPXX:APT:SSLS:DDSSNVI:LKVYP:VVR:SXGXH,
RVPSTXX:APV:SSLS:DNGRVLL:LKVYP:VEE:XGXL,
ASAAPXX:VPQ:SSLS:VGRKPKV:LKVYP:VRS:XKXS,
ASASPXX:VSQ:SSLS:IGKTPKI:LKVYP:VKS:XKXS,
ASASPXX:VPQ:SSLS:VGRTPKV:LKVYP:VKS:XKXS,
NDEGLEX:VPT:SSLS:RIKPHQGQH:LKVYP:QHN:KXEXR,
NDEGLEX:VPT:SSLS:RIKPHQGQH:LKVYP:EHS:QXEXR,
SSVKXQP:SRV:SSLS:EYVRKKPKL:LKVYP:EEH:LEXAXA,
RNVQXRP:TQV:SSLS:EIVRKKPIF:LKVYP:EDH:LAXKXE,
KIPKAXX:APT:NAIS:DENEKVV:LKKYR:VVR:GXGXR,
GIPEPXX:APT:NAIS:DENKNVV:LKKYR:VVR:SXAXR,

SIPKAXX:APT:NAIS:DEYDKVV:LKKYR:VVR:GXGXR,

AVPKAXX:APT:NAIS:DSSNNVI:LKKYR:VVR:AXGXH,

KVGKAXX:APT:NAIS:DDMGVPT:LKKYR:VVR:XGXR,

KASKAXX:APT:NAIS:DKGVVTY:LKKYR:VVR:EXGXR,

GSAGPXX:APT:NAIS:NDKQQII:LKKYR:VVR:RXGXS,

AAPASXX:APT:NAIS:DAANNVV:LKKYR:VVR:AXGXR,

STPPTXX:APT:NAIS:DSANNVV:LKKYR:VVR:SXGXR,

RVPSTXX:APT:NAIS:DNGRVLL:LKKYR:VVR:XGXL,

ASAAPXX:APT:NAIS:VGRKPKV:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS:IGKTPKI:LKKYR:VVR:XKXS,

ASASPXX:APT:NAIS:VGRTPKV:LKKYR:VVR:XKXS,

KIPKAXX:VPT:NAIS:DENEKVV:LKKYR:VVE:GXGXR,

GIPEPXX:VPE:NAIS:DENKNVV:LKKYR:TVE:SXAXR,

SIPKAXX:VPT:NAIS:DEYDKVV:LKKYR:VVE:GXGXR,

AVPKAXX:APT:NAIS:DSSNNVI:LKKYR:VVK:AXGXH,

KVGKAXX:VPT:NAIS:DDMGVPT:LKKYR:VAE:XGXR,

KASKAXX:VPT:NAIS:DKGVVTY:LKKYR:AVS:EXGXR,

GSAGPXX:TPT:NAIS:NDKQQII:LKKYR:VVD:RXGXS,

AAPASXX:VPA:NAIS:DAANNVV:LKKYR:VVE:AXGXR,

STPPTXX:VPT:NAIS:DSANNVV:LKKYR:VVE:SXGXR,

RVPSTXX:APV:NAIS:DNGRVLL:LKKYR:VEE:XGXL,

ASAAPXX:VPQ:NAIS:VGRKPKV:LKKYR:VRS:XKXS,

ASASPXX:VSQ:NAIS:IGKTPKI:LKKYR:VKS:XKXS,

ASASPXX:VPQ:NAIS:VGRTPKV:LKKYR:VKS:XKXS,

NDEGLEX:VPT:NAIS:RIKPHQGQH:LKKYR:QHN:KXEXR,

NDEGLEX:VPT:NAIS:RIKPHQGQH:LKKYR:EHS:QXEXR,

SSVKXQP:SRV:NAIS:EYVRKKPKL:LKKYR:EEH:LEXAXA,

RNVQXRP:TQV:NAIS:EIVRKKPIF:LKKYR:EDH:LAXKXE,

KIPKAXX:APT:SATS:DENEKVV:LRKHR:VVK:GXGXR,

GIPEPXX:APT:SATS:DENKNVV:LRKHR:VVK:SXAXR,

SIPKAXX:APT:SATS:DEYDKVV:LRKHR:VVK:GXGXR,

HVTKPTX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

YVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

TVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:AXGXH,

KVGKAXX:APT:SATS:DDMGVPT:LRKHR:VVK:XGXR,

KASKAXX:APT:SATS:DKGVVTY:LRKHR:VVK:EXGXR,

GSAGPXX:APT:SATS:NDKQQII:LRKHR:VVK:RXGXS,

AAPASXX:APT:SATS:DAANNVV:LRKHR:VVK:AXGXR,

STPPTXX:APT:SATS:DSANNVV:LRKHR:VVK:SXGXR,

HVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVK:SXGXH,

RVPSTXX:APT:SATS:DNGRVLL:LRKHR:VVK:XGXL,

ASAAPXX:APT:SATS:VGRKPKV:LRKHR:VVK:XKXS,

ASASPXX:APT:SATS:IGKTPKI:LRKHR:VVK:XKXS,

ASASPXX:APT:SATS:VGRTPKV:LRKHR:VVK:XKXS,
KIPKAXX:VPT:SATS:DENEKVV:LRKHR:VVE:GXGXR,
GIPEPXX:VPE:SATS:DENKNVV:LRKHR:TVE:SXAXR,
SIPKAXX:VPT:SATS:DEYDKVV:LRKHR:VVE:GXGXR,
HVTKPTX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,
YVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,
TVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:AXGXH,
KVGKAXX:VPT:SATS:DDMGVPT:LRKHR:VAE:XGXR,
KASKAXX:VPT:SATS:DKGVVTY:LRKHR:AVS:EXGXR,
GSAGPXX:TPT:SATS:NDKQQII:LRKHR:VVD:RXGXS,
AAPASXX:VPA:SATS:DAANNVV:LRKHR:VVE:AXGXR,
STPPTXX:VPT:SATS:DSANNVV:LRKHR:VVE:SXGXR,
HVPKPXX:APT:SATS:DDSSNVI:LRKHR:VVR:SXGXH,
RVPSTXX:APV:SATS:DNGRVLL:LRKHR:VEE:XGXL,
ASAAPXX:VPQ:SATS:VGRKPKV:LRKHR:VRS:XKXS,
ASASPXX:VSQ:SATS:IGKTPKI:LRKHR:VKS:XKXS,
ASASPXX:VPQ:SATS:VGRTPKV:LRKHR:VKS:XKXS,
NDEGLEX:VPT:SATS:RIKPHQGQH:LRKHR:QHN:KXEXR,
NDEGLEX:VPT:SATS:RIKPHQGQH:LRKHR:EHS:QXEXR,
SSVKXQP:SRV:SATS:EYVRKKPKL:LRKHR:EEH:LEXAXA,
RNVQXRP:TQV:SATS:EIVRKKPIF:LRKHR:EDH:LAXKXE,
KIPKAXX:VPT:SPIS:DENEKVV:LKYHY:VAE:GXGXR,
GIPEPXX:VPT:SPIS:DENKNVV:LKYHY:VAE:SXAXR,
SIPKAXX:VPT:SPIS:DEYDKVV:LKYHY:VAE:GXGXR,
HVTKPTX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
YVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
TVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:AXGXH,
AVPKAXX:VPT:SPIS:DSSNNVI:LKYHY:VAE:AXGXH,
KASKAXX:VPT:SPIS:DKGVVTY:LKYHY:VAE:EXGXR,
GSAGPXX:VPT:SPIS:NDKQQII:LKYHY:VAE:RXGXS,
AAPASXX:VPT:SPIS:DAANNVV:LKYHY:VAE:AXGXR,
STPPTXX:VPT:SPIS:DSANNVV:LKYHY:VAE:SXGXR,
HVPKPXX:VPT:SPIS:DDSSNVI:LKYHY:VAE:SXGXH,
RVPSTXX:VPT:SPIS:DNGRVLL:LKYHY:VAE:XGXL,
ASAAPXX:VPT:SPIS:VGRKPKV:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS:IGKTPKI:LKYHY:VAE:XKXS,
ASASPXX:VPT:SPIS:VGRTPKV:LKYHY:VAE:XKXS,
KIPKAXX:VPT:SPIS:DENEKVV:LKYHY:VVE:GXGXR,
GIPEPXX:VPE:SPIS:DENKNVV:LKYHY:TVE:SXAXR,
SIPKAXX:VPT:SPIS:DEYDKVV:LKYHY:VVE:GXGXR,
HVTKPTX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
YVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
TVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:AXGXH,

AVPKAXX:APT:SPIS:DSSNNVI:LKYHY:VVK:AXGXH,
KASKAXX:VPT:SPIS:DKGVVTY:LKYHY:AVS:EXGXR,
GSAGPXX:TPT:SPIS:NDKQQII:LKYHY:VVD:RXGXS,
AAPASXX:VPA:SPIS:DAANNVV:LKYHY:VVE:AXGXR,
STPPTXX:VPT:SPIS:DSANNVV:LKYHY:VVE:SXGXR,
HVPKPXX:APT:SPIS:DDSSNVI:LKYHY:VVR:SXGXH,
RVPSTXX:APV:SPIS:DNGRVLL:LKYHY:VEE:XGXL,
ASAAPXX:VPQ:SPIS:VGRKPKV:LKYHY:VRS:XKXS,
ASASPXX:VSQ:SPIS:IGKTPKI:LKYHY:VKS:XKXS,
ASASPXX:VPQ:SPIS:VGRTPKV:LKYHY:VKS:XKXS,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:QHN:KXEXR,
NDEGLEX:VPT:SPIS:RIKPHQGQH:LKYHY:EHS:QXEXR,
SSVKXQP:SRV:SPIS:EYVRKKPKL:LKYHY:EEH:LEXAXA,
RNVQXRP:TQV:SPIS:EIVRKKPIF:LKYHY:EDH:LAXKXE,
KIPKAXX:VPT:EPIS:DENEKVV:KFKYE:AVS:GXGXR,
GIPEPXX:VPT:EPIS:DENKNVV:KFKYE:AVS:SXAXR,
SIPKAXX:VPT:EPIS:DEYDKVV:KFKYE:AVS:GXGXR,
HVTKPTX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,
YVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,
TVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:AXGXH,
AVPKAXX:VPT:EPIS:DSSNNVI:KFKYE:AVS:AXGXH,
KVGKAXX:VPT:EPIS:DDMGVPT:KFKYE:AVS:XGXR,
GSAGPXX:VPT:EPIS:NDKQQII:KFKYE:AVS:RXGXS,
AAPASXX:VPT:EPIS:DAANNVV:KFKYE:AVS:AXGXR,
STPPTXX:VPT:EPIS:DSANNVV:KFKYE:AVS:SXGXR,
HVPKPXX:VPT:EPIS:DDSSNVI:KFKYE:AVS:SXGXH,
RVPSTXX:VPT:EPIS:DNGRVLL:KFKYE:AVS:XGXL,
ASAAPXX:VPT:EPIS:VGRKPKV:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS:IGKTPKI:KFKYE:AVS:XKXS,
ASASPXX:VPT:EPIS:VGRTPKV:KFKYE:AVS:XKXS,
KIPKAXX:VPT:EPIS:DENEKVV:KFKYE:VVE:GXGXR,
GIPEPXX:VPE:EPIS:DENKNVV:KFKYE:TVE:SXAXR,
SIPKAXX:VPT:EPIS:DEYDKVV:KFKYE:VVE:GXGXR,
HVTKPTX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,
YVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,
TVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:AXGXH,
AVPKAXX:APT:EPIS:DSSNNVI:KFKYE:VVK:AXGXH,
KVGKAXX:VPT:EPIS:DDMGVPT:KFKYE:VAE:XGXR,
GSAGPXX:TPT:EPIS:NDKQQII:KFKYE:VVD:RXGXS,
AAPASXX:VPA:EPIS:DAANNVV:KFKYE:VVE:AXGXR,
STPPTXX:VPT:EPIS:DSANNVV:KFKYE:VVE:SXGXR,
HVPKPXX:APT:EPIS:DDSSNVI:KFKYE:VVR:SXGXH,
RVPSTXX:APV:EPIS:DNGRVLL:KFKYE:VEE:XGXL,

ASAAPXX:VPQ:EPIS:VGRKPKV:KFKYE:VRS:XKXS,

ASASPXX:VSQ:EPIS:IGKTPKI:KFKYE:VKS:XKXS,

ASASPXX:VPQ:EPIS:VGRTPKV:KFKYE:VKS:XKXS,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:QHN:KXEXR,

NDEGLEX:VPT:EPIS:RIKPHQGQH:KFKYE:EHS:QXEXR,

SSVKXQP:SRV:EPIS:EYVRKKPKL:KFKYE:EEH:LEXAXA,

RNVQXRP:TQV:EPIS:EIVRKKPIF:KFKYE:EDH:LAXKXE,

KIPKAXX:TPT:SPIN:DENEKVV:YGKIP:VVD:GXGXR,

GIPEPXX:TPT:SPIN:DENKNVV:YGKIP:VVD:SXAXR,

SIPKAXX:TPT:SPIN:DEYDKVV:YGKIP:VVD:GXGXR,

HVTKPTX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

YVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

TVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:AXGXH,

AVPKAXX:TPT:SPIN:DSSNNVI:YGKIP:VVD:AXGXH,

KVGKAXX:TPT:SPIN:DDMGVPT:YGKIP:VVD:XGXR,

KASKAXX:TPT:SPIN:DKGVVTY:YGKIP:VVD:EXGXR,

AAPASXX:TPT:SPIN:DAANNVV:YGKIP:VVD:AXGXR,

STPPTXX:TPT:SPIN:DSANNVV:YGKIP:VVD:SXGXR,

HVPKPXX:TPT:SPIN:DDSSNVI:YGKIP:VVD:SXGXH,

RVPSTXX:TPT:SPIN:DNGRVLL:YGKIP:VVD:XGXL,

ASAAPXX:TPT:SPIN:VGRKPKV:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN:IGKTPKI:YGKIP:VVD:XKXS,

ASASPXX:TPT:SPIN:VGRTPKV:YGKIP:VVD:XKXS,

KIPKAXX:VPT:SPIN:DENEKVV:YGKIP:VVE:GXGXR,

GIPEPXX:VPE:SPIN:DENKNVV:YGKIP:TVE:SXAXR,

SIPKAXX:VPT:SPIN:DEYDKVV:YGKIP:VVE:GXGXR,

HVTKPTX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

YVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

TVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:AXGXH,

AVPKAXX:APT:SPIN:DSSNNVI:YGKIP:VVK:AXGXH,

KVGKAXX:VPT:SPIN:DDMGVPT:YGKIP:VAE:XGXR,

KASKAXX:VPT:SPIN:DKGVVTY:YGKIP:AVS:EXGXR,

AAPASXX:VPA:SPIN:DAANNVV:YGKIP:VVE:AXGXR,

STPPTXX:VPT:SPIN:DSANNVV:YGKIP:VVE:SXGXR,

HVPKPXX:APT:SPIN:DDSSNVI:YGKIP:VVR:SXGXH,

RVPSTXX:APV:SPIN:DNGRVLL:YGKIP:VEE:XGXL,

ASAAPXX:VPQ:SPIN:VGRKPKV:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN:IGKTPKI:YGKIP:VKS:XKXS,

ASASPXX:VPQ:SPIN:VGRTPKV:YGKIP:VKS:XKXS,

NDEGLEX:VPT:SPIN:RIKPHQGQH:YGKIP:QHN:KXEXR,

NDEGLEX:VPT:SPIN:RIKPHQGQH:YGKIP:EHS:QXEXR,

SSVKXQP:SRV:SPIN:EYVRKKPKL:YGKIP:EEH:LEXAXA,

RNVQXRP:TQV:SPIN:EIVRKKPIF:YGKIP:EDH:LAXKXE,

KIPKAXX:VPA:SPIS:DENEKVV:YKQYE:VVE:GXGXR,

GIPEPXX:VPA:SPIS:DENKNVV:YKQYE:VVE:SXAXR,
SIPKAXX:VPA:SPIS:DEYDKVV:YKQYE:VVE:GXGXR,
HVTKPTX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
YVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
TVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:AXGXH,
AVPKAXX:VPA:SPIS:DSSNNVI:YKQYE:VVE:AXGXH,
KVGKAXX:VPA:SPIS:DDMGVPT:YKQYE:VVE:XGXR,
KASKAXX:VPA:SPIS:DKGVVTY:YKQYE:VVE:EXGXR,
GSAGPXX:VPA:SPIS:NDKQQII:YKQYE:VVE:RXGXS,
STPPTXX:VPA:SPIS:DSANNVV:YKQYE:VVE:SXGXR,
HVPKPXX:VPA:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
RVPSTXX:VPA:SPIS:DNGRVLL:YKQYE:VVE:XGXL,
ASAAPXX:VPA:SPIS:VGRKPKV:YKQYE:VVE:XKXS,
ASASPXX:VPA:SPIS:IGKTPKI:YKQYE:VVE:XKXS,
ASASPXX:VPA:SPIS:VGRTPKV:YKQYE:VVE:XKXS,
KIPKAXX:VPT:SPIS:DENEKVV:YKQYE:VVE:GXGXR,
GIPEPXX:VPE:SPIS:DENKNVV:YKQYE:TVE:SXAXR,
SIPKAXX:VPT:SPIS:DEYDKVV:YKQYE:VVE:GXGXR,
HVTKPTX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,
YVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,
TVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:AXGXH,
AVPKAXX:APT:SPIS:DSSNNVI:YKQYE:VVK:AXGXH,
KVGKAXX:VPT:SPIS:DDMGVPT:YKQYE:VAE:XGXR,
KASKAXX:VPT:SPIS:DKGVVTY:YKQYE:AVS:EXGXR,
GSAGPXX:TPT:SPIS:NDKQQII:YKQYE:VVD:RXGXS,
STPPTXX:VPT:SPIS:DSANNVV:YKQYE:VVE:SXGXR,
HVPKPXX:APT:SPIS:DDSSNVI:YKQYE:VVR:SXGXH,
RVPSTXX:APV:SPIS:DNGRVLL:YKQYE:VEE:XGXL,
ASAAPXX:VPQ:SPIS:VGRKPKV:YKQYE:VRS:XKXS,
ASASPXX:VSQ:SPIS:IGKTPKI:YKQYE:VKS:XKXS,
ASASPXX:VPQ:SPIS:VGRTPKV:YKQYE:VKS:XKXS,
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NDEGLEX:VPT:SPIS:RIKPHQGQH:YKQYE:EHS:QXEXR,
SSVKXQP:SRV:SPIS:EYVRKKPKL:YKQYE:EEH:LEXAXA,
RNVQXRP:TQV:SPIS:EIVRKKPIF:YKQYE:EDH:LAXKXE,
GIPEPXX:VPT:SPIS:DENKNVV:YKQYE:VVE:SXAXR,
HVTKPTX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
YVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
TVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:AXGXH,
AVPKAXX:VPT:SPIS:DSSNNVI:YKQYE:VVE:AXGXH,
KVGKAXX:VPT:SPIS:DDMGVPT:YKQYE:VVE:XGXR,
KASKAXX:VPT:SPIS:DKGVVTY:YKQYE:VVE:EXGXR,

GSAGPXX:VPT:SPIS:NDKQQII:YKQYE:VVE:RXGXS,
AAPASXX:VPT:SPIS:DAANNVV:YKQYE:VVE:AXGXR,
HVPKPXX:VPT:SPIS:DDSSNVI:YKQYE:VVE:SXGXH,
RVPSTXX:VPT:SPIS:DNGRVLL:YKQYE:VVE:XGXL,
ASAAPXX:VPT:SPIS:VGRKPKV:YKQYE:VVE:XKXS,
ASASPXX:VPT:SPIS:IGKTPKI:YKQYE:VVE:XKXS,
ASASPXX:VPT:SPIS:VGRTPKV:YKQYE:VVE:XKXS,
AAPASXX:VPA:SPIS:DAANNVV:YKQYE:VVE:AXGXR,
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GIPEPXX:APV:KPLS:DENKNVV:DHHKD:VEE:SXAXR,
SIPKAXX:APV:KPLS:DEYDKVV:DHHKD:VEE:GXGXR,
HVTKPTX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
YVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
TVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:AXGXH,
AVPKAXX:APV:KPLS:DSSNNVI:DHHKD:VEE:AXGXH,
KVGKAXX:APV:KPLS:DDMGVPT:DHHKD:VEE:XGXR,
KASKAXX:APV:KPLS:DKGVVTY:DHHKD:VEE:EXGXR,
GSAGPXX:APV:KPLS:NDKQQII:DHHKD:VEE:RXGXS,
AAPASXX:APV:KPLS:DAANNVV:DHHKD:VEE:AXGXR,
STPPTXX:APV:KPLS:DSANNVV:DHHKD:VEE:SXGXR,
HVPKPXX:APV:KPLS:DDSSNVI:DHHKD:VEE:SXGXH,
ASAAPXX:APV:KPLS:VGRKPKV:DHHKD:VEE:XKXS,
ASASPXX:APV:KPLS:IGKTPKI:DHHKD:VEE:XKXS,
ASASPXX:APV:KPLS:VGRTPKV:DHHKD:VEE:XKXS,
KIPKAXX:VPT:KPLS:DENEKVV:DHHKD:VVE:GXGXR,
GIPEPXX:VPE:KPLS:DENKNVV:DHHKD:TVE:SXAXR,
SIPKAXX:VPT:KPLS:DEYDKVV:DHHKD:VVE:GXGXR,
HVTKPTX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
YVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
TVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:AXGXH,
AVPKAXX:APT:KPLS:DSSNNVI:DHHKD:VVK:AXGXH,
KVGKAXX:VPT:KPLS:DDMGVPT:DHHKD:VAE:XGXR,
KASKAXX:VPT:KPLS:DKGVVTY:DHHKD:AVS:EXGXR,
GSAGPXX:TPT:KPLS:NDKQQII:DHHKD:VVD:RXGXS,
AAPASXX:VPA:KPLS:DAANNVV:DHHKD:VVE:AXGXR,
STPPTXX:VPT:KPLS:DSANNVV:DHHKD:VVE:SXGXR,
HVPKPXX:APT:KPLS:DDSSNVI:DHHKD:VVR:SXGXH,
ASAAPXX:VPQ:KPLS:VGRKPKV:DHHKD:VRS:XKXS,
ASASPXX:VSQ:KPLS:IGKTPKI:DHHKD:VKS:XKXS,
ASASPXX:VPQ:KPLS:VGRTPKV:DHHKD:VKS:XKXS,
NDEGLEX:VPT:KPLS:RIKPHQGQH:DHHKD:QHN:KXEXR,
NDEGLEX:VPT:KPLS:RIKPHQGQH:DHHKD:EHS:QXEXR,

SSVKXQP:SRV:KPLS:EYVRKKPKL:DHHKD:EEH:LEXAXA,

RNVQXRP:TQV:KPLS:EIVRKKPIF:DHHKD:EDH:LAXKXE,

KIPKAXX:VPQ:EPLP:DENEKVV:EQLSN:VRS:GXGXR,

GIPEPXX:VPQ:EPLP:DENKNVV:EQLSN:VRS:SXAXR,

SIPKAXX:VPQ:EPLP:DEYDKVV:EQLSN:VRS:GXGXR,

HVTKPTX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

YVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

TVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:AXGXH,

AVPKAXX:VPQ:EPLP:DSSNNVI:EQLSN:VRS:AXGXH,

KVGKAXX:VPQ:EPLP:DDMGVPT:EQLSN:VRS:XGXR,

KASKAXX:VPQ:EPLP:DKGVVTY:EQLSN:VRS:EXGXR,

GSAGPXX:VPQ:EPLP:NDKQQII:EQLSN:VRS:RXGXS,

AAPASXX:VPQ:EPLP:DAANNVV:EQLSN:VRS:AXGXR,

STPPTXX:VPQ:EPLP:DSANNVV:EQLSN:VRS:SXGXR,

HVPKPXX:VPQ:EPLP:DDSSNVI:EQLSN:VRS:SXGXH,

RVPSTXX:VPQ:EPLP:DNGRVLL:EQLSN:VRS:XGXL,

ASASPXX:VPQ:EPLP:IGKTPKI:EQLSN:VRS:XKXS,

ASASPXX:VPQ:EPLP:VGRTPKV:EQLSN:VRS:XKXS,

KIPKAXX:VPT:EPLP:DENEKVV:EQLSN:VVE:GXGXR,

GIPEPXX:VPE:EPLP:DENKNVV:EQLSN:TVE:SXAXR,

SIPKAXX:VPT:EPLP:DEYDKVV:EQLSN:VVE:GXGXR,

HVTKPTX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

YVPKPXX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

TVPKPXX:APT:EPLP:DDSSNVI:EQLSN:VVR:AXGXH,

AVPKAXX:APT:EPLP:DSSNNVI:EQLSN:VVK:AXGXH,

KVGKAXX:VPT:EPLP:DDMGVPT:EQLSN:VAE:XGXR,

KASKAXX:VPT:EPLP:DKGVVTY:EQLSN:AVS:EXGXR,

GSAGPXX:TPT:EPLP:NDKQQII:EQLSN:VVD:RXGXS,

AAPASXX:VPA:EPLP:DAANNVV:EQLSN:VVE:AXGXR,

STPPTXX:VPT:EPLP:DSANNVV:EQLSN:VVE:SXGXR,

HVPKPXX:APT:EPLP:DDSSNVI:EQLSN:VVR:SXGXH,

RVPSTXX:APV:EPLP:DNGRVLL:EQLSN:VEE:XGXL,

ASASPXX:VSQ:EPLP:IGKTPKI:EQLSN:VKS:XKXS,

ASASPXX:VPQ:EPLP:VGRTPKV:EQLSN:VKS:XKXS,

NDEGLEX:VPT:EPLP:RIKPHQGQH:EQLSN:QHN:KXEXR,

NDEGLEX:VPT:EPLP:RIKPHQGQH:EQLSN:EHS:QXEXR,

SSVKXQP:SRV:EPLP:EYVRKKPKL:EQLSN:EEH:LEXAXA,

RNVQXRP:TQV:EPLP:EIVRKKPIF:EQLSN:EDH:LAXKXE,

KIPKAXX:VSQ:EPLT:DENEKVV:EQLSN:VKS:GXGXR,

GIPEPXX:VSQ:EPLT:DENKNVV:EQLSN:VKS:SXAXR,

SIPKAXX:VSQ:EPLT:DEYDKVV:EQLSN:VKS:GXGXR,

HVTKPTX:VSQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,

YVPKPXX:VSQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,
TVPKPXX:VSQ:EPLT:DDSSNVI:EQLSN:VKS:AXGXH,
AVPKAXX:VSQ:EPLT:DSSNNVI:EQLSN:VKS:AXGXH,
KVGKAXX:VSQ:EPLT:DDMGVPT:EQLSN:VKS:XGXR,
KASKAXX:VSQ:EPLT:DKGVVTY:EQLSN:VKS:EXGXR,
GSAGPXX:VSQ:EPLT:NDKQQII:EQLSN:VKS:RXGXS,
AAPASXX:VSQ:EPLT:DAANNVV:EQLSN:VKS:AXGXR,
STPPTXX:VSQ:EPLT:DSANNVV:EQLSN:VKS:SXGXR,
HVPKPXX:VSQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,
RVPSTXX:VSQ:EPLT:DNGRVLL:EQLSN:VKS:XGXL,
ASAAPXX:VSQ:EPLT:VGRKPKV:EQLSN:VKS:XKXS,
ASASPXX:VSQ:EPLT:VGRTPKV:EQLSN:VKS:XKXS,
KIPKAXX:VPT:EPLT:DENEKVV:EQLSN:VVE:GXGXR,
GIPEPXX:VPE:EPLT:DENKNVV:EQLSN:TVE:SXAXR,
SIPKAXX:VPT:EPLT:DEYDKVV:EQLSN:VVE:GXGXR,
HVTKPTX:APT:EPLT:DDSSNVI:EQLSN:VVR:SXGXH,
YVPKPXX:APT:EPLT:DDSSNVI:EQLSN:VVR:SXGXH,
TVPKPXX:APT:EPLT:DDSSNVI:EQLSN:VVR:AXGXH,
AVPKAXX:APT:EPLT:DSSNNVI:EQLSN:VVK:AXGXH,
KVGKAXX:VPT:EPLT:DDMGVPT:EQLSN:VAE:XGXR,
KASKAXX:VPT:EPLT:DKGVVTY:EQLSN:AVS:EXGXR,
GSAGPXX:TPT:EPLT:NDKQQII:EQLSN:VVD:RXGXS,
AAPASXX:VPA:EPLT:DAANNVV:EQLSN:VVE:AXGXR,
STPPTXX:VPT:EPLT:DSANNVV:EQLSN:VVE:SXGXR,
HVPKPXX:APT:EPLT:DDSSNVI:EQLSN:VVR:SXGXH,
RVPSTXX:APV:EPLT:DNGRVLL:EQLSN:VEE:XGXL,
ASAAPXX:VPQ:EPLT:VGRKPKV:EQLSN:VRS:XKXS,
NDEGLEX:VPT:EPLT:RIKPHQGQH:EQLSN:QHN:KXEXR,
NDEGLEX:VPT:EPLT:RIKPHQGQH:EQLSN:EHS:QXEXR,
SSVKXQP:SRV:EPLT:EYVRKKPKL:EQLSN:EEH:LEXAXA,
RNVQXRP:TQV:EPLT:EIVRKKPIF:EQLSN:EDH:LAXKXE,
KIPKAXX:VPQ:EPLT:DENEKVV:EQLSN:VKS:GXGXR,
GIPEPXX:VPQ:EPLT:DENKNVV:EQLSN:VKS:SXAXR,
SIPKAXX:VPQ:EPLT:DEYDKVV:EQLSN:VKS:GXGXR,
HVTKPTX:VPQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,
YVPKPXX:VPQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,
TVPKPXX:VPQ:EPLT:DDSSNVI:EQLSN:VKS:AXGXH,
AVPKAXX:VPQ:EPLT:DSSNNVI:EQLSN:VKS:AXGXH,
KVGKAXX:VPQ:EPLT:DDMGVPT:EQLSN:VKS:XGXR,
KASKAXX:VPQ:EPLT:DKGVVTY:EQLSN:VKS:EXGXR,
GSAGPXX:VPQ:EPLT:NDKQQII:EQLSN:VKS:RXGXS,
AAPASXX:VPQ:EPLT:DAANNVV:EQLSN:VKS:AXGXR,

STPPTXX:VPQ:EPLT:DSANNVV:EQLSN:VKS:SXGXR,

HVPKPXX:VPQ:EPLT:DDSSNVI:EQLSN:VKS:SXGXH,

RVPSTXX:VPQ:EPLT:DNGRVLL:EQLSN:VKS:XGXL,

ASAAPXX:VPQ:EPLT:VGRKPKV:EQLSN:VKS:XKXS,

ASASPXX:VPQ:EPLT:IGKTPKI:EQLSN:VKS:XKXS,

NDEGLEX:VPT:SNIT:RIKPHQGQH:IGEMS:QHN:QXEXR,

KIPKAXX:VPT:SNIT:DENEKVV:IGEMS:VVE:GXGXR,

GIPEPXX:VPE:SNIT:DENKNVV:IGEMS:TVE:SXAXR,

SIPKAXX:VPT:SNIT:DEYDKVV:IGEMS:VVE:GXGXR,

HVTKPTX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,

YVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,

TVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:AXGXH,

AVPKAXX:APT:SNIT:DSSNNVI:IGEMS:VVK:AXGXH,

KVGKAXX:VPT:SNIT:DDMGVPT:IGEMS:VAE:XGXR,

KASKAXX:VPT:SNIT:DKGVVTY:IGEMS:AVS:EXGXR,

GSAGPXX:TPT:SNIT:NDKQQII:IGEMS:VVD:RXGXS,

AAPASXX:VPA:SNIT:DAANNVV:IGEMS:VVE:AXGXR,

STPPTXX:VPT:SNIT:DSANNVV:IGEMS:VVE:SXGXR,

HVPKPXX:APT:SNIT:DDSSNVI:IGEMS:VVR:SXGXH,

RVPSTXX:APV:SNIT:DNGRVLL:IGEMS:VEE:XGXL,

ASAAPXX:VPQ:SNIT:VGRKPKV:IGEMS:VRS:XKXS,

ASASPXX:VSQ:SNIT:IGKTPKI:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT:VGRTPKV:IGEMS:VKS:XKXS,

NDEGLEX:VPT:SNIT:RIKPHQGQH:IGEMS:EHS:QXEXR,

SSVKXQP:SRV:SNIT:EYVRKKPKL:IGEMS:EEH:LEXAXA,

RNVQXRP:TQV:SNIT:EIVRKKPIF:IGEMS:EDH:LAXKXE,

NDEGLEX:VPT:SNIT:RIKPHQGQH:LGEMS:EHS:KXEXR,

KIPKAXX:VPT:SNIT:DENEKVV:LGEMS:VVE:GXGXR,

GIPEPXX:VPE:SNIT:DENKNVV:LGEMS:TVE:SXAXR,

SIPKAXX:VPT:SNIT:DEYDKVV:LGEMS:VVE:GXGXR,

HVTKPTX:APT:SNIT:DDSSNVI:LGEMS:VVR:SXGXH,

YVPKPXX:APT:SNIT:DDSSNVI:LGEMS:VVR:SXGXH,

TVPKPXX:APT:SNIT:DDSSNVI:LGEMS:VVR:AXGXH,

AVPKAXX:APT:SNIT:DSSNNVI:LGEMS:VVK:AXGXH,

KVGKAXX:VPT:SNIT:DDMGVPT:LGEMS:VAE:XGXR,

KASKAXX:VPT:SNIT:DKGVVTY:LGEMS:AVS:EXGXR,

GSAGPXX:TPT:SNIT:NDKQQII:LGEMS:VVD:RXGXS,

AAPASXX:VPA:SNIT:DAANNVV:LGEMS:VVE:AXGXR,

STPPTXX:VPT:SNIT:DSANNVV:LGEMS:VVE:SXGXR,

HVPKPXX:APT:SNIT:DDSSNVI:LGEMS:VVR:SXGXH,

RVPSTXX:APV:SNIT:DNGRVLL:LGEMS:VEE:XGXL,

ASAAPXX:VPQ:SNIT:VGRKPKV:LGEMS:VRS:XKXS,

ASASPXX:VSQ:SNIT:IGKTPKI:LGEMS:VKS:XKXS,

ASASPXX:VPQ:SNIT:VGRTPKV:LGEMS:VKS:XKXS,

NDEGLEX:VPT:SNIT:RIKPHQGQH:LGEMS:QHN:KXEXR,

SSVKXQP:SRV:SNIT:EYVRKKPKL:LGEMS:EEH:LEXAXA,

RNVQXRP:TQV:SNIT:EIVRKKPIF:LGEMS:EDH:LAXKXE,

RNVQXRP:SRV:RSVK:EIVRKKPIF:KEVQV:EEH:LAXKXE,

KIPKAXX:VPT:RSVK:DENEKVV:KEVQV:VVE:GXGXR,

GIPEPXX:VPE:RSVK:DENKNVV:KEVQV:TVE:SXAXR,

SIPKAXX:VPT:RSVK:DEYDKVV:KEVQV:VVE:GXGXR,

HVTKPTX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,

YVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,

TVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:AXGXH,

AVPKAXX:APT:RSVK:DSSNNVI:KEVQV:VVK:AXGXH,

KVGKAXX:VPT:RSVK:DDMGVPT:KEVQV:VAE:XGXR,

KASKAXX:VPT:RSVK:DKGVVTY:KEVQV:AVS:EXGXR,

GSAGPXX:TPT:RSVK:NDKQQII:KEVQV:VVD:RXGXS,

AAPASXX:VPA:RSVK:DAANNVV:KEVQV:VVE:AXGXR,

STPPTXX:VPT:RSVK:DSANNVV:KEVQV:VVE:SXGXR,

HVPKPXX:APT:RSVK:DDSSNVI:KEVQV:VVR:SXGXH,

RVPSTXX:APV:RSVK:DNGRVLL:KEVQV:VEE:XGXL,

ASAAPXX:VPQ:RSVK:VGRKPKV:KEVQV:VRS:XKXS,

ASASPXX:VSQ:RSVK:IGKTPKI:KEVQV:VKS:XKXS,

ASASPXX:VPQ:RSVK:VGRTPKV:KEVQV:VKS:XKXS,

NDEGLEX:VPT:RSVK:RIKPHQGQH:KEVQV:QHN:KXEXR,

NDEGLEX:VPT:RSVK:RIKPHQGQH:KEVQV:EHS:QXEXR,

RNVQXRP:TQV:RSVK:EIVRKKPIF:KEVQV:EDH:LAXKXE,

SSVKXQP:TQV:RPVQ:EYVRKKPKL:KKATV:EDH:LEXAXA,

KIPKAXX:VPT:RPVQ:DENEKVV:KKATV:VVE:GXGXR,

GIPEPXX:VPE:RPVQ:DENKNVV:KKATV:TVE:SXAXR,

SIPKAXX:VPT:RPVQ:DEYDKVV:KKATV:VVE:GXGXR,

HVTKPTX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,

YVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,

TVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:AXGXH,

AVPKAXX:APT:RPVQ:DSSNNVI:KKATV:VVK:AXGXH,

KVGKAXX:VPT:RPVQ:DDMGVPT:KKATV:VAE:XGXR,

KASKAXX:VPT:RPVQ:DKGVVTY:KKATV:AVS:EXGXR,

GSAGPXX:TPT:RPVQ:NDKQQII:KKATV:VVD:RXGXS,

AAPASXX:VPA:RPVQ:DAANNVV:KKATV:VVE:AXGXR,

STPPTXX:VPT:RPVQ:DSANNVV:KKATV:VVE:SXGXR,

HVPKPXX:APT:RPVQ:DDSSNVI:KKATV:VVR:SXGXH,

RVPSTXX:APV:RPVQ:DNGRVLL:KKATV:VEE:XGXL,

ASAAPXX:VPQ:RPVQ:VGRKPKV:KKATV:VRS:XKXS,

ASASPXX:VSQ:RPVQ:IGKTPKI:KKATV:VKS:XKXS,

ASASPXX:VPQ:RPVQ:VGRTPKV:KKATV:VKS:XKXS,
NDEGLEX:VPT:RPVQ:RIKPHQGQH:KKATV:QHN:KXEXR,
NDEGLEX:VPT:RPVQ:RIKPHQGQH:KKATV:EHS:QXEXR and
SSVKXQP:SRV:RPVQ:EYVRKKPKL:KKATV:EEH:LEXAXA.

In particular, in certain embodiments, the heptuplet PEP7:PEP3:PEP12:LINKER:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS-AA[17]-LYL:DENKNVV:LKNYQ:VVE:SXAXR, SIPKAXX:VPT:SAIS-AA[17]-LYL:DEYDKVV:LKNYQ:VVE:GXGXR, HVTKPTX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, YVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:AXGXH, AVPKAXX:VPT:SAIS-AA[17]-LYL:DSSNNVI:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:DDMGVPT:LKNYQ:VVE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:DKGVVTY:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS-AA[17]-LYL:NDKQQII:LKNYQ:VVE:RXGXS, AAPASXX:VPT:SAIS-AA[17]-LYL:DAANNVV:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS-AA[17]-LYL:DSANNVV:LKNYQ:VVE:SXGXR, HVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS-AA[17]-LYL:DNGRVLL:LKNYQ:VVE:XGXL, ASAAPXX:VPT:SAIS-AA[17]-LYL:VGRKPKV:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:IGKTPKI:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:VGRTPKV:LKNYQ:VVE:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:VVE:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:VVE:QXEXR, SSVKXQP:VPT:SAIS-AA[17]-LYL:EYVRKKPKL:LKNYQ:VVE:LEXAXA, RNVQXRP:VPT:SAIS-AA[17]-LYL:EIVRKKPIF:LKNYQ:VVE:LAXKXE, GIPEPXX:VPE:SAIS-AA[17]-LYL:DENKNVV:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, YVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:AXGXH, AVPKAXX:APT:SAIS-AA[17]-LYL:DSSNNVI:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:DDMGVPT:LKNYQ:VAE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:DKGVVTY:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS-AA[17]-LYL:NDKQQII:LKNYQ:VVD:RXGXS, AAPASXX:VPA:SAIS-AA[17]-LYL:DAANNVV:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, RVPSTXX:APV:SAIS-AA[17]-LYL:DNGRVLL:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS-AA[17]-LYL:VGRKPKV:LKNYQ:VRS:XKXS, ASASPXX:VSQ:SAIS-AA[17]-LYL:IGKTPKI:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS-AA[17]-LYL:VGRTPKV:LKNYQ:VKS:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:EHS:QXEXR, SSVKXQP:SRV:SAIS-AA[17]-LYL:EYVRKKPKL:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS-AA[17]-LYL:EIVRKKPIF:LKNYQ:EDH:LAXKXE, KIPKAXX:VPE:SSLS-AA[17]-LFF:DENEKVV:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS-AA[17]-LFF:DEYDKVV:LKVYP:TVE:GXGXR, HVTKPTX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, YVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, TVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:AXGXH, AVPKAXX:VPE:SSLS-AA[17]-LFF:DSSNNVI:LKVYP:TVE:AXGXH, KVGKAXX:VPE:SSLS-AA[17]-LFF:DDMGVPT:LKVYP:TVE:XGXR, KASKAXX:VPE:SSLS-AA[17]-LFF:DKGVVTY:LKVYP:TVE:EXGXR, GSAGPXX:VPE:SSLS-AA[17]-LFF:NDKQQII:LKVYP:TVE:RXGXS, AAPASXX:VPE:SSLS-AA[17]-LFF:DAANNVV:LKVYP:TVE:AXGXR, STPPTXX:VPE:SSLS-AA[17]-LFF:DSANNVV:LKVYP:TVE:SXGXR, HVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, RVPSTXX:VPE:SSLS-AA[17]-

LFF:DNGRVLL:LKVYP:TVE:XGXL, ASAAPXX:VPE:SSLS-AA[17]-LFF:VGRKPKV:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:IGKTPKI:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:VGRTPKV:LKVYP:TVE:XKXS, NDEGLEX:VPE:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:TVE:KXEXR, NDEGLEX:VPE:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:TVE:QXEXR, SSVKXQP:VPE:SSLS-AA[17]-LFF:EYVRKKPKL:LKVYP:TVE:LEXAXA, RNVQXRP:VPE:SSLS-AA[17]-LFF:EIVRKKPIF:LKVYP:TVE:LAXKXE, KIPKAXX:VPT:SSLS-AA[17]-LFF:DENEKVV:LKVYP:VVE:GXGXR, SIPKAXX:VPT:SSLS-AA[17]-LFF:DEYDKVV:LKVYP:VVE:GXGXR, HVTKPTX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, YVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, TVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:AXGXH, AVPKAXX:APT:SSLS-AA[17]-LFF:DSSNNVI:LKVYP:VVK:AXGXH, KVGKAXX:VPT:SSLS-AA[17]-LFF:DDMGVPT:LKVYP:VAE:XGXR, KASKAXX:VPT:SSLS-AA[17]-LFF:DKGVVTY:LKVYP:AVS:EXGXR, GSAGPXX:TPT:SSLS-AA[17]-LFF:NDKQQII:LKVYP:VVD:RXGXS, AAPASXX:VPA:SSLS-AA[17]-LFF:DAANNVV:LKVYP:VVE:AXGXR, STPPTXX:VPT:SSLS-AA[17]-LFF:DSANNVV:LKVYP:VVE:SXGXR, HVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, RVPSTXX:APV:SSLS-AA[17]-LFF:DNGRVLL:LKVYP:VEE:XGXL, ASAAPXX:VPQ:SSLS-AA[17]-LFF:VGRKPKV:LKVYP:VRS:XKXS, ASASPXX:VSQ:SSLS-AA[17]-LFF:IGKTPKI:LKVYP:VKS:XKXS, ASASPXX:VPQ:SSLS-AA[17]-LFF:VGRTPKV:LKVYP:VKS:XKXS, NDEGLEX:VPT:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:QHN:KXEXR, NDEGLEX:VPT:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:EHS:QXEXR, SSVKXQP:SRV:SSLS-AA[17]-LFF:EYVRKKPKL:LKVYP:EEH:LEXAXA, RNVQXRP:TQV:SSLS-AA[17]-LFF:EIVRKKPIF:LKVYP:EDH:LAXKXE, KIPKAXX:VPT:SAIS-AA[17]-LYL:DENEKVV:LKNYQ:VVE:GXGXR, KIPKAXX:APT:NAIS-AA[17]-LYF:DENEKVV:LKKYR:VVR:GXGXR, GIPEPXX:APT:NAIS-AA[17]-LYF:DENKNVV:LKKYR:VVR:SXAXR, SIPKAXX:APT:NAIS-AA[17]-LYF:DEYDKVV:LKKYR:VVR:GXGXR, YVPKPXX:APT:NAIS-AA[17]-LYF:DDSSNVI:LKKYR:VVR:SXGXH, TVPKPXX:APT:NAIS-AA[17]-LYF:DDSSNVI:LKKYR:VVR:AXGXH, AVPKAXX:APT:NAIS-AA[17]-LYF:DSSNNVI:LKKYR:VVR:AXGXH, KVGKAXX:APT:NAIS-AA[17]-LYF:DDMGVPT:LKKYR:VVR:XGXR, KASKAXX:APT:NAIS-AA[17]-LYF:DKGVVTY:LKKYR:VVR:EXGXR, GSAGPXX:APT:NAIS-AA[17]-LYF:NDKQQII:LKKYR:VVR:RXGXS, AAPASXX:APT:NAIS-AA[17]-LYF:DAANNVV:LKKYR:VVR:AXGXR, STPPTXX:APT:NAIS-AA[17]-LYF:DSANNVV:LKKYR:VVR:SXGXR, HVPKPXX:APT:NAIS-AA[17]-LYF:DDSSNVI:LKKYR:VVR:SXGXH, RVPSTXX:APT:NAIS-AA[17]-LYF:DNGRVLL:LKKYR:VVR:XGXL, ASAAPXX:APT:NAIS-AA[17]-LYF:VGRKPKV:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:IGKTPKI:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:VGRTPKV:LKKYR:VVR:XKXS, NDEGLEX:APT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:VVR:KXEXR, NDEGLEX:APT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:VVR:QXEXR, SSVKXQP:APT:NAIS-AA[17]-LYF:EYVRKKPKL:LKKYR:VVR:LEXAXA, RNVQXRP:APT:NAIS-AA[17]-LYF:EIVRKKPIF:LKKYR:VVR:LAXKXE, KIPKAXX:VPT:NAIS-AA[17]-LYF:DENEKVV:LKKYR:VVE:GXGXR, GIPEPXX:VPE:NAIS-AA[17]-LYF:DENKNVV:LKKYR:TVE:SXAXR, SIPKAXX:VPT:NAIS-AA[17]-LYF:DEYDKVV:LKKYR:VVE:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:DSSNNVI:LKKYR:VVK:AXGXH, KVGKAXX:VPT:NAIS-AA[17]-LYF:DDMGVPT:LKKYR:VAE:XGXR, KASKAXX:VPT:NAIS-AA[17]-LYF:DKGVVTY:LKKYR:AVS:EXGXR, GSAGPXX:TPT:NAIS-AA[17]-LYF:NDKQQII:LKKYR:VVD:RXGXS, AAPASXX:VPA:NAIS-AA[17]-LYF:DAANNVV:LKKYR:VVE:AXGXR, STPPTXX:VPT:NAIS-AA[17]-LYF:DSANNVV:LKKYR:VVE:SXGXR, RVPSTXX:APV:NAIS-AA[17]-LYF:DNGRVLL:LKKYR:VEE:XGXL, ASAAPXX:VPQ:NAIS-AA[17]-LYF:VGRKPKV:LKKYR:VRS:XKXS, ASASPXX:VSQ:NAIS-AA[17]-

LYF:IGKTPKI:LKKYR:VKS:XKXS, ASASPXX:VPQ:NAIS-AA[17]-LYF:VGRTPKV:LKKYR:VKS:XKXS, NDEGLEX:VPT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:QHN:KXEXR, NDEGLEX:VPT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:EHS:QXEXR, SSVKXQP:SRV:NAIS-AA[17]-LYF:EYVRKKPKL:LKKYR:EEH:LEXAXA, RNVQXRP:TQV:NAIS-AA[17]-LYF:EIVRKKPIF:LKKYR:EDH:LAXKXE, HVTKPTX:APT:NAIS-AA[17]-LYF:DDSSNVI:LKKYR:VVR:SXGXH, KIPKAXX:APT:SATS-AA[17]-LYY:DENEKVV:LRKHR:VVK:GXGXR, GIPEPXX:APT:SATS-AA[17]-LYY:DENKNVV:LRKHR:VVK:SXAXR, SIPKAXX:APT:SATS-AA[17]-LYY:DEYDKVV:LRKHR:VVK:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:AXGXH, KVGKAXX:APT:SATS-AA[17]-LYY:DDMGVPT:LRKHR:VVK:XGXR, KASKAXX:APT:SATS-AA[17]-LYY:DKGVVTY:LRKHR:VVK:EXGXR, GSAGPXX:APT:SATS-AA[17]-LYY:NDKQQII:LRKHR:VVK:RXGXS, AAPASXX:APT:SATS-AA[17]-LYY:DAANNVV:LRKHR:VVK:AXGXR, STPPTXX:APT:SATS-AA[17]-LYY:DSANNVV:LRKHR:VVK:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, RVPSTXX:APT:SATS-AA[17]-LYY:DNGRVLL:LRKHR:VVK:XGXL, ASAAPXX:APT:SATS-AA[17]-LYY:VGRKPKV:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:IGKTPKI:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:VGRTPKV:LRKHR:VVK:XKXS, NDEGLEX:APT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:VVK:KXEXR, NDEGLEX:APT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:VVK:QXEXR, SSVKXQP:APT:SATS-AA[17]-LYY:EYVRKKPKL:LRKHR:VVK:LEXAXA, RNVQXRP:APT:SATS-AA[17]-LYY:EIVRKKPIF:LRKHR:VVK:LAXKXE, KIPKAXX:VPT:SATS-AA[17]-LYY:DENEKVV:LRKHR:VVE:GXGXR, GIPEPXX:VPE:SATS-AA[17]-LYY:DENKNVV:LRKHR:TVE:SXAXR, SIPKAXX:VPT:SATS-AA[17]-LYY:DEYDKVV:LRKHR:VVE:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:AXGXH, KVGKAXX:VPT:SATS-AA[17]-LYY:DDMGVPT:LRKHR:VAE:XGXR, KASKAXX:VPT:SATS-AA[17]-LYY:DKGVVTY:LRKHR:AVS:EXGXR, GSAGPXX:TPT:SATS-AA[17]-LYY:NDKQQII:LRKHR:VVD:RXGXS, AAPASXX:VPA:SATS-AA[17]-LYY:DAANNVV:LRKHR:VVE:AXGXR, STPPTXX:VPT:SATS-AA[17]-LYY:DSANNVV:LRKHR:VVE:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, RVPSTXX:APV:SATS-AA[17]-LYY:DNGRVLL:LRKHR:VEE:XGXL, ASAAPXX:VPQ:SATS-AA[17]-LYY:VGRKPKV:LRKHR:VRS:XKXS, ASASPXX:VSQ:SATS-AA[17]-LYY:IGKTPKI:LRKHR:VKS:XKXS, ASASPXX:VPQ:SATS-AA[17]-LYY:VGRTPKV:LRKHR:VKS:XKXS, NDEGLEX:VPT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:QHN:KXEXR, NDEGLEX:VPT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:EHS:QXEXR, SSVKXQP:SRV:SATS-AA[17]-LYY:EYVRKKPKL:LRKHR:EEH:LEXAXA, RNVQXRP:TQV:SATS-AA[17]-LYY:EIVRKKPIF:LRKHR:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:DENEKVV:LKYHY:VAE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LYK:DENKNVV:LKYHY:VAE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:DEYDKVV:LKYHY:VAE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LYK:DSSNNVI:LKYHY:VAE:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:DKGVVTY:LKYHY:VAE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LYK:NDKQQII:LKYHY:VAE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LYK:DAANNVV:LKYHY:VAE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:DSANNVV:LKYHY:VAE:SXGXR,

HVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LYK:DNGRVLL:LKYHY:VAE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LYK:VGRKPKV:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:IGKTPKI:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:VGRTPKV:LKYHY:VAE:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:VAE:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:VAE:QXEXR, SSVKXQP:VPT:SPIS-AA[17]-LYK:EYVRKKPKL:LKYHY:VAE:LEXAXA, RNVQXRP:VPT:SPIS-AA[17]-LYK:EIVRKKPIF:LKYHY:VAE:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:DENEKVV:LKYHY:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYK:DENKNVV:LKYHY:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:DEYDKVV:LKYHY:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYK:DSSNNVI:LKYHY:VVK:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:DKGVVTY:LKYHY:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYK:NDKQQII:LKYHY:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LYK:DAANNVV:LKYHY:VVE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:DSANNVV:LKYHY:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYK:DNGRVLL:LKYHY:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYK:VGRKPKV:LKYHY:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYK:IGKTPKI:LKYHY:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYK:VGRTPKV:LKYHY:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYK:EYVRKKPKL:LKYHY:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYK:EIVRKKPIF:LKYHY:EDH:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:DENEKVV:KFKYE:AVS:GXGXR, GIPEPXX:VPT:EPIS-AA[17]-LYL:DENKNVV:KFKYE:AVS:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:DEYDKVV:KFKYE:AVS:GXGXR, HVTKPTX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, YVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, TVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:AXGXH, AVPKAXX:VPT:EPIS-AA[17]-LYL:DSSNNVI:KFKYE:AVS:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:DDMGVPT:KFKYE:AVS:XGXR, GSAGPXX:VPT:EPIS-AA[17]-LYL:NDKQQII:KFKYE:AVS:RXGXS, AAPASXX:VPT:EPIS-AA[17]-LYL:DAANNVV:KFKYE:AVS:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:DSANNVV:KFKYE:AVS:SXGXR, HVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, RVPSTXX:VPT:EPIS-AA[17]-LYL:DNGRVLL:KFKYE:AVS:XGXL, ASAAPXX:VPT:EPIS-AA[17]-LYL:VGRKPKV:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:IGKTPKI:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:VGRTPKV:KFKYE:AVS:XKXS, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:AVS:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:AVS:QXEXR, SSVKXQP:VPT:EPIS-AA[17]-LYL:EYVRKKPKL:KFKYE:AVS:LEXAXA, RNVQXRP:VPT:EPIS-AA[17]-LYL:EIVRKKPIF:KFKYE:AVS:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:DENEKVV:KFKYE:VVE:GXGXR, GIPEPXX:VPE:EPIS-AA[17]-LYL:DENKNVV:KFKYE:TVE:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:DEYDKVV:KFKYE:VVE:GXGXR, HVTKPTX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:SXGXH, YVPKPXX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:SXGXH, TVPKPXX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:AXGXH, AVPKAXX:APT:EPIS-AA[17]-LYL:DSSNNVI:KFKYE:VVK:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:DDMGVPT:KFKYE:VAE:XGXR, GSAGPXX:TPT:EPIS-AA[17]-LYL:NDKQQII:KFKYE:VVD:RXGXS, AAPASXX:VPA:EPIS-AA[17]-LYL:DAANNVV:KFKYE:VVE:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:DSANNVV:KFKYE:VVE:SXGXR, HVPKPXX:APT:EPIS-AA[17]-

LYL:DDSSNVI:KFKYE:VVR:SXGXH, RVPSTXX:APV:EPIS-AA[17]-LYL:DNGRVLL:KFKYE:VEE:XGXL, ASAAPXX:VPQ:EPIS-AA[17]-LYL:VGRKPKV:KFKYE:VRS:XKXS, ASASPXX:VSQ:EPIS-AA[17]-LYL:IGKTPKI:KFKYE:VKS:XKXS, ASASPXX:VPQ:EPIS-AA[17]-LYL:VGRTPKV:KFKYE:VKS:XKXS, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:QHN:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:EHS:QXEXR, SSVKXQP:SRV:EPIS-AA[17]-LYL:EYVRKKPKL:KFKYE:EEH:LEXAXA, RNVQXRP:TQV:EPIS-AA[17]-LYL:EIVRKKPIF:KFKYE:EDH:LAXKXE, KIPKAXX:TPT:SPIN-AA[17]-LYF:DENEKVV:YGKIP:VVD:GXGXR, GIPEPXX:TPT:SPIN-AA[17]-LYF:DENKNVV:YGKIP:VVD:SXAXR, SIPKAXX:TPT:SPIN-AA[17]-LYF:DEYDKVV:YGKIP:VVD:GXGXR, HVTKPTX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, YVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, TVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:AXGXH, AVPKAXX:TPT:SPIN-AA[17]-LYF:DSSNNVI:YGKIP:VVD:AXGXH, KVGKAXX:TPT:SPIN-AA[17]-LYF:DDMGVPT:YGKIP:VVD:XGXR, KASKAXX:TPT:SPIN-AA[17]-LYF:DKGVVTY:YGKIP:VVD:EXGXR, AAPASXX:TPT:SPIN-AA[17]-LYF:DAANNVV:YGKIP:VVD:AXGXR, STPPTXX:TPT:SPIN-AA[17]-LYF:DSANNVV:YGKIP:VVD:SXGXR, HVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, RVPSTXX:TPT:SPIN-AA[17]-LYF:DNGRVLL:YGKIP:VVD:XGXL, ASAAPXX:TPT:SPIN-AA[17]-LYF:VGRKPKV:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:IGKTPKI:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:VGRTPKV:YGKIP:VVD:XKXS, NDEGLEX:TPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:VVD:KXEXR, NDEGLEX:TPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:VVD:QXEXR, SSVKXQP:TPT:SPIN-AA[17]-LYF:EYVRKKPKL:YGKIP:VVD:LEXAXA, RNVQXRP:TPT:SPIN-AA[17]-LYF:EIVRKKPIF:YGKIP:VVD:LAXKXE, KIPKAXX:VPT:SPIN-AA[17]-LYF:DENEKVV:YGKIP:VVE:GXGXR, GIPEPXX:VPE:SPIN-AA[17]-LYF:DENKNVV:YGKIP:TVE:SXAXR, SIPKAXX:VPT:SPIN-AA[17]-LYF:DEYDKVV:YGKIP:VVE:GXGXR, HVTKPTX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, YVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, TVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:AXGXH, AVPKAXX:APT:SPIN-AA[17]-LYF:DSSNNVI:YGKIP:VVK:AXGXH, KVGKAXX:VPT:SPIN-AA[17]-LYF:DDMGVPT:YGKIP:VAE:XGXR, KASKAXX:VPT:SPIN-AA[17]-LYF:DKGVVTY:YGKIP:AVS:EXGXR, AAPASXX:VPA:SPIN-AA[17]-LYF:DAANNVV:YGKIP:VVE:AXGXR, STPPTXX:VPT:SPIN-AA[17]-LYF:DSANNVV:YGKIP:VVE:SXGXR, HVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, RVPSTXX:APV:SPIN-AA[17]-LYF:DNGRVLL:YGKIP:VEE:XGXL, ASAAPXX:VPQ:SPIN-AA[17]-LYF:VGRKPKV:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN-AA[17]-LYF:IGKTPKI:YGKIP:VKS:XKXS, ASASPXX:VPQ:SPIN-AA[17]-LYF:VGRTPKV:YGKIP:VKS:XKXS, NDEGLEX:VPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:QHN:KXEXR, NDEGLEX:VPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:EHS:QXEXR, SSVKXQP:SRV:SPIN-AA[17]-LYF:EYVRKKPKL:YGKIP:EEH:LEXAXA, RNVQXRP:TQV:SPIN-AA[17]-LYF:EIVRKKPIF:YGKIP:EDH:LAXKXE, KIPKAXX:VPA:SPIS-AA[17]-LYI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPA:SPIS-AA[17]-LYI:DENKNVV:YKQYE:VVE:SXAXR, SIPKAXX:VPA:SPIS-AA[17]-LYI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:SXGXH, YVPKPXX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:SXGXH, TVPKPXX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:AXGXH, AVPKAXX:VPA:SPIS-AA[17]-LYI:DSSNNVI:YKQYE:VVE:AXGXH, KVGKAXX:VPA:SPIS-AA[17]-LYI:DDMGVPT:YKQYE:VVE:XGXR, KASKAXX:VPA:SPIS-AA[17]-LYI:DKGVVTY:YKQYE:VVE:EXGXR, GSAGPXX:VPA:SPIS-AA[17]-LYI:NDKQQII:YKQYE:VVE:RXGXS, STPPTXX:VPA:SPIS-AA[17]-LYI:DSANNVV:YKQYE:VVE:SXGXR, HVPKPXX:VPA:SPIS-AA[17]-

LYI:DDSSNVI:YKQYE:VVE:SXGXH, RVPSTXX:VPA:SPIS-AA[17]-LYI:DNGRVLL:YKQYE:VVE:XGXL, ASAAPXX:VPA:SPIS-AA[17]-LYI:VGRKPKV:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:IGKTPKI:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:VGRTPKV:YKQYE:VVE:XKXS, NDEGLEX:VPA:SPIS-AA[17]-LYI:RIKPHQGQH:YKQYE:VVE:KXEXR, NDEGLEX:VPA:SPIS-AA[17]-LYI:RIKPHQGQH:YKQYE:VVE:QXEXR, SSVKXQP:VPA:SPIS-AA[17]-LYI:EYVRKKPKL:YKQYE:VVE:LEXAXA, RNVQXRP:VPA:SPIS-AA[17]-LYI:EIVRKKPIF:YKQYE:VVE:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYI:DENKNVV:YKQYE:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYI:DSSNNVI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LYI:DDMGVPT:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LYI:DKGVVTY:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYI:NDKQQII:YKQYE:VVD:RXGXS, STPPTXX:VPT:SPIS-AA[17]-LYI:DSANNVV:YKQYE:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYI:DNGRVLL:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYI:VGRKPKV:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYI:IGKTPKI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYI:VGRTPKV:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYI:RIKPHQGQH:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYI:RIKPHQGQH:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYI:EYVRKKPKL:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYI:EIVRKKPIF:YKQYE:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LFI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LFI:DENKNVV:YKQYE:VVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LFI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LFI:DSSNNVI:YKQYE:VVE:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:DDMGVPT:YKQYE:VVE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:DKGVVTY:YKQYE:VVE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LFI:NDKQQII:YKQYE:VVE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LFI:DAANNVV:YKQYE:VVE:AXGXR, HVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LFI:DNGRVLL:YKQYE:VVE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LFI:VGRKPKV:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:IGKTPKI:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:VGRTPKV:YKQYE:VVE:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:VVE:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:VVE:QXEXR, SSVKXQP:VPT:SPIS-AA[17]-LFI:EYVRKKPKL:YKQYE:VVE:LEXAXA, RNVQXRP:VPT:SPIS-AA[17]-LFI:EIVRKKPIF:YKQYE:VVE:LAXKXE, GIPEPXX:VPE:SPIS-AA[17]-LFI:DENKNVV:YKQYE:TVE:SXAXR, HVTKPTX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LFI:DSSNNVI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:DDMGVPT:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:DKGVVTY:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LFI:NDKQQII:YKQYE:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LFI:DAANNVV:YKQYE:VVE:AXGXR, HVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LFI:DNGRVLL:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-

LFI:VGRKPKV:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LFI:IGKTPKI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LFI:VGRTPKV:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LFI:EYVRKKPKL:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LFI:EIVRKKPIF:YKQYE:EDH:LAXKXE, KIPKAXX:APV:KPLS-AA[17]-LYV:DENEKVV:DHHKD:VEE:GXGXR, GIPEPXX:APV:KPLS-AA[17]-LYV:DENKNVV:DHHKD:VEE:SXAXR, SIPKAXX:APV:KPLS-AA[17]-LYV:DEYDKVV:DHHKD:VEE:GXGXR, HVTKPTX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, YVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, TVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:AXGXH, AVPKAXX:APV:KPLS-AA[17]-LYV:DSSNNVI:DHHKD:VEE:AXGXH, KVGKAXX:APV:KPLS-AA[17]-LYV:DDMGVPT:DHHKD:VEE:XGXR, KASKAXX:APV:KPLS-AA[17]-LYV:DKGVVTY:DHHKD:VEE:EXGXR, GSAGPXX:APV:KPLS-AA[17]-LYV:NDKQQII:DHHKD:VEE:RXGXS, AAPASXX:APV:KPLS-AA[17]-LYV:DAANNVV:DHHKD:VEE:AXGXR, STPPTXX:APV:KPLS-AA[17]-LYV:DSANNVV:DHHKD:VEE:SXGXR, HVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, ASAAPXX:APV:KPLS-AA[17]-LYV:VGRKPKV:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:IGKTPKI:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:VGRTPKV:DHHKD:VEE:XKXS, NDEGLEX:APV:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:VEE:KXEXR, NDEGLEX:APV:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:VEE:QXEXR, SSVKXQP:APV:KPLS-AA[17]-LYV:EYVRKKPKL:DHHKD:VEE:LEXAXA, RNVQXRP:APV:KPLS-AA[17]-LYV:EIVRKKPIF:DHHKD:VEE:LAXKXE, KIPKAXX:VPT:KPLS-AA[17]-LYV:DENEKVV:DHHKD:VVE:GXGXR, GIPEPXX:VPE:KPLS-AA[17]-LYV:DENKNVV:DHHKD:TVE:SXAXR, SIPKAXX:VPT:KPLS-AA[17]-LYV:DEYDKVV:DHHKD:VVE:GXGXR, HVTKPTX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, YVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, TVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:AXGXH, AVPKAXX:APT:KPLS-AA[17]-LYV:DSSNNVI:DHHKD:VVK:AXGXH, KVGKAXX:VPT:KPLS-AA[17]-LYV:DDMGVPT:DHHKD:VAE:XGXR, KASKAXX:VPT:KPLS-AA[17]-LYV:DKGVVTY:DHHKD:AVS:EXGXR, GSAGPXX:TPT:KPLS-AA[17]-LYV:NDKQQII:DHHKD:VVD:RXGXS, AAPASXX:VPA:KPLS-AA[17]-LYV:DAANNVV:DHHKD:VVE:AXGXR, STPPTXX:VPT:KPLS-AA[17]-LYV:DSANNVV:DHHKD:VVE:SXGXR, HVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, ASAAPXX:VPQ:KPLS-AA[17]-LYV:VGRKPKV:DHHKD:VRS:XKXS, ASASPXX:VSQ:KPLS-AA[17]-LYV:IGKTPKI:DHHKD:VKS:XKXS, ASASPXX:VPQ:KPLS-AA[17]-LYV:VGRTPKV:DHHKD:VKS:XKXS, NDEGLEX:VPT:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:QHN:KXEXR, NDEGLEX:VPT:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:EHS:QXEXR, SSVKXQP:SRV:KPLS-AA[17]-LYV:EYVRKKPKL:DHHKD:EEH:LEXAXA, RNVQXRP:TQV:KPLS-AA[17]-LYV:EIVRKKPIF:DHHKD:EDH:LAXKXE, KIPKAXX:VPQ:EPLP-AA[17]-VYY:DENEKVV:EQLSN:VRS:GXGXR, GIPEPXX:VPQ:EPLP-AA[17]-VYY:DENKNVV:EQLSN:VRS:SXAXR, SIPKAXX:VPQ:EPLP-AA[17]-VYY:DEYDKVV:EQLSN:VRS:GXGXR, HVTKPTX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, YVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, TVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:AXGXH, AVPKAXX:VPQ:EPLP-AA[17]-VYY:DSSNNVI:EQLSN:VRS:AXGXH, KVGKAXX:VPQ:EPLP-AA[17]-VYY:DDMGVPT:EQLSN:VRS:XGXR, KASKAXX:VPQ:EPLP-AA[17]-VYY:DKGVVTY:EQLSN:VRS:EXGXR,

GSAGPXX:VPQ:EPLP-AA[17]-VYY:NDKQQII:EQLSN:VRS:RXGXS, AAPASXX:VPQ:EPLP-AA[17]-VYY:DAANNVV:EQLSN:VRS:AXGXR, STPPTXX:VPQ:EPLP-AA[17]-VYY:DSANNVV:EQLSN:VRS:SXGXR, HVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, RVPSTXX:VPQ:EPLP-AA[17]-VYY:DNGRVLL:EQLSN:VRS:XGXL, ASASPXX:VPQ:EPLP-AA[17]-VYY:IGKTPKI:EQLSN:VRS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:VGRTPKV:EQLSN:VRS:XKXS, NDEGLEX:VPQ:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:VRS:KXEXR, NDEGLEX:VPQ:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:VRS:QXEXR, SSVKXQP:VPQ:EPLP-AA[17]-VYY:EYVRKKPKL:EQLSN:VRS:LEXAXA, RNVQXRP:VPQ:EPLP-AA[17]-VYY:EIVRKKPIF:EQLSN:VRS:LAXKXE, KIPKAXX:VPT:EPLP-AA[17]-VYY:DENEKVV:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLP-AA[17]-VYY:DENKNVV:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLP-AA[17]-VYY:DEYDKVV:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLP-AA[17]-VYY:DSSNNVI:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLP-AA[17]-VYY:DDMGVPT:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLP-AA[17]-VYY:DKGVVTY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLP-AA[17]-VYY:NDKQQII:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLP-AA[17]-VYY:DAANNVV:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLP-AA[17]-VYY:DSANNVV:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLP-AA[17]-VYY:DNGRVLL:EQLSN:VEE:XGXL, ASASPXX:VSQ:EPLP-AA[17]-VYY:IGKTPKI:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:VGRTPKV:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLP-AA[17]-VYY:EYVRKKPKL:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLP-AA[17]-VYY:EIVRKKPIF:EQLSN:EDH:LAXKXE, KIPKAXX:VSQ:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VKS:GXGXR, GIPEPXX:VSQ:EPLT-AA[17]-LYY:DENKNVV:EQLSN:VKS:SXAXR, SIPKAXX:VSQ:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VKS:GXGXR, HVTKPTX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, YVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, TVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:AXGXH, AVPKAXX:VSQ:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VKS:AXGXH, KVGKAXX:VSQ:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VKS:XGXR, KASKAXX:VSQ:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:VKS:EXGXR, GSAGPXX:VSQ:EPLT-AA[17]-LYY:NDKQQII:EQLSN:VKS:RXGXS, AAPASXX:VSQ:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VKS:AXGXR, STPPTXX:VSQ:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VKS:SXGXR, HVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, RVPSTXX:VSQ:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VKS:XGXL, ASAAPXX:VSQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VKS:XKXS, ASASPXX:VSQ:EPLT-AA[17]-LYY:VGRTPKV:EQLSN:VKS:XKXS, NDEGLEX:VSQ:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:VKS:KXEXR, NDEGLEX:VSQ:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:VKS:QXEXR, SSVKXQP:VSQ:EPLT-AA[17]-LYY:EYVRKKPKL:EQLSN:VKS:LEXAXA, RNVQXRP:VSQ:EPLT-AA[17]-LYY:EIVRKKPIF:EQLSN:VKS:LAXKXE, KIPKAXX:VPT:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLT-AA[17]-LYY:DENKNVV:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLT-AA[17]-

LYY:DDSSNVI:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLT-AA[17]-LYY:NDKQQII:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VEE:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VRS:XKXS, ASASPXX:VPQ:EPLT-AA[17]-LYY:VGRTPKV:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLT-AA[17]-LYY:EYVRKKPKL:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT-AA[17]-LYY:EIVRKKPIF:EQLSN:EDH:LAXKXE, KIPKAXX:VPQ:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VKS:GXGXR, GIPEPXX:VPQ:EPLT-AA[17]-LYY:DENKNVV:EQLSN:VKS:SXAXR, SIPKAXX:VPQ:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VKS:GXGXR, HVTKPTX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, YVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, TVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:AXGXH, AVPKAXX:VPQ:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VKS:AXGXH, KVGKAXX:VPQ:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VKS:XGXR, KASKAXX:VPQ:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT-AA[17]-LYY:NDKQQII:EQLSN:VKS:RXGXS, AAPASXX:VPQ:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VKS:SXGXR, HVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VKS:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLT-AA[17]-LYY:IGKTPKI:EQLSN:VKS:XKXS, NDEGLEX:VPQ:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:VKS:KXEXR, NDEGLEX:VPQ:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:VKS:QXEXR, SSVKXQP:VPQ:EPLT-AA[17]-LYY:EYVRKKPKL:EQLSN:VKS:LEXAXA, RNVQXRP:VPQ:EPLT-AA[17]-LYY:EIVRKKPIF:EQLSN:VKS:LAXKXE, ASASPXX:VSQ:EPLT-AA[17]-LYY:IGKTPKI:EQLSN:VKS:XKXS, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:IGEMS:QHN:GXGXR, GIPEPXX:VPT:SNIT-AA[17]-QIM:DENKNVV:IGEMS:QHN:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:IGEMS:QHN:GXGXR, HVTKPTX:VPT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:QHN:SXGXH, YVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:QHN:SXGXH, TVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:QHN:AXGXH, AVPKAXX:VPT:SNIT-AA[17]-QIM:DSSNNVI:IGEMS:QHN:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:IGEMS:QHN:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:IGEMS:QHN:EXGXR, GSAGPXX:VPT:SNIT-AA[17]-QIM:NDKQQII:IGEMS:QHN:RXGXS, AAPASXX:VPT:SNIT-AA[17]-QIM:DAANNVV:IGEMS:QHN:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:IGEMS:QHN:SXGXR, HVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:QHN:SXGXH, RVPSTXX:VPT:SNIT-AA[17]-QIM:DNGRVLL:IGEMS:QHN:XGXL, ASAAPXX:VPT:SNIT-AA[17]-QIM:VGRKPKV:IGEMS:QHN:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:IGKTPKI:IGEMS:QHN:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:VGRTPKV:IGEMS:QHN:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:IGEMS:QHN:QXEXR, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:IGEMS:QHN:KXEXR, SSVKXQP:VPT:SNIT-AA[17]-QIM:EYVRKKPKL:IGEMS:QHN:LEXAXA, RNVQXRP:VPT:SNIT-AA[17]-

QIM:EIVRKKPIF:IGEMS:QHN:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:IGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:DENKNVV:IGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:IGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:DSSNNVI:IGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:IGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:IGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:NDKQQII:IGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:DAANNVV:IGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:IGEMS:VVE:SXGXR, HVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:DNGRVLL:IGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:VGRKPKV:IGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGKTPKI:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:VGRTPKV:IGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:IGEMS:EHS:QXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:EYVRKKPKL:IGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:EIVRKKPIF:IGEMS:EDH:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:LGEMS:EHS:GXGXR, GIPEPXX:VPT:SNIT-AA[17]-QIM:DENKNVV:LGEMS:EHS:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:LGEMS:EHS:GXGXR, HVTKPTX:VPT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:EHS:SXGXH, YVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:EHS:SXGXH, TVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:EHS:AXGXH, AVPKAXX:VPT:SNIT-AA[17]-QIM:DSSNNVI:LGEMS:EHS:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:LGEMS:EHS:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:LGEMS:EHS:EXGXR, GSAGPXX:VPT:SNIT-AA[17]-QIM:NDKQQII:LGEMS:EHS:RXGXS, AAPASXX:VPT:SNIT-AA[17]-QIM:DAANNVV:LGEMS:EHS:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:LGEMS:EHS:SXGXR, HVPKPXX:VPT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:EHS:SXGXH, RVPSTXX:VPT:SNIT-AA[17]-QIM:DNGRVLL:LGEMS:EHS:XGXL, ASAAPXX:VPT:SNIT-AA[17]-QIM:VGRKPKV:LGEMS:EHS:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:IGKTPKI:LGEMS:EHS:XKXS, ASASPXX:VPT:SNIT-AA[17]-QIM:VGRTPKV:LGEMS:EHS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:LGEMS:EHS:KXEXR, SSVKXQP:VPT:SNIT-AA[17]-QIM:EYVRKKPKL:LGEMS:EHS:LEXAXA, RNVQXRP:VPT:SNIT-AA[17]-QIM:EIVRKKPIF:LGEMS:EHS:LAXKXE, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:LGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:DENKNVV:LGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:DSSNNVI:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:LGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:NDKQQII:LGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:DAANNVV:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:LGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:DNGRVLL:LGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:VGRKPKV:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGKTPKI:LGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:VGRTPKV:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:LGEMS:QHN:KXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:EYVRKKPKL:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-

QIM:EIVRKKPIF:LGEMS:EDH:LAXKXE, KIPKAXX:SRV:RSVK-AA[17]-AKV:DENEKVV:KEVQV:EEH:GXGXR, GIPEPXX:SRV:RSVK-AA[17]-AKV:DENKNVV:KEVQV:EEH:SXAXR, SIPKAXX:SRV:RSVK-AA[17]-AKV:DEYDKVV:KEVQV:EEH:GXGXR, HVTKPTX:SRV:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:EEH:SXGXH, YVPKPXX:SRV:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:EEH:SXGXH, TVPKPXX:SRV:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:EEH:AXGXH, AVPKAXX:SRV:RSVK-AA[17]-AKV:DSSNNVI:KEVQV:EEH:AXGXH, KVGKAXX:SRV:RSVK-AA[17]-AKV:DDMGVPT:KEVQV:EEH:XGXR, KASKAXX:SRV:RSVK-AA[17]-AKV:DKGVVTY:KEVQV:EEH:EXGXR, GSAGPXX:SRV:RSVK-AA[17]-AKV:NDKQQII:KEVQV:EEH:RXGXS, AAPASXX:SRV:RSVK-AA[17]-AKV:DAANNVV:KEVQV:EEH:AXGXR, STPPTXX:SRV:RSVK-AA[17]-AKV:DSANNVV:KEVQV:EEH:SXGXR, HVPKPXX:SRV:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:EEH:SXGXH, RVPSTXX:SRV:RSVK-AA[17]-AKV:DNGRVLL:KEVQV:EEH:XGXL, ASAAPXX:SRV:RSVK-AA[17]-AKV:VGRKPKV:KEVQV:EEH:XKXS, ASASPXX:SRV:RSVK-AA[17]-AKV:IGKTPKI:KEVQV:EEH:XKXS, ASASPXX:SRV:RSVK-AA[17]-AKV:VGRTPKV:KEVQV:EEH:XKXS, NDEGLEX:SRV:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:EEH:KXEXR, NDEGLEX:SRV:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:EEH:QXEXR, RNVQXRP:SRV:RSVK-AA[17]-AKV:EIVRKKPIF:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK-AA[17]-AKV:DENEKVV:KEVQV:VVE:GXGXR, GIPEPXX:VPE:RSVK-AA[17]-AKV:DENKNVV:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK-AA[17]-AKV:DEYDKVV:KEVQV:VVE:GXGXR, HVTKPTX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, TVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK-AA[17]-AKV:DSSNNVI:KEVQV:VVK:AXGXH, KVGKAXX:VPT:RSVK-AA[17]-AKV:DDMGVPT:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK-AA[17]-AKV:DKGVVTY:KEVQV:AVS:EXGXR, GSAGPXX:TPT:RSVK-AA[17]-AKV:NDKQQII:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK-AA[17]-AKV:DAANNVV:KEVQV:VVE:AXGXR, STPPTXX:VPT:RSVK-AA[17]-AKV:DSANNVV:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, RVPSTXX:APV:RSVK-AA[17]-AKV:DNGRVLL:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK-AA[17]-AKV:VGRKPKV:KEVQV:VRS:XKXS, ASASPXX:VSQ:RSVK-AA[17]-AKV:IGKTPKI:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK-AA[17]-AKV:VGRTPKV:KEVQV:VKS:XKXS, NDEGLEX:VPT:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:EHS:QXEXR, RNVQXRP:TQV:RSVK-AA[17]-AKV:EIVRKKPIF:KEVQV:EDH:LAXKXE, KIPKAXX:TQV:RPVQ-AA[17]-RKI:DENEKVV:KKATV:EDH:GXGXR, GIPEPXX:TQV:RPVQ-AA[17]-RKI:DENKNVV:KKATV:EDH:SXAXR, SIPKAXX:TQV:RPVQ-AA[17]-RKI:DEYDKVV:KKATV:EDH:GXGXR, HVTKPTX:TQV:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:EDH:SXGXH, YVPKPXX:TQV:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:EDH:SXGXH, TVPKPXX:TQV:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:EDH:AXGXH, AVPKAXX:TQV:RPVQ-AA[17]-RKI:DSSNNVI:KKATV:EDH:AXGXH, KVGKAXX:TQV:RPVQ-AA[17]-RKI:DDMGVPT:KKATV:EDH:XGXR, KASKAXX:TQV:RPVQ-AA[17]-RKI:DKGVVTY:KKATV:EDH:EXGXR, GSAGPXX:TQV:RPVQ-AA[17]-RKI:NDKQQII:KKATV:EDH:RXGXS, AAPASXX:TQV:RPVQ-AA[17]-RKI:DAANNVV:KKATV:EDH:AXGXR, STPPTXX:TQV:RPVQ-AA[17]-RKI:DSANNVV:KKATV:EDH:SXGXR, HVPKPXX:TQV:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:EDH:SXGXH, RVPSTXX:TQV:RPVQ-AA[17]-RKI:DNGRVLL:KKATV:EDH:XGXL, ASAAPXX:TQV:RPVQ-AA[17]-RKI:VGRKPKV:KKATV:EDH:XKXS, ASASPXX:TQV:RPVQ-AA[17]-RKI:IGKTPKI:KKATV:EDH:XKXS, ASASPXX:TQV:RPVQ-AA[17]-RKI:VGRTPKV:KKATV:EDH:XKXS,

NDEGLEX:TQV:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:EDH:KXEXR, NDEGLEX:TQV:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:EDH:QXEXR, SSVKXQP:TQV:RPVQ-AA[17]-RKI:EYVRKKPKL:KKATV:EDH:LEXAXA, KIPKAXX:VPT:RPVQ-AA[17]-RKI:DENEKVV:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ-AA[17]-RKI:DENKNVV:KKATV:TVE:SXAXR, SIPKAXX:VPT:RPVQ-AA[17]-RKI:DEYDKVV:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:SXGXH, YVPKPXX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:AXGXH, AVPKAXX:APT:RPVQ-AA[17]-RKI:DSSNNVI:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ-AA[17]-RKI:DDMGVPT:KKATV:VAE:XGXR, KASKAXX:VPT:RPVQ-AA[17]-RKI:DKGVVTY:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ-AA[17]-RKI:NDKQQII:KKATV:VVD:RXGXS, AAPASXX:VPA:RPVQ-AA[17]-RKI:DAANNVV:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ-AA[17]-RKI:DSANNVV:KKATV:VVE:SXGXR, HVPKPXX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ-AA[17]-RKI:DNGRVLL:KKATV:VEE:XGXL, ASAAPXX:VPQ:RPVQ-AA[17]-RKI:VGRKPKV:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ-AA[17]-RKI:IGKTPKI:KKATV:VKS:XKXS, ASASPXX:VPQ:RPVQ-AA[17]-RKI:VGRTPKV:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:QHN:KXEXR, NDEGLEX:VPT:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ-AA[17]-RKI:EYVRKKPKL:KKATV:EEH:LEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T). More particularly, the heptuplet PEP7:PEP3:PEP12:LINKER:PEP2:PEP4:PEP8 is selected from the group consisting of GIPEPXX:VPT:SAIS-AA[17]-LYL:DENKNVV:LKNYQ:VVE:SXAXR, HVTKPTX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, YVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:AXGXH, AVPKAXX:VPT:SAIS-AA[17]-LYL:DSSNNVI:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:DDMGVPT:LKNYQ:VVE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:DKGVVTY:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS-AA[17]-LYL:NDKQQII:LKNYQ:VVE:RXGXS, AAPASXX:VPT:SAIS-AA[17]-LYL:DAANNVV:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS-AA[17]-LYL:DSANNVV:LKNYQ:VVE:SXGXR, HVPKPXX:VPT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVE:SXGXH, RVPSTXX:VPT:SAIS-AA[17]-LYL:DNGRVLL:LKNYQ:VVE:XGXL, ASAAPXX:VPT:SAIS-AA[17]-LYL:VGRKPKV:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:IGKTPKI:LKNYQ:VVE:XKXS, ASASPXX:VPT:SAIS-AA[17]-LYL:VGRTPKV:LKNYQ:VVE:XKXS, GIPEPXX:VPE:SAIS-AA[17]-LYL:DENKNVV:LKNYQ:TVE:SXAXR, HVTKPTX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, YVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, TVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:AXGXH, AVPKAXX:APT:SAIS-AA[17]-LYL:DSSNNVI:LKNYQ:VVK:AXGXH, KVGKAXX:VPT:SAIS-AA[17]-LYL:DDMGVPT:LKNYQ:VAE:XGXR, KASKAXX:VPT:SAIS-AA[17]-LYL:DKGVVTY:LKNYQ:AVS:EXGXR, GSAGPXX:TPT:SAIS-AA[17]-LYL:NDKQQII:LKNYQ:VVD:RXGXS, AAPASXX:VPA:SAIS-AA[17]-LYL:DAANNVV:LKNYQ:VVE:AXGXR, HVPKPXX:APT:SAIS-AA[17]-LYL:DDSSNVI:LKNYQ:VVR:SXGXH, RVPSTXX:APV:SAIS-AA[17]-LYL:DNGRVLL:LKNYQ:VEE:XGXL, ASAAPXX:VPQ:SAIS-AA[17]-LYL:VGRKPKV:LKNYQ:VRS:XKXS, ASASPXX:VSQ:SAIS-AA[17]-LYL:IGKTPKI:LKNYQ:VKS:XKXS, ASASPXX:VPQ:SAIS-AA[17]-LYL:VGRTPKV:LKNYQ:VKS:XKXS, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:QHN:KXEXR, NDEGLEX:VPT:SAIS-AA[17]-LYL:RIKPHQGQH:LKNYQ:EHS:QXEXR, SSVKXQP:SRV:SAIS-AA[17]-LYL:EYVRKKPKL:LKNYQ:EEH:LEXAXA, RNVQXRP:TQV:SAIS-AA[17]-

LYL:EIVRKKPIF:LKNYQ:EDH:LAXKXE, KIPKAXX:VPE:SSLS-AA[17]-LFF:DENEKVV:LKVYP:TVE:GXGXR, SIPKAXX:VPE:SSLS-AA[17]-LFF:DEYDKVV:LKVYP:TVE:GXGXR, HVTKPTX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, YVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, TVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:AXGXH, AVPKAXX:VPE:SSLS-AA[17]-LFF:DSSNNVI:LKVYP:TVE:AXGXH, KVGKAXX:VPE:SSLS-AA[17]-LFF:DDMGVPT:LKVYP:TVE:XGXR, KASKAXX:VPE:SSLS-AA[17]-LFF:DKGVVTY:LKVYP:TVE:EXGXR, GSAGPXX:VPE:SSLS-AA[17]-LFF:NDKQQII:LKVYP:TVE:RXGXS, AAPASXX:VPE:SSLS-AA[17]-LFF:DAANNVV:LKVYP:TVE:AXGXR, STPPTXX:VPE:SSLS-AA[17]-LFF:DSANNVV:LKVYP:TVE:SXGXR, HVPKPXX:VPE:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:TVE:SXGXH, RVPSTXX:VPE:SSLS-AA[17]-LFF:DNGRVLL:LKVYP:TVE:XGXL, ASAAPXX:VPE:SSLS-AA[17]-LFF:VGRKPKV:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:IGKTPKI:LKVYP:TVE:XKXS, ASASPXX:VPE:SSLS-AA[17]-LFF:VGRTPKV:LKVYP:TVE:XKXS, KIPKAXX:VPT:SSLS-AA[17]-LFF:DENEKVV:LKVYP:VVE:GXGXR, SIPKAXX:VPT:SSLS-AA[17]-LFF:DEYDKVV:LKVYP:VVE:GXGXR, HVTKPTX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, YVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, TVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:AXGXH, AVPKAXX:APT:SSLS-AA[17]-LFF:DSSNNVI:LKVYP:VVK:AXGXH, KVGKAXX:VPT:SSLS-AA[17]-LFF:DDMGVPT:LKVYP:VAE:XGXR, KASKAXX:VPT:SSLS-AA[17]-LFF:DKGVVTY:LKVYP:AVS:EXGXR, GSAGPXX:TPT:SSLS-AA[17]-LFF:NDKQQII:LKVYP:VVD:RXGXS, AAPASXX:VPA:SSLS-AA[17]-LFF:DAANNVV:LKVYP:VVE:AXGXR, STPPTXX:VPT:SSLS-AA[17]-LFF:DSANNVV:LKVYP:VVE:SXGXR, HVPKPXX:APT:SSLS-AA[17]-LFF:DDSSNVI:LKVYP:VVR:SXGXH, RVPSTXX:APV:SSLS-AA[17]-LFF:DNGRVLL:LKVYP:VEE:XGXL, ASAAPXX:VPQ:SSLS-AA[17]-LFF:VGRKPKV:LKVYP:VRS:XKXS, ASASPXX:VSQ:SSLS-AA[17]-LFF:IGKTPKI:LKVYP:VKS:XKXS, ASASPXX:VPQ:SSLS-AA[17]-LFF:VGRTPKV:LKVYP:VKS:XKXS, NDEGLEX:VPT:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:QHN:KXEXR, NDEGLEX:VPT:SSLS-AA[17]-LFF:RIKPHQGQH:LKVYP:EHS:QXEXR, SSVKXQP:SRV:SSLS-AA[17]-LFF:EYVRKKPKL:LKVYP:EEH:LEXAXA, RNVQXRP:TQV:SSLS-AA[17]-LFF:EIVRKKPIF:LKVYP:EDH:LAXKXE, KIPKAXX:APT:NAIS-AA[17]-LYF:DENEKVV:LKKYR:VVR:GXGXR, GIPEPXX:APT:NAIS-AA[17]-LYF:DENKNVV:LKKYR:VVR:SXAXR, SIPKAXX:APT:NAIS-AA[17]-LYF:DEYDKVV:LKKYR:VVR:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:DSSNNVI:LKKYR:VVR:AXGXH, KVGKAXX:APT:NAIS-AA[17]-LYF:DDMGVPT:LKKYR:VVR:XGXR, KASKAXX:APT:NAIS-AA[17]-LYF:DKGVVTY:LKKYR:VVR:EXGXR, GSAGPXX:APT:NAIS-AA[17]-LYF:NDKQQII:LKKYR:VVR:RXGXS, AAPASXX:APT:NAIS-AA[17]-LYF:DAANNVV:LKKYR:VVR:AXGXR, STPPTXX:APT:NAIS-AA[17]-LYF:DSANNVV:LKKYR:VVR:SXGXR, RVPSTXX:APT:NAIS-AA[17]-LYF:DNGRVLL:LKKYR:VVR:XGXL, ASAAPXX:APT:NAIS-AA[17]-LYF:VGRKPKV:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:IGKTPKI:LKKYR:VVR:XKXS, ASASPXX:APT:NAIS-AA[17]-LYF:VGRTPKV:LKKYR:VVR:XKXS, KIPKAXX:VPT:NAIS-AA[17]-LYF:DENEKVV:LKKYR:VVE:GXGXR, GIPEPXX:VPE:NAIS-AA[17]-LYF:DENKNVV:LKKYR:TVE:SXAXR, SIPKAXX:VPT:NAIS-AA[17]-LYF:DEYDKVV:LKKYR:VVE:GXGXR, AVPKAXX:APT:NAIS-AA[17]-LYF:DSSNNVI:LKKYR:VVK:AXGXH, KVGKAXX:VPT:NAIS-AA[17]-LYF:DDMGVPT:LKKYR:VAE:XGXR, KASKAXX:VPT:NAIS-AA[17]-LYF:DKGVVTY:LKKYR:AVS:EXGXR, GSAGPXX:TPT:NAIS-AA[17]-LYF:NDKQQII:LKKYR:VVD:RXGXS, AAPASXX:VPA:NAIS-AA[17]-LYF:DAANNVV:LKKYR:VVE:AXGXR, STPPTXX:VPT:NAIS-AA[17]-LYF:DSANNVV:LKKYR:VVE:SXGXR, RVPSTXX:APV:NAIS-AA[17]-LYF:DNGRVLL:LKKYR:VEE:XGXL, ASAAPXX:VPQ:NAIS-AA[17]-LYF:VGRKPKV:LKKYR:VRS:XKXS, ASASPXX:VSQ:NAIS-AA[17]-LYF:IGKTPKI:LKKYR:VKS:XKXS,

ASASPXX:VPQ:NAIS-AA[17]-LYF:VGRTPKV:LKKYR:VKS:XKXS, NDEGLEX:VPT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:QHN:KXEXR, NDEGLEX:VPT:NAIS-AA[17]-LYF:RIKPHQGQH:LKKYR:EHS:QXEXR, SSVKXQP:SRV:NAIS-AA[17]-LYF:EYVRKKPKL:LKKYR:EEH:LEXAXA, RNVQXRP:TQV:NAIS-AA[17]-LYF:EIVRKKPIF:LKKYR:EDH:LAXKXE, KIPKAXX:APT:SATS-AA[17]-LYY:DENEKVV:LRKHR:VVK:GXGXR, GIPEPXX:APT:SATS-AA[17]-LYY:DENKNVV:LRKHR:VVK:SXAXR, SIPKAXX:APT:SATS-AA[17]-LYY:DEYDKVV:LRKHR:VVK:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:AXGXH, KVGKAXX:APT:SATS-AA[17]-LYY:DDMGVPT:LRKHR:VVK:XGXR, KASKAXX:APT:SATS-AA[17]-LYY:DKGVVTY:LRKHR:VVK:EXGXR, GSAGPXX:APT:SATS-AA[17]-LYY:NDKQQII:LRKHR:VVK:RXGXS, AAPASXX:APT:SATS-AA[17]-LYY:DAANNVV:LRKHR:VVK:AXGXR, STPPTXX:APT:SATS-AA[17]-LYY:DSANNVV:LRKHR:VVK:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVK:SXGXH, RVPSTXX:APT:SATS-AA[17]-LYY:DNGRVLL:LRKHR:VVK:XGXL, ASAAPXX:APT:SATS-AA[17]-LYY:VGRKPKV:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:IGKTPKI:LRKHR:VVK:XKXS, ASASPXX:APT:SATS-AA[17]-LYY:VGRTPKV:LRKHR:VVK:XKXS, KIPKAXX:VPT:SATS-AA[17]-LYY:DENEKVV:LRKHR:VVE:GXGXR, GIPEPXX:VPE:SATS-AA[17]-LYY:DENKNVV:LRKHR:TVE:SXAXR, SIPKAXX:VPT:SATS-AA[17]-LYY:DEYDKVV:LRKHR:VVE:GXGXR, HVTKPTX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, YVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, TVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:AXGXH, KVGKAXX:VPT:SATS-AA[17]-LYY:DDMGVPT:LRKHR:VAE:XGXR, KASKAXX:VPT:SATS-AA[17]-LYY:DKGVVTY:LRKHR:AVS:EXGXR, GSAGPXX:TPT:SATS-AA[17]-LYY:NDKQQII:LRKHR:VVD:RXGXS, AAPASXX:VPA:SATS-AA[17]-LYY:DAANNVV:LRKHR:VVE:AXGXR, STPPTXX:VPT:SATS-AA[17]-LYY:DSANNVV:LRKHR:VVE:SXGXR, HVPKPXX:APT:SATS-AA[17]-LYY:DDSSNVI:LRKHR:VVR:SXGXH, RVPSTXX:APV:SATS-AA[17]-LYY:DNGRVLL:LRKHR:VEE:XGXL, ASAAPXX:VPQ:SATS-AA[17]-LYY:VGRKPKV:LRKHR:VRS:XKXS, ASASPXX:VSQ:SATS-AA[17]-LYY:IGKTPKI:LRKHR:VKS:XKXS, ASASPXX:VPQ:SATS-AA[17]-LYY:VGRTPKV:LRKHR:VKS:XKXS, NDEGLEX:VPT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:QHN:KXEXR, NDEGLEX:VPT:SATS-AA[17]-LYY:RIKPHQGQH:LRKHR:EHS:QXEXR, SSVKXQP:SRV:SATS-AA[17]-LYY:EYVRKKPKL:LRKHR:EEH:LEXAXA, RNVQXRP:TQV:SATS-AA[17]-LYY:EIVRKKPIF:LRKHR:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LYK:DENEKVV:LKYHY:VAE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LYK:DENKNVV:LKYHY:VAE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYK:DEYDKVV:LKYHY:VAE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LYK:DSSNNVI:LKYHY:VAE:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:DKGVVTY:LKYHY:VAE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LYK:NDKQQII:LKYHY:VAE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LYK:DAANNVV:LKYHY:VAE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:DSANNVV:LKYHY:VAE:SXGXR, HVPKPXX:VPT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VAE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LYK:DNGRVLL:LKYHY:VAE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LYK:VGRKPKV:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:IGKTPKI:LKYHY:VAE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LYK:VGRTPKV:LKYHY:VAE:XKXS, KIPKAXX:VPT:SPIS-AA[17]-LYK:DENEKVV:LKYHY:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYK:DENKNVV:LKYHY:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-

LYK:DEYDKVV:LKYHY:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYK:DSSNNVI:LKYHY:VVK:AXGXH, KASKAXX:VPT:SPIS-AA[17]-LYK:DKGVVTY:LKYHY:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYK:NDKQQII:LKYHY:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LYK:DAANNVV:LKYHY:VVE:AXGXR, STPPTXX:VPT:SPIS-AA[17]-LYK:DSANNVV:LKYHY:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYK:DDSSNVI:LKYHY:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYK:DNGRVLL:LKYHY:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYK:VGRKPKV:LKYHY:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYK:IGKTPKI:LKYHY:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYK:VGRTPKV:LKYHY:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYK:RIKPHQGQH:LKYHY:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYK:EYVRKKPKL:LKYHY:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYK:EIVRKKPIF:LKYHY:EDH:LAXKXE, KIPKAXX:VPT:EPIS-AA[17]-LYL:DENEKVV:KFKYE:AVS:GXGXR, GIPEPXX:VPT:EPIS-AA[17]-LYL:DENKNVV:KFKYE:AVS:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:DEYDKVV:KFKYE:AVS:GXGXR, HVTKPTX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, YVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, TVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:AXGXH, AVPKAXX:VPT:EPIS-AA[17]-LYL:DSSNNVI:KFKYE:AVS:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:DDMGVPT:KFKYE:AVS:XGXR, GSAGPXX:VPT:EPIS-AA[17]-LYL:NDKQQII:KFKYE:AVS:RXGXS, AAPASXX:VPT:EPIS-AA[17]-LYL:DAANNVV:KFKYE:AVS:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:DSANNVV:KFKYE:AVS:SXGXR, HVPKPXX:VPT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:AVS:SXGXH, RVPSTXX:VPT:EPIS-AA[17]-LYL:DNGRVLL:KFKYE:AVS:XGXL, ASAAPXX:VPT:EPIS-AA[17]-LYL:VGRKPKV:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:IGKTPKI:KFKYE:AVS:XKXS, ASASPXX:VPT:EPIS-AA[17]-LYL:VGRTPKV:KFKYE:AVS:XKXS, KIPKAXX:VPT:EPIS-AA[17]-LYL:DENEKVV:KFKYE:VVE:GXGXR, GIPEPXX:VPE:EPIS-AA[17]-LYL:DENKNVV:KFKYE:TVE:SXAXR, SIPKAXX:VPT:EPIS-AA[17]-LYL:DEYDKVV:KFKYE:VVE:GXGXR, HVTKPTX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:SXGXH, YVPKPXX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:SXGXH, TVPKPXX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:AXGXH, AVPKAXX:APT:EPIS-AA[17]-LYL:DSSNNVI:KFKYE:VVK:AXGXH, KVGKAXX:VPT:EPIS-AA[17]-LYL:DDMGVPT:KFKYE:VAE:XGXR, GSAGPXX:TPT:EPIS-AA[17]-LYL:NDKQQII:KFKYE:VVD:RXGXS, AAPASXX:VPA:EPIS-AA[17]-LYL:DAANNVV:KFKYE:VVE:AXGXR, STPPTXX:VPT:EPIS-AA[17]-LYL:DSANNVV:KFKYE:VVE:SXGXR, HVPKPXX:APT:EPIS-AA[17]-LYL:DDSSNVI:KFKYE:VVR:SXGXH, RVPSTXX:APV:EPIS-AA[17]-LYL:DNGRVLL:KFKYE:VEE:XGXL, ASAAPXX:VPQ:EPIS-AA[17]-LYL:VGRKPKV:KFKYE:VRS:XKXS, ASASPXX:VSQ:EPIS-AA[17]-LYL:IGKTPKI:KFKYE:VKS:XKXS, ASASPXX:VPQ:EPIS-AA[17]-LYL:VGRTPKV:KFKYE:VKS:XKXS, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:QHN:KXEXR, NDEGLEX:VPT:EPIS-AA[17]-LYL:RIKPHQGQH:KFKYE:EHS:QXEXR, SSVKXQP:SRV:EPIS-AA[17]-LYL:EYVRKKPKL:KFKYE:EEH:LEXAXA, RNVQXRP:TQV:EPIS-AA[17]-LYL:EIVRKKPIF:KFKYE:EDH:LAXKXE, KIPKAXX:TPT:SPIN-AA[17]-LYF:DENEKVV:YGKIP:VVD:GXGXR, GIPEPXX:TPT:SPIN-AA[17]-LYF:DENKNVV:YGKIP:VVD:SXAXR, SIPKAXX:TPT:SPIN-AA[17]-LYF:DEYDKVV:YGKIP:VVD:GXGXR, HVTKPTX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, YVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, TVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:AXGXH, AVPKAXX:TPT:SPIN-AA[17]-LYF:DSSNNVI:YGKIP:VVD:AXGXH,

KVGKAXX:TPT:SPIN-AA[17]-LYF:DDMGVPT:YGKIP:VVD:XGXR, KASKAXX:TPT:SPIN-AA[17]-LYF:DKGVVTY:YGKIP:VVD:EXGXR, AAPASXX:TPT:SPIN-AA[17]-LYF:DAANNVV:YGKIP:VVD:AXGXR, STPPTXX:TPT:SPIN-AA[17]-LYF:DSANNVV:YGKIP:VVD:SXGXR, HVPKPXX:TPT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVD:SXGXH, RVPSTXX:TPT:SPIN-AA[17]-LYF:DNGRVLL:YGKIP:VVD:XGXL, ASAAPXX:TPT:SPIN-AA[17]-LYF:VGRKPKV:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:IGKTPKI:YGKIP:VVD:XKXS, ASASPXX:TPT:SPIN-AA[17]-LYF:VGRTPKV:YGKIP:VVD:XKXS, KIPKAXX:VPT:SPIN-AA[17]-LYF:DENEKVV:YGKIP:VVE:GXGXR, GIPEPXX:VPE:SPIN-AA[17]-LYF:DENKNVV:YGKIP:TVE:SXAXR, SIPKAXX:VPT:SPIN-AA[17]-LYF:DEYDKVV:YGKIP:VVE:GXGXR, HVTKPTX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, YVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, TVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:AXGXH, AVPKAXX:APT:SPIN-AA[17]-LYF:DSSNNVI:YGKIP:VVK:AXGXH, KVGKAXX:VPT:SPIN-AA[17]-LYF:DDMGVPT:YGKIP:VAE:XGXR, KASKAXX:VPT:SPIN-AA[17]-LYF:DKGVVTY:YGKIP:AVS:EXGXR, AAPASXX:VPA:SPIN-AA[17]-LYF:DAANNVV:YGKIP:VVE:AXGXR, STPPTXX:VPT:SPIN-AA[17]-LYF:DSANNVV:YGKIP:VVE:SXGXR, HVPKPXX:APT:SPIN-AA[17]-LYF:DDSSNVI:YGKIP:VVR:SXGXH, RVPSTXX:APV:SPIN-AA[17]-LYF:DNGRVLL:YGKIP:VEE:XGXL, ASAAPXX:VPQ:SPIN-AA[17]-LYF:VGRKPKV:YGKIP:VRS:XKXS, ASASPXX:VSQ:SPIN-AA[17]-LYF:IGKTPKI:YGKIP:VKS:XKXS, ASASPXX:VPQ:SPIN-AA[17]-LYF:VGRTPKV:YGKIP:VKS:XKXS, NDEGLEX:VPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:QHN:KXEXR, NDEGLEX:VPT:SPIN-AA[17]-LYF:RIKPHQGQH:YGKIP:EHS:QXEXR, SSVKXQP:SRV:SPIN-AA[17]-LYF:EYVRKKPKL:YGKIP:EEH:LEXAXA, RNVQXRP:TQV:SPIN-AA[17]-LYF:EIVRKKPIF:YGKIP:EDH:LAXKXE, KIPKAXX:VPA:SPIS-AA[17]-LYI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPA:SPIS-AA[17]-LYI:DENKNVV:YKQYE:VVE:SXAXR, SIPKAXX:VPA:SPIS-AA[17]-LYI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:SXGXH, YVPKPXX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:SXGXH, TVPKPXX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:AXGXH, AVPKAXX:VPA:SPIS-AA[17]-LYI:DSSNNVI:YKQYE:VVE:AXGXH, KVGKAXX:VPA:SPIS-AA[17]-LYI:DDMGVPT:YKQYE:VVE:XGXR, KASKAXX:VPA:SPIS-AA[17]-LYI:DKGVVTY:YKQYE:VVE:EXGXR, GSAGPXX:VPA:SPIS-AA[17]-LYI:NDKQQII:YKQYE:VVE:RXGXS, STPPTXX:VPA:SPIS-AA[17]-LYI:DSANNVV:YKQYE:VVE:SXGXR, HVPKPXX:VPA:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVE:SXGXH, RVPSTXX:VPA:SPIS-AA[17]-LYI:DNGRVLL:YKQYE:VVE:XGXL, ASAAPXX:VPA:SPIS-AA[17]-LYI:VGRKPKV:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:IGKTPKI:YKQYE:VVE:XKXS, ASASPXX:VPA:SPIS-AA[17]-LYI:VGRTPKV:YKQYE:VVE:XKXS, KIPKAXX:VPT:SPIS-AA[17]-LYI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPE:SPIS-AA[17]-LYI:DENKNVV:YKQYE:TVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LYI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LYI:DSSNNVI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LYI:DDMGVPT:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LYI:DKGVVTY:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LYI:NDKQQII:YKQYE:VVD:RXGXS, STPPTXX:VPT:SPIS-AA[17]-LYI:DSANNVV:YKQYE:VVE:SXGXR, HVPKPXX:APT:SPIS-AA[17]-LYI:DDSSNVI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LYI:DNGRVLL:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LYI:VGRKPKV:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LYI:IGKTPKI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LYI:VGRTPKV:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-

LYI:RIKPHQGQH:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LYI:RIKPHQGQH:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LYI:EYVRKKPKL:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LYI:EIVRKKPIF:YKQYE:EDH:LAXKXE, KIPKAXX:VPT:SPIS-AA[17]-LFI:DENEKVV:YKQYE:VVE:GXGXR, GIPEPXX:VPT:SPIS-AA[17]-LFI:DENKNVV:YKQYE:VVE:SXAXR, SIPKAXX:VPT:SPIS-AA[17]-LFI:DEYDKVV:YKQYE:VVE:GXGXR, HVTKPTX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, YVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, TVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:AXGXH, AVPKAXX:VPT:SPIS-AA[17]-LFI:DSSNNVI:YKQYE:VVE:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:DDMGVPT:YKQYE:VVE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:DKGVVTY:YKQYE:VVE:EXGXR, GSAGPXX:VPT:SPIS-AA[17]-LFI:NDKQQII:YKQYE:VVE:RXGXS, AAPASXX:VPT:SPIS-AA[17]-LFI:DAANNVV:YKQYE:VVE:AXGXR, HVPKPXX:VPT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVE:SXGXH, RVPSTXX:VPT:SPIS-AA[17]-LFI:DNGRVLL:YKQYE:VVE:XGXL, ASAAPXX:VPT:SPIS-AA[17]-LFI:VGRKPKV:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:IGKTPKI:YKQYE:VVE:XKXS, ASASPXX:VPT:SPIS-AA[17]-LFI:VGRTPKV:YKQYE:VVE:XKXS, GIPEPXX:VPE:SPIS-AA[17]-LFI:DENKNVV:YKQYE:TVE:SXAXR, HVTKPTX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, YVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, TVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:AXGXH, AVPKAXX:APT:SPIS-AA[17]-LFI:DSSNNVI:YKQYE:VVK:AXGXH, KVGKAXX:VPT:SPIS-AA[17]-LFI:DDMGVPT:YKQYE:VAE:XGXR, KASKAXX:VPT:SPIS-AA[17]-LFI:DKGVVTY:YKQYE:AVS:EXGXR, GSAGPXX:TPT:SPIS-AA[17]-LFI:NDKQQII:YKQYE:VVD:RXGXS, AAPASXX:VPA:SPIS-AA[17]-LFI:DAANNVV:YKQYE:VVE:AXGXR, HVPKPXX:APT:SPIS-AA[17]-LFI:DDSSNVI:YKQYE:VVR:SXGXH, RVPSTXX:APV:SPIS-AA[17]-LFI:DNGRVLL:YKQYE:VEE:XGXL, ASAAPXX:VPQ:SPIS-AA[17]-LFI:VGRKPKV:YKQYE:VRS:XKXS, ASASPXX:VSQ:SPIS-AA[17]-LFI:IGKTPKI:YKQYE:VKS:XKXS, ASASPXX:VPQ:SPIS-AA[17]-LFI:VGRTPKV:YKQYE:VKS:XKXS, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:QHN:KXEXR, NDEGLEX:VPT:SPIS-AA[17]-LFI:RIKPHQGQH:YKQYE:EHS:QXEXR, SSVKXQP:SRV:SPIS-AA[17]-LFI:EYVRKKPKL:YKQYE:EEH:LEXAXA, RNVQXRP:TQV:SPIS-AA[17]-LFI:EIVRKKPIF:YKQYE:EDH:LAXKXE, KIPKAXX:APV:KPLS-AA[17]-LYV:DENEKVV:DHHKD:VEE:GXGXR, GIPEPXX:APV:KPLS-AA[17]-LYV:DENKNVV:DHHKD:VEE:SXAXR, SIPKAXX:APV:KPLS-AA[17]-LYV:DEYDKVV:DHHKD:VEE:GXGXR, HVTKPTX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, YVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, TVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:AXGXH, AVPKAXX:APV:KPLS-AA[17]-LYV:DSSNNVI:DHHKD:VEE:AXGXH, KVGKAXX:APV:KPLS-AA[17]-LYV:DDMGVPT:DHHKD:VEE:XGXR, KASKAXX:APV:KPLS-AA[17]-LYV:DKGVVTY:DHHKD:VEE:EXGXR, GSAGPXX:APV:KPLS-AA[17]-LYV:NDKQQII:DHHKD:VEE:RXGXS, AAPASXX:APV:KPLS-AA[17]-LYV:DAANNVV:DHHKD:VEE:AXGXR, STPPTXX:APV:KPLS-AA[17]-LYV:DSANNVV:DHHKD:VEE:SXGXR, HVPKPXX:APV:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VEE:SXGXH, ASAAPXX:APV:KPLS-AA[17]-LYV:VGRKPKV:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:IGKTPKI:DHHKD:VEE:XKXS, ASASPXX:APV:KPLS-AA[17]-LYV:VGRTPKV:DHHKD:VEE:XKXS, KIPKAXX:VPT:KPLS-AA[17]-LYV:DENEKVV:DHHKD:VVE:GXGXR, GIPEPXX:VPE:KPLS-AA[17]-LYV:DENKNVV:DHHKD:TVE:SXAXR, SIPKAXX:VPT:KPLS-AA[17]-LYV:DEYDKVV:DHHKD:VVE:GXGXR, HVTKPTX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, YVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, TVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:AXGXH, AVPKAXX:APT:KPLS-AA[17]-LYV:DSSNNVI:DHHKD:VVK:AXGXH,

KVGKAXX:VPT:KPLS-AA[17]-LYV:DDMGVPT:DHHKD:VAE:XGXR, KASKAXX:VPT:KPLS-AA[17]-LYV:DKGVVTY:DHHKD:AVS:EXGXR, GSAGPXX:TPT:KPLS-AA[17]-LYV:NDKQQII:DHHKD:VVD:RXGXS, AAPASXX:VPA:KPLS-AA[17]-LYV:DAANNVV:DHHKD:VVE:AXGXR, STPPTXX:VPT:KPLS-AA[17]-LYV:DSANNVV:DHHKD:VVE:SXGXR, HVPKPXX:APT:KPLS-AA[17]-LYV:DDSSNVI:DHHKD:VVR:SXGXH, ASAAPXX:VPQ:KPLS-AA[17]-LYV:VGRKPKV:DHHKD:VRS:XKXS, ASASPXX:VSQ:KPLS-AA[17]-LYV:IGKTPKI:DHHKD:VKS:XKXS, ASASPXX:VPQ:KPLS-AA[17]-LYV:VGRTPKV:DHHKD:VKS:XKXS, NDEGLEX:VPT:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:QHN:KXEXR, NDEGLEX:VPT:KPLS-AA[17]-LYV:RIKPHQGQH:DHHKD:EHS:QXEXR, SSVKXQP:SRV:KPLS-AA[17]-LYV:EYVRKKPKL:DHHKD:EEH:LEXAXA, RNVQXRP:TQV:KPLS-AA[17]-LYV:EIVRKKPIF:DHHKD:EDH:LAXKXE, KIPKAXX:VPQ:EPLP-AA[17]-VYY:DENEKVV:EQLSN:VRS:GXGXR, GIPEPXX:VPQ:EPLP-AA[17]-VYY:DENKNVV:EQLSN:VRS:SXAXR, SIPKAXX:VPQ:EPLP-AA[17]-VYY:DEYDKVV:EQLSN:VRS:GXGXR, HVTKPTX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, YVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, TVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:AXGXH, AVPKAXX:VPQ:EPLP-AA[17]-VYY:DSSNNVI:EQLSN:VRS:AXGXH, KVGKAXX:VPQ:EPLP-AA[17]-VYY:DDMGVPT:EQLSN:VRS:XGXR, KASKAXX:VPQ:EPLP-AA[17]-VYY:DKGVVTY:EQLSN:VRS:EXGXR, GSAGPXX:VPQ:EPLP-AA[17]-VYY:NDKQQII:EQLSN:VRS:RXGXS, AAPASXX:VPQ:EPLP-AA[17]-VYY:DAANNVV:EQLSN:VRS:AXGXR, STPPTXX:VPQ:EPLP-AA[17]-VYY:DSANNVV:EQLSN:VRS:SXGXR, HVPKPXX:VPQ:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VRS:SXGXH, RVPSTXX:VPQ:EPLP-AA[17]-VYY:DNGRVLL:EQLSN:VRS:XGXL, ASASPXX:VPQ:EPLP-AA[17]-VYY:IGKTPKI:EQLSN:VRS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:VGRTPKV:EQLSN:VRS:XKXS, KIPKAXX:VPT:EPLP-AA[17]-VYY:DENEKVV:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLP-AA[17]-VYY:DENKNVV:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLP-AA[17]-VYY:DEYDKVV:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLP-AA[17]-VYY:DSSNNVI:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLP-AA[17]-VYY:DDMGVPT:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLP-AA[17]-VYY:DKGVVTY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLP-AA[17]-VYY:NDKQQII:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLP-AA[17]-VYY:DAANNVV:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLP-AA[17]-VYY:DSANNVV:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLP-AA[17]-VYY:DDSSNVI:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLP-AA[17]-VYY:DNGRVLL:EQLSN:VEE:XGXL, ASASPXX:VSQ:EPLP-AA[17]-VYY:IGKTPKI:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLP-AA[17]-VYY:VGRTPKV:EQLSN:VKS:XKXS, NDEGLEX:VPT:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLP-AA[17]-VYY:RIKPHQGQH:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLP-AA[17]-VYY:EYVRKKPKL:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLP-AA[17]-VYY:EIVRKKPIF:EQLSN:EDH:LAXKXE, KIPKAXX:VSQ:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VKS:GXGXR, GIPEPXX:VSQ:EPLT-AA[17]-LYY:DENKNVV:EQLSN:VKS:SXAXR, SIPKAXX:VSQ:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VKS:GXGXR, HVTKPTX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, YVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, TVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:AXGXH, AVPKAXX:VSQ:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VKS:AXGXH, KVGKAXX:VSQ:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VKS:XGXR, KASKAXX:VSQ:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:VKS:EXGXR, GSAGPXX:VSQ:EPLT-AA[17]-

LYY:NDKQQII:EQLSN:VKS:RXGXS, AAPASXX:VSQ:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VKS:AXGXR, STPPTXX:VSQ:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VKS:SXGXR, HVPKPXX:VSQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, RVPSTXX:VSQ:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VKS:XGXL, ASAAPXX:VSQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VKS:XKXS, ASASPXX:VSQ:EPLT-AA[17]-LYY:VGRTPKV:EQLSN:VKS:XKXS, KIPKAXX:VPT:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VVE:GXGXR, GIPEPXX:VPE:EPLT-AA[17]-LYY:DENKNVV:EQLSN:TVE:SXAXR, SIPKAXX:VPT:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VVE:GXGXR, HVTKPTX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:SXGXH, YVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:SXGXH, TVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:AXGXH, AVPKAXX:APT:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VVK:AXGXH, KVGKAXX:VPT:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VAE:XGXR, KASKAXX:VPT:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:AVS:EXGXR, GSAGPXX:TPT:EPLT-AA[17]-LYY:NDKQQII:EQLSN:VVD:RXGXS, AAPASXX:VPA:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VVE:AXGXR, STPPTXX:VPT:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VVE:SXGXR, HVPKPXX:APT:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VVR:SXGXH, RVPSTXX:APV:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VEE:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VRS:XKXS, NDEGLEX:VPT:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:QHN:KXEXR, NDEGLEX:VPT:EPLT-AA[17]-LYY:RIKPHQGQH:EQLSN:EHS:QXEXR, SSVKXQP:SRV:EPLT-AA[17]-LYY:EYVRKKPKL:EQLSN:EEH:LEXAXA, RNVQXRP:TQV:EPLT-AA[17]-LYY:EIVRKKPIF:EQLSN:EDH:LAXKXE, KIPKAXX:VPQ:EPLT-AA[17]-LYY:DENEKVV:EQLSN:VKS:GXGXR, GIPEPXX:VPQ:EPLT-AA[17]-LYY:DENKNVV:EQLSN:VKS:SXAXR, SIPKAXX:VPQ:EPLT-AA[17]-LYY:DEYDKVV:EQLSN:VKS:GXGXR, HVTKPTX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, YVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, TVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:AXGXH, AVPKAXX:VPQ:EPLT-AA[17]-LYY:DSSNNVI:EQLSN:VKS:AXGXH, KVGKAXX:VPQ:EPLT-AA[17]-LYY:DDMGVPT:EQLSN:VKS:XGXR, KASKAXX:VPQ:EPLT-AA[17]-LYY:DKGVVTY:EQLSN:VKS:EXGXR, GSAGPXX:VPQ:EPLT-AA[17]-LYY:NDKQQII:EQLSN:VKS:RXGXS, AAPASXX:VPQ:EPLT-AA[17]-LYY:DAANNVV:EQLSN:VKS:AXGXR, STPPTXX:VPQ:EPLT-AA[17]-LYY:DSANNVV:EQLSN:VKS:SXGXR, HVPKPXX:VPQ:EPLT-AA[17]-LYY:DDSSNVI:EQLSN:VKS:SXGXH, RVPSTXX:VPQ:EPLT-AA[17]-LYY:DNGRVLL:EQLSN:VKS:XGXL, ASAAPXX:VPQ:EPLT-AA[17]-LYY:VGRKPKV:EQLSN:VKS:XKXS, ASASPXX:VPQ:EPLT-AA[17]-LYY:IGKTPKI:EQLSN:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:IGEMS:QHN:QXEXR, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:IGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:DENKNVV:IGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:IGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:DSSNNVI:IGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:IGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:IGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:NDKQQII:IGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:DAANNVV:IGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:IGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:IGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:DNGRVLL:IGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:VGRKPKV:IGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGKTPKI:IGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:VGRTPKV:IGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:IGEMS:EHS:QXEXR,

SSVKXQP:SRV:SNIT-AA[17]-QIM:EYVRKKPKL:IGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:EIVRKKPIF:IGEMS:EDH:LAXKXE, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:LGEMS:EHS:KXEXR, KIPKAXX:VPT:SNIT-AA[17]-QIM:DENEKVV:LGEMS:VVE:GXGXR, GIPEPXX:VPE:SNIT-AA[17]-QIM:DENKNVV:LGEMS:TVE:SXAXR, SIPKAXX:VPT:SNIT-AA[17]-QIM:DEYDKVV:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, YVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:AXGXH, AVPKAXX:APT:SNIT-AA[17]-QIM:DSSNNVI:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT-AA[17]-QIM:DDMGVPT:LGEMS:VAE:XGXR, KASKAXX:VPT:SNIT-AA[17]-QIM:DKGVVTY:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT-AA[17]-QIM:NDKQQII:LGEMS:VVD:RXGXS, AAPASXX:VPA:SNIT-AA[17]-QIM:DAANNVV:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT-AA[17]-QIM:DSANNVV:LGEMS:VVE:SXGXR, HVPKPXX:APT:SNIT-AA[17]-QIM:DDSSNVI:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT-AA[17]-QIM:DNGRVLL:LGEMS:VEE:XGXL, ASAAPXX:VPQ:SNIT-AA[17]-QIM:VGRKPKV:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT-AA[17]-QIM:IGKTPKI:LGEMS:VKS:XKXS, ASASPXX:VPQ:SNIT-AA[17]-QIM:VGRTPKV:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT-AA[17]-QIM:RIKPHQGQH:LGEMS:QHN:KXEXR, SSVKXQP:SRV:SNIT-AA[17]-QIM:EYVRKKPKL:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT-AA[17]-QIM:EIVRKKPIF:LGEMS:EDH:LAXKXE, RNVQXRP:SRV:RSVK-AA[17]-AKV:EIVRKKPIF:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK-AA[17]-AKV:DENEKVV:KEVQV:VVE:GXGXR, GIPEPXX:VPE:RSVK-AA[17]-AKV:DENKNVV:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK-AA[17]-AKV:DEYDKVV:KEVQV:VVE:GXGXR, HVTKPTX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, TVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK-AA[17]-AKV:DSSNNVI:KEVQV:VVK:AXGXH, KVGKAXX:VPT:RSVK-AA[17]-AKV:DDMGVPT:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK-AA[17]-AKV:DKGVVTY:KEVQV:AVS:EXGXR, GSAGPXX:TPT:RSVK-AA[17]-AKV:NDKQQII:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK-AA[17]-AKV:DAANNVV:KEVQV:VVE:AXGXR, STPPTXX:VPT:RSVK-AA[17]-AKV:DSANNVV:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK-AA[17]-AKV:DDSSNVI:KEVQV:VVR:SXGXH, RVPSTXX:APV:RSVK-AA[17]-AKV:DNGRVLL:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK-AA[17]-AKV:VGRKPKV:KEVQV:VRS:XKXS, ASASPXX:VSQ:RSVK-AA[17]-AKV:IGKTPKI:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK-AA[17]-AKV:VGRTPKV:KEVQV:VKS:XKXS, NDEGLEX:VPT:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK-AA[17]-AKV:RIKPHQGQH:KEVQV:EHS:QXEXR, RNVQXRP:TQV:RSVK-AA[17]-AKV:EIVRKKPIF:KEVQV:EDH:LAXKXE, SSVKXQP:TQV:RPVQ-AA[17]-RKI:EYVRKKPKL:KKATV:EDH:LEXAXA, KIPKAXX:VPT:RPVQ-AA[17]-RKI:DENEKVV:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ-AA[17]-RKI:DENKNVV:KKATV:TVE:SXAXR, SIPKAXX:VPT:RPVQ-AA[17]-RKI:DEYDKVV:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:SXGXH, YVPKPXX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ-AA[17]-RKI:DDSSNVI:KKATV:VVR:AXGXH, AVPKAXX:APT:RPVQ-AA[17]-RKI:DSSNNVI:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ-AA[17]-RKI:DDMGVPT:KKATV:VAE:XGXR, KASKAXX:VPT:RPVQ-AA[17]-RKI:DKGVVTY:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ-AA[17]-RKI:NDKQQII:KKATV:VVD:RXGXS, AAPASXX:VPA:RPVQ-AA[17]-RKI:DAANNVV:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ-AA[17]-RKI:DSANNVV:KKATV:VVE:SXGXR, HVPKPXX:APT:RPVQ-AA[17]-

RKI:DDSSNVI:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ-AA[17]-RKI:DNGRVLL:KKATV:VEE:XGXL, ASAAPXX:VPQ:RPVQ-AA[17]-RKI:VGRKPKV:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ-AA[17]-RKI:IGKTPKI:KKATV:VKS:XKXS, ASASPXX:VPQ:RPVQ-AA[17]-RKI:VGRTPKV:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:QHN:KXEXR, NDEGLEX:VPT:RPVQ-AA[17]-RKI:RIKPHQGQH:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ-AA[17]-RKI:EYVRKKPKL:KKATV:EEH:LEXAXA; and wherein AA[17] is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S (in particular is selected from the group consisting of M, I, L, V and T).

In particular, in certain embodiments, the heptuplet PEP7:PEP5:PEP1:LINKER:PEP2:PEP6:PEP8 is selected from the group consisting of GIPEPXX:VPTKM:SAIS:DENKNVV:LKNYQ:NMVVE:SXAXR,
SIPKAXX:VPTEL:SAIS:DEYDKVV:LKNYQ:EMVVE:GXGXR,
HVTKPTX:VPTKL:SAIS:DDSSNVI:LKNYQ:NMVVE:SXGXH,
YVPKPXX:VPTKL:SAIS:DDSSNVI:LKNYQ:NMVVE:SXGXH,
TVPKPXX:VPTQL:SAIS:DDSSNVI:LKNYQ:NMVVE:AXGXH,
AVPKAXX:VPTKL:SAIS:DSSNNVI:LKNYQ:NMVVE:AXGXH,
KVGKAXX:VPTKL:SAIS:DDMGVPT:LKNYQ:EGMSVVE:XGXR,
KASKAXX:VPTKL:SAIS:DKGVVTY:LKNYQ:GMVVE:EXGXR,
GSAGPXX:VPTKM:SAIS:NDKQQII:LKNYQ:GMVVE:RXGXS,
AAPASXX:VPTRL:SAIS:DAANNVV:LKNYQ:DMVVE:AXGXR,
STPPTXX:VPTRL:SAIS:DSANNVV:LKNYQ:DMVVE:SXGXR,
HVPKPXX:VPTKL:SAIS:DDSSNVI:LKNYQ:NMVVE:SXGXH,
RVPSTXX:VPTKT:SAIS:DNGRVLL:LKNYQ:MIVVE:XGXL,
ASAAPXX:VPTAL:SAIS:VGRKPKV:LKNYQ:MIVVE:XKXS,
ASASPXX:VPTDL:SAIS:IGKTPKI:LKNYQ:MIVVE:XKXS,
ASASPXX:VPTDL:SAIS:VGRTPKV:LKNYQ:MVVVE:XKXS,
NDEGLXS:VPTEE:SAIS:RIKPHQGQH:LKNYQ:FLVVE:KXEXR,
NDEGLXS:VPTGQ:SAIS:RIKPHQGQH:LKNYQ:LEVVE:QXEXR,
SSVKXQP:VPTHH:SAIS:EYVRKKPKL:LKNYQ:RLVVE:LEXAXA,
RNVQXRP:VPTQL:SAIS:EIVRKKPIF:LKNYQ:TLVVE:LAXKXE,
GIPEPXX:VPEKM:SAIS:DENKNVV:LKNYQ:NMTVE:SXAXR,
HVTKPTX:APTKL:SAIS:DDSSNVI:LKNYQ:NMVVR:SXGXH,
YVPKPXX:APTKL:SAIS:DDSSNVI:LKNYQ:NMVVR:SXGXH,
TVPKPXX:APTQL:SAIS:DDSSNVI:LKNYQ:NMVVR:AXGXH,
AVPKAXX:APTKL:SAIS:DSSNNVI:LKNYQ:NMVVK:AXGXH,
KVGKAXX:VPTKL:SAIS:DDMGVPT:LKNYQ:EGMSVAE:XGXR,
KASKAXX:VPTKL:SAIS:DKGVVTY:LKNYQ:GMAVS:EXGXR,
GSAGPXX:TPTKM:SAIS:NDKQQII:LKNYQ:GMVVD:RXGXS,
AAPASXX:VPARL:SAIS:DAANNVV:LKNYQ:DMVVE:AXGXR,
HVPKPXX:APTKL:SAIS:DDSSNVI:LKNYQ:NMVVR:SXGXH,
RVPSTXX:APVKT:SAIS:DNGRVLL:LKNYQ:MIVEE:XGXL,
ASAAPXX:VPQAL:SAIS:VGRKPKV:LKNYQ:MIVRS:XKXS,
ASASPXX:VSQDL:SAIS:IGKTPKI:LKNYQ:MIVKS:XKXS,

ASASPXX:VPQDL:SAIS:VGRTPKV:LKNYQ:MVVKS:XKXS,

NDEGLXS:VPTEE:SAIS:RIKPHQGQH:LKNYQ:FLQHN:KXEXR,

NDEGLXS:VPTGQ:SAIS:RIKPHQGQH:LKNYQ:LEEHS:QXEXR,

SSVKXQP:SRVHH:SAIS:EYVRKKPKL:LKNYQ:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SAIS:EIVRKKPIF:LKNYQ:TLEDH:LAXKXE,

KIPKAXX:VPEEL:SSLS:DENEKVV:LKVYP:DMTVE:GXGXR,

SIPKAXX:VPEEL:SSLS:DEYDKVV:LKVYP:EMTVE:GXGXR,

HVTKPTX:VPEKL:SSLS:DDSSNVI:LKVYP:NMTVE:SXGXH,

YVPKPXX:VPEKL:SSLS:DDSSNVI:LKVYP:NMTVE:SXGXH,

TVPKPXX:VPEQL:SSLS:DDSSNVI:LKVYP:NMTVE:AXGXH,

AVPKAXX:VPEKL:SSLS:DSSNNVI:LKVYP:NMTVE:AXGXH,

KVGKAXX:VPEKL:SSLS:DDMGVPT:LKVYP:EGMSTVE:XGXR,

KASKAXX:VPEKL:SSLS:DKGVVTY:LKVYP:GMTVE:EXGXR,

GSAGPXX:VPEKM:SSLS:NDKQQII:LKVYP:GMTVE:RXGXS,

AAPASXX:VPERL:SSLS:DAANNVV:LKVYP:DMTVE:AXGXR,

STPPTXX:VPERL:SSLS:DSANNVV:LKVYP:DMTVE:SXGXR,

HVPKPXX:VPEKL:SSLS:DDSSNVI:LKVYP:NMTVE:SXGXH,

RVPSTXX:VPEKT:SSLS:DNGRVLL:LKVYP:MITVE:XGXL,

ASAAPXX:VPEAL:SSLS:VGRKPKV:LKVYP:MITVE:XKXS,

ASASPXX:VPEDL:SSLS:IGKTPKI:LKVYP:MITVE:XKXS,

ASASPXX:VPEDL:SSLS:VGRTPKV:LKVYP:MVTVE:XKXS,

NDEGLXS:VPEEE:SSLS:RIKPHQGQH:LKVYP:FLTVE:KXEXR,

NDEGLXS:VPEGQ:SSLS:RIKPHQGQH:LKVYP:LETVE:QXEXR,

SSVKXQP:VPEHH:SSLS:EYVRKKPKL:LKVYP:RLTVE:LEXAXA,

RNVQXRP:VPEQL:SSLS:EIVRKKPIF:LKVYP:TLTVE:LAXKXE,

KIPKAXX:VPTEL:SSLS:DENEKVV:LKVYP:DMVVE:GXGXR,

SIPKAXX:VPTEL:SSLS:DEYDKVV:LKVYP:EMVVE:GXGXR,

HVTKPTX:APTKL:SSLS:DDSSNVI:LKVYP:NMVVR:SXGXH,

YVPKPXX:APTKL:SSLS:DDSSNVI:LKVYP:NMVVR:SXGXH,

TVPKPXX:APTQL:SSLS:DDSSNVI:LKVYP:NMVVR:AXGXH,

AVPKAXX:APTKL:SSLS:DSSNNVI:LKVYP:NMVVK:AXGXH,

KVGKAXX:VPTKL:SSLS:DDMGVPT:LKVYP:EGMSVAE:XGXR,

KASKAXX:VPTKL:SSLS:DKGVVTY:LKVYP:GMAVS:EXGXR,

GSAGPXX:TPTKM:SSLS:NDKQQII:LKVYP:GMVVD:RXGXS,

AAPASXX:VPARL:SSLS:DAANNVV:LKVYP:DMVVE:AXGXR,

STPPTXX:VPTRL:SSLS:DSANNVV:LKVYP:DMVVE:SXGXR,

HVPKPXX:APTKL:SSLS:DDSSNVI:LKVYP:NMVVR:SXGXH,

RVPSTXX:APVKT:SSLS:DNGRVLL:LKVYP:MIVEE:XGXL,

ASAAPXX:VPQAL:SSLS:VGRKPKV:LKVYP:MIVRS:XKXS,

ASASPXX:VSQDL:SSLS:IGKTPKI:LKVYP:MIVKS:XKXS,

ASASPXX:VPQDL:SSLS:VGRTPKV:LKVYP:MVVKS:XKXS,

NDEGLXS:VPTEE:SSLS:RIKPHQGQH:LKVYP:FLQHN:KXEXR,

NDEGLXS:VPTGQ:SSLS:RIKPHQGQH:LKVYP:LEEHS:QXEXR,

SSVKXQP:SRVHH:SSLS:EYVRKKPKL:LKVYP:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SSLS:EIVRKKPIF:LKVYP:TLEDH:LAXKXE,

KIPKAXX:VPTEL:SAIS:DENEKVV:LKNYQ:DMVVE:GXGXR,

KIPKAXX:APTEL:NAIS:DENEKVV:LKKYR:DMVVR:GXGXR,

GIPEPXX:APTKM:NAIS:DENKNVV:LKKYR:NMVVR:SXAXR,

SIPKAXX:APTEL:NAIS:DEYDKVV:LKKYR:EMVVR:GXGXR,

YVPKPXX:APTKL:NAIS:DDSSNVI:LKKYR:NMVVR:SXGXH,

TVPKPXX:APTQL:NAIS:DDSSNVI:LKKYR:NMVVR:AXGXH,

AVPKAXX:APTKL:NAIS:DSSNNVI:LKKYR:NMVVR:AXGXH,

KVGKAXX:APTKL:NAIS:DDMGVPT:LKKYR:EGMSVVR:XGXR,

KASKAXX:APTKL:NAIS:DKGVVTY:LKKYR:GMVVR:EXGXR,

GSAGPXX:APTKM:NAIS:NDKQQII:LKKYR:GMVVR:RXGXS,

AAPASXX:APTRL:NAIS:DAANNVV:LKKYR:DMVVR:AXGXR,

STPPTXX:APTRL:NAIS:DSANNVV:LKKYR:DMVVR:SXGXR,

HVPKPXX:APTKL:NAIS:DDSSNVI:LKKYR:NMVVR:SXGXH,

RVPSTXX:APTKT:NAIS:DNGRVLL:LKKYR:MIVVR:XGXL,

ASAAPXX:APTAL:NAIS:VGRKPKV:LKKYR:MIVVR:XKXS,

ASASPXX:APTDL:NAIS:IGKTPKI:LKKYR:MIVVR:XKXS,

ASASPXX:APTDL:NAIS:VGRTPKV:LKKYR:MVVVR:XKXS,

NDEGLXS:APTEE:NAIS:RIKPHQGQH:LKKYR:FLVVR:KXEXR,

NDEGLXS:APTGQ:NAIS:RIKPHQGQH:LKKYR:LEVVR:QXEXR,

SSVKXQP:APTHH:NAIS:EYVRKKPKL:LKKYR:RLVVR:LEXAXA,

RNVQXRP:APTQL:NAIS:EIVRKKPIF:LKKYR:TLVVR:LAXKXE,

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GIPEPXX:VPEKM:NAIS:DENKNVV:LKKYR:NMTVE:SXAXR,

SIPKAXX:VPTEL:NAIS:DEYDKVV:LKKYR:EMVVE:GXGXR,

AVPKAXX:APTKL:NAIS:DSSNNVI:LKKYR:NMVVK:AXGXH,

KVGKAXX:VPTKL:NAIS:DDMGVPT:LKKYR:EGMSVAE:XGXR,

KASKAXX:VPTKL:NAIS:DKGVVTY:LKKYR:GMAVS:EXGXR,

GSAGPXX:TPTKM:NAIS:NDKQQII:LKKYR:GMVVD:RXGXS,

AAPASXX:VPARL:NAIS:DAANNVV:LKKYR:DMVVE:AXGXR,

STPPTXX:VPTRL:NAIS:DSANNVV:LKKYR:DMVVE:SXGXR,

RVPSTXX:APVKT:NAIS:DNGRVLL:LKKYR:MIVEE:XGXL,

ASAAPXX:VPQAL:NAIS:VGRKPKV:LKKYR:MIVRS:XKXS,

ASASPXX:VSQDL:NAIS:IGKTPKI:LKKYR:MIVKS:XKXS,

ASASPXX:VPQDL:NAIS:VGRTPKV:LKKYR:MVVKS:XKXS,

NDEGLXS:VPTEE:NAIS:RIKPHQGQH:LKKYR:FLQHN:KXEXR,

NDEGLXS:VPTGQ:NAIS:RIKPHQGQH:LKKYR:LEEHS:QXEXR,

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RNVQXRP:TQVQL:NAIS:EIVRKKPIF:LKKYR:TLEDH:LAXKXE,

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GIPEPXX:APTKM:SATS:DENKNVV:LRKHR:NMVVK:SXAXR,

SIPKAXX:APTEL:SATS:DEYDKVV:LRKHR:EMVVK:GXGXR,

HVTKPTX:APTKL:SATS:DDSSNVI:LRKHR:NMVVK:SXGXH,

YVPKPXX:APTKL:SATS:DDSSNVI:LRKHR:NMVVK:SXGXH,

TVPKPXX:APTQL:SATS:DDSSNVI:LRKHR:NMVVK:AXGXH,

KVGKAXX:APTKL:SATS:DDMGVPT:LRKHR:EGMSVVK:XGXR,

KASKAXX:APTKL:SATS:DKGVVTY:LRKHR:GMVVK:EXGXR,

GSAGPXX:APTKM:SATS:NDKQQII:LRKHR:GMVVK:RXGXS,

AAPASXX:APTRL:SATS:DAANNVV:LRKHR:DMVVK:AXGXR,

STPPTXX:APTRL:SATS:DSANNVV:LRKHR:DMVVK:SXGXR,

HVPKPXX:APTKL:SATS:DDSSNVI:LRKHR:NMVVK:SXGXH,

RVPSTXX:APTKT:SATS:DNGRVLL:LRKHR:MIVVK:XGXL,

ASAAPXX:APTAL:SATS:VGRKPKV:LRKHR:MIVVK:XKXS,

ASASPXX:APTDL:SATS:IGKTPKI:LRKHR:MIVVK:XKXS,

ASASPXX:APTDL:SATS:VGRTPKV:LRKHR:MVVVK:XKXS,

NDEGLXS:APTEE:SATS:RIKPHQGQH:LRKHR:FLVVK:KXEXR,

NDEGLXS:APTGQ:SATS:RIKPHQGQH:LRKHR:LEVVK:QXEXR,

SSVKXQP:APTHH:SATS:EYVRKKPKL:LRKHR:RLVVK:LEXAXA,

RNVQXRP:APTQL:SATS:EIVRKKPIF:LRKHR:TLVVK:LAXKXE,

KIPKAXX:VPTEL:SATS:DENEKVV:LRKHR:DMVVE:GXGXR,

GIPEPXX:VPEKM:SATS:DENKNVV:LRKHR:NMTVE:SXAXR,

SIPKAXX:VPTEL:SATS:DEYDKVV:LRKHR:EMVVE:GXGXR,

HVTKPTX:APTKL:SATS:DDSSNVI:LRKHR:NMVVR:SXGXH,

YVPKPXX:APTKL:SATS:DDSSNVI:LRKHR:NMVVR:SXGXH,

TVPKPXX:APTQL:SATS:DDSSNVI:LRKHR:NMVVR:AXGXH,

KVGKAXX:VPTKL:SATS:DDMGVPT:LRKHR:EGMSVAE:XGXR,

KASKAXX:VPTKL:SATS:DKGVVTY:LRKHR:GMAVS:EXGXR,

GSAGPXX:TPTKM:SATS:NDKQQII:LRKHR:GMVVD:RXGXS,

AAPASXX:VPARL:SATS:DAANNVV:LRKHR:DMVVE:AXGXR,

STPPTXX:VPTRL:SATS:DSANNVV:LRKHR:DMVVE:SXGXR,

HVPKPXX:APTKL:SATS:DDSSNVI:LRKHR:NMVVR:SXGXH,

RVPSTXX:APVKT:SATS:DNGRVLL:LRKHR:MIVEE:XGXL,

ASAAPXX:VPQAL:SATS:VGRKPKV:LRKHR:MIVRS:XKXS,

ASASPXX:VSQDL:SATS:IGKTPKI:LRKHR:MIVKS:XKXS,

ASASPXX:VPQDL:SATS:VGRTPKV:LRKHR:MVVKS:XKXS,

NDEGLXS:VPTEE:SATS:RIKPHQGQH:LRKHR:FLQHN:KXEXR,

NDEGLXS:VPTGQ:SATS:RIKPHQGQH:LRKHR:LEEHS:QXEXR,

SSVKXQP:SRVHH:SATS:EYVRKKPKL:LRKHR:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SATS:EIVRKKPIF:LRKHR:TLEDH:LAXKXE,

KIPKAXX:VPTEL:SPIS:DENEKVV:LKYHY:DMVAE:GXGXR,

GIPEPXX:VPTKM:SPIS:DENKNVV:LKYHY:NMVAE:SXAXR,

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 240

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 240

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

1. A pharmaceutical association for use in the treatment, prevention and/or diagnostic of a neoplastic disease, said association comprising at least one growth factor receptor-binding compound, which activates at least one growth factor receptor of a neoplastic cell, and at least one bioactive carrier forming at least one covalent or non-covalent interaction with said at least one growth factor receptor-binding compound, and wherein said association reduces or suppresses, in the neoplastic cell, the gene expression of at least one cyclin D and/or reduces or suppresses the formation of at least one complex formed between said at least one cyclin D and at least one of cyclin dependent-kinase 4 or 6.

2. A pharmaceutical association for a use according to claim 1, wherein said growth factor receptor-binding compound is a non-cyclic growth factor receptor-binding compound having a growth factor receptor activating capability and has a molecular weight of less than 8,000 Daltons.

3. A pharmaceutical association for a use according to claim 1, wherein said growth factor receptor-binding compound is a cyclic growth factor receptor-binding compound having a growth factor receptor activating capability and has a molecular weight of less than 7,000 Daltons.

4. A pharmaceutical association for a use according to any one of claims 1 to 3, wherein said growth factor receptor-binding compound comprises a peptide with four amino acids PEP1, and a peptide with five amino acids PEP2; wherein PEP1 is selected from the group consisting of SAIS, SSLS, NAIS, SATS, SPIS, EPIS, SPIN, KPLS, EPLP, EPLT, SNIT, RSVK and RPVQ ; and wherein PEP2 is selected from the group consisting of LKNYQ, LKVYP, LKKYR, LRKHR, LKYHY, KFKYE, YGKIP, YKQYE, DHHKD, EQLSN, IGEMS, LGEMS, KEVQV and KKATV.

5. A pharmaceutical association for a use according to any one of claims 1 to 4, wherein said growth factor receptor is selected from the group consisting of epidermal growth factor receptors, fibroblast growth factor receptors, vascular endothelial growth factor receptors, nerve growth factor receptors, insulin receptor family, Trk receptor family, Eph receptor family, AXL receptor family, LTK receptor family, TIE receptor family, ROR receptor family, DDR receptor family, RET receptor family, KLG receptor family, RYK receptor family, MuSK receptor family, hepatocyte growth factor receptors, somatomedin or insulin-like growth factor receptors, platelet-derived growth factor receptors, and transforming growth factor beta superfamily proteins.

6. A pharmaceutical association for a use according to any one of claims 1 to 5, wherein the gene expression of cyclin D is reduced or suppressed during phase G1 of the cell cycle of the neoplastic cell.

7. A pharmaceutical association for a use according to claim 6, wherein the gene expression of cyclin D is reduced or suppressed during the entire duration of phase G1 of the cell cycle of the neoplastic cell.

8. A pharmaceutical association for a use according to any one of claims 1 to 7, wherein said treatment restores a function of at least one impaired cell cycle checkpoint.

9. A pharmaceutical association for a use according to claim 8, wherein said cell cycle checkpoint is a cell adhesion checkpoint.

10. A pharmaceutical association for a use according to any one of claims 1 to 9, wherein said treatment comprises down-regulating the expression or activity of a GTPase.

11. A pharmaceutical association for a use according to any one of claims 1 to 10, wherein said treatment is an extracellular treatment.

12. A pharmaceutical association for a use according to any one of claims 1 to 11, wherein said treatment is a non-mutagenic treatment.

13. A pharmaceutical association for a use according to any one of claims 1 to 12, wherein said treatment converts a neoplastic cell into a non-neoplastic cell.

14. A pharmaceutical association for a use according to any one of claims 1 to 13, wherein said treatment induces the differentiation of said neoplastic cell.

15. A pharmaceutical association for a use according to any one of claims 1 to 14, wherein said treatment induces the quiescence of said neoplastic cell.

16. A pharmaceutical association for a use according to any one of claims 1 to 15, wherein said treatment inhibits cell division and/or cell proliferation of said neoplastic cell.

17. A pharmaceutical association for a use according to any one of claims 1 to 16, wherein said treatment promotes anti-mitogen activity, tumour suppressor activity, anti-oncogenic activity or any combination thereof in said neoplastic cell.

18. A pharmaceutical association for a use according to any one of claims 1 to 17, wherein said growth factor receptor-binding compound comprises a peptide with eight amino acids PEP12, and a peptide with five amino acids PEP2 ; wherein PEP12 is a peptide of general formula PEP1-AA^{17}-PEP11; wherein AA^{17} is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S ; wherein PEP11 is a peptide with 3 amino acids of general formula AA^{18}-AA^{19}-AA^{20}; wherein AA^{18} is selected from the group consisting of L, V, Q, A and R; wherein AA^{19} is selected from the group consisting of F, W, H, Y, I and K; wherein AA^{20} is selected from the group consisting of L, F, Y, K, I, V and M.

19. A pharmaceutical association for a use according to claim 18, wherein PEP11 is selected from the

group consisting of LYL, LFF, LYF, LYY, LYK, LYI, LFI, LYV, VYY, QIM, AKV and RKI.

20. A pharmaceutical association for a use according to any one of claims 4 to 19, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3 and a peptide with three amino acids PEP4 ; wherein PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV ; and wherein PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH.

21. A pharmaceutical association for a use according to any one of claims 4 to 20, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5 and a peptide with between five and seven amino acids PEP6; wherein PEP5 is a peptide of general formula PEP3-AA^{11}-AA^{12}; wherein PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H ; wherein PEP6 is a peptide of general formula AA^{26}-AA^{27}-AA^{28}-AA^{29}-PEP4; wherein PEP4 is selected from the group consisting of VVE, TVE, VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S.

22. A pharmaceutical association for a use according to claim 21, wherein PEP5 is selected from the group consisting of VPTEL, VPEKM, APTKL, APTQL, VPTKL, TPTKM, VPARL, VPTRL, APVKT, VPQAL, VSQDL, VPQDL, VPTEE, VPTGQ, SRVHH and TQVQL.

23. A pharmaceutical association for a use according to claim 21 or 22, wherein PEP6 is selected from the group consisting of DMVVE, NMTVE, EMVVE, NMVVR, NMVVK, EGMSVAE, GMAVS, GMVVD, MIVEE, MIVRS, MIVKS, MVVKS, FLQHN, LEEHS, RLEEH and TLEDH.

24. A pharmaceutical association for a use according to any one of claims 4 to 23, wherein said growth factor receptor-binding compound comprises a peptide with between six and twelve amino acids PEP9 and a peptide with between six and eleven amino acids PEP10 ; wherein PEP9 is a peptide of general formula PEP7-PEP5; wherein PEP5 is a peptide of formula PEP3-AA^{11}-AA^{12}; wherein PEP3 is selected from the group consisting of VPT, VPE, APT, TPT, VPA, APV, VPQ, VSQ, SRV and TQV; wherein AA^{11} is selected from the group consisting of E, K, Q, R, A, D, G and H; and wherein AA^{12} is selected from the group consisting of L, M, T, E, Q and H; wherein PEP7 is an amino acid or a peptide with between two and seven amino acids of general formula AA^{1}-AA^{2}-AA^{3}-AA^{4}-AA^{5}-AA^{6}-AA^{7}; wherein AA^{1}, AA^{2}, AA^{3}, AA^{4}, and AA^{5} are independently absent or AA^{I} as defined herein; wherein AA^{6} is absent or selected from the group consisting of S, T, C, E, Q, P and R; wherein AA^{7} is absent or is selected from the group consisting of S, T, C, E, Q, P and R ; wherein PEP10 is a peptide of general formula PEP6-PEP8; wherein PEP6 is a peptide of formula AA^{26}-AA^{27}-AA^{28}-AA^{29}-PEP4; wherein PEP4 is selected from the group consisting of VVE, TVE,

VVR, VVK, VAE, AVS, VVD, VEE, VRS, VKS, QHN, EHS, EEH and EDH; wherein AA^{26} is absent or selected from the group consisting of AA^{III} amino acids, preferably is absent or is E; wherein AA^{27} and AA^{28} are independently selected from the group consisting of AA^{III} and AA^{V} amino acids; and wherein AA^{29} is absent or selected from the group consisting of AA^{II} amino acids, preferably is absent or is S; wherein PEP8 is an amino acid or a peptide with between two and six amino acids of general formula AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38}; AA^{33} is absent or is selected from the group consisting of AA^{I} amino acids at the exception of AA^{VI} amino acids; AA^{34} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{35} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{36} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{37} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{38} is absent or is selected from the group consisting of AA^{I}.

25. A pharmaceutical association for a use according to claim 24, wherein PEP9 is selected from the group consisting of KIPKAXXVPTEL, GIPEPXXVPEKM, SIPKAXXVPTEL, HVTKPTXAPTKL, YVPKPXXAPTKL, TVPKPXXAPTQL, AVPKAXXAPTKL, KVGKAXXVPTKL, KASKAXXVPTKL, GSAGPXXTPTKM, AAPASXXVPARL, STPPTXXVPTRL, HVPKPXXAPTKL, RVPSTXXAPVKT, ASAAPXXVPQAL, ASASPXXVSQDL, ASASPXXVPQDL, NDEGLEXVPTEE, NDEGLEXVPTGQ, SSVKXQPSRVHH and RNVQXRPTQVQL; and wherein X is C or S.

26. A pharmaceutical association for a use according to claim 24 or 25, wherein PEP10 is selected from the group consisting of DMVVEGXGXR, NMTVESXAXR, EMVVEGXGXR, NMVVRSXGXH, NMVVRAXGXH, NMVVKAXGXH, EGMSVAEXGXR, GMAVSEXGXR, GMVVDRXGXS, DMVVEAXGXR, DMVVESXGXR, MIVEEXGXL, MIVRSXKXS, MIVKSXKXS, MVVKSXKXS, FLQHNKXEXR, LEEHSQXEXR, RLEEHLEXAXA and TLEDHLAXKXE; and wherein X is C or S.

27. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3 and a peptide with between five and seven amino acids PEP6.

28. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3 and a peptide with between six and eleven amino acids PEP10.

29. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5 and a peptide with three amino acids PEP4.

30. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with between six and twelve amino acids PEP9 and a peptide with three amino acids PEP4.

31. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5 and a peptide with between six and eleven amino acids PEP10.

32. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with between six and twelve amino acids PEP9 and a peptide with between five and seven amino acids PEP6.

33. A pharmaceutical association for a use according to any one of claims 4 to 26, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3, an amino acid or a peptide with between two and seven amino acids PEP7, and a peptide with three amino acids PEP4; wherein PEP7 is an amino acid or a peptide with between two and seven amino acids of general formula AA^1-AA^2-AA^3-AA^4-AA^5-AA^6-AA^7; wherein AA^1, AA^2, AA^3, AA^4, and AA^5 are independently absent or AA^I; wherein AA^6 is absent or selected from the group consisting of S, T, C, E, Q, P and R; wherein AA^7 is absent or is selected from the group consisting of S, T, C, E, Q, P and R; wherein at least one of AA^1, AA^2, AA^3, AA^4, AA^5, AA^6 or AA^7 is not absent; wherein PEP8 is an amino acid or a peptide with between two and six amino acids of general formula AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38}; wherein AA^{33} is absent or is selected from the group consisting of AA^I amino acids at the exception of AA^{VI} amino acids; AA^{34} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{35} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{36} is absent or is selected from the group consisting of AA^{III} and AA^{IV} amino acids; wherein AA^{37} is absent or is selected from the group consisting of AA^{II} amino acids, preferably is S or C; wherein AA^{38} is absent or is selected from the group consisting of AA^I; and wherein at least one of AA^{33}, AA^{34}, AA^{35}, AA^{36}, AA^{37} or AA^{38} is not absent.

34. A pharmaceutical association for a use according to claim 33, wherein PEP7 is selected from the group consisting of KIPKAXX, GIPEPXX, SIPKAXX, HVTKPTX, YVPKPXX, TVPKPXX, AVPKAXX, KVGKAXX, KASKAXX, GSAGPXX, AAPASXX, STPPTXX, HVPKPXX, RVPSTXX, ASAAPXX, ASASPXX, NDEGLEX, SSVKXQP and RNVQXRP; and wherein X is C or S.

35. A pharmaceutical association for a use according to claim 33 or 34, wherein PEP8 is selected from the group consisting of GXGXR, SXAXR, SXGXH, AXGXH, XGXR, EXGXR, RXGXS, AXGXR, SXGXR, XGXL, XKXS, KXEXR, QXEXR, LEXAXA and LAXKXE; and wherein X is C or S.

36. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3, an amino acid or a peptide with between two and seven amino acids PEP7, and a peptide with between five and seven amino acids PEP6.

37. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3, an amino

acid or a peptide with between two and seven amino acids PEP7, and a peptide with between six and eleven amino acids PEP10.

38. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3, an amino acid or a peptide with between two and seven amino acids PEP7, a peptide with three amino acids PEP4, and an amino acid or a peptide with between two and six amino acids PEP8.

39. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with three amino acids PEP3, an amino acid or a peptide with between two and seven amino acids PEP7, a peptide with between five and seven amino acids PEP6, and an amino acid or a peptide with between two and six amino acids PEP8.

40. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5, an amino acid or a peptide with between two and seven amino acids PEP7, and a peptide with three amino acids PEP4.

41. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5, an amino acid or a peptide with between two and seven amino acids PEP7, and a peptide with between five and seven amino acids PEP6.

42. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5, an amino acid or a peptide with between two and seven amino acids PEP7, and a peptide with between six and eleven amino acids PEP10.

43. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5, an amino acid or a peptide with between two and seven amino acids PEP7, a peptide with three amino acids PEP4, and an amino acid or a peptide with between two and six amino acids PEP8.

44. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with five amino acids PEP5, an amino acid or a peptide with between two and seven amino acids PEP7, a peptide with between five and seven amino acids PEP6, and an amino acid or a peptide with between two and six amino acids PEP8.

45. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with between six and twelve amino acids

PEP9, a peptide with three amino acids PEP4, and an amino acid or a peptide with between two and six amino acids PEP8.

46. A pharmaceutical association for a use according to any one of claims 4 to 35, wherein said growth factor receptor-binding compound comprises a peptide with between six and twelve amino acids PEP9, a peptide with between five and seven amino acids PEP6, and an amino acid or a peptide with between two and six amino acids PEP8.

47. A pharmaceutical association for a use according to any one of claims 1 to 46, wherein said growth factor receptor-binding compound comprises a peptide, a variant or analog thereof, or a peptidomimetic having the following general formula (Ia):

PEP(A)-LINKER-PEP(B) (Ia)

wherein one end of LINKER interacts covalently with one end of PEP(A); wherein another end of LINKER interacts covalently with one end of PEP(B); wherein PEP(A) comprises PEP1 or PEP12 and at least one amino acid or peptide selected from the group consisiting of PEP3, PEP5, PEP7 and PEP9; wherein PEP(B) comprises PEP2 and at least one amino acid or peptide selected from the group consisting of PEP4, PEP6, PEP8 and PEP10; wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight comprised between about 28 and about 2,000 Da.

48. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 46, wherein said growth factor receptor-binding compound has the following general formula (Ia):

PEP(A)-LINKER-PEP(B) (Ia)

wherein one end of LINKER interacts covalently with one end of PEP(A); wherein another end of LINKER interacts covalently with one end of PEP(B); wherein PEP(A) comprises at least one amino acid or peptide selected from the group consisiting of PEP1, PEP12, PEP3, PEP5, PEP7 and PEP9; wherein PEP(B) comprises at least one amino acid or peptide selected from the group consisting of PEP2, PEP4, PEP6, PEP8 and PEP10; wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight comprised between about 28 and about 2,000 Da.

49. A pharmaceutical association for a use according to any one of claims 1 to 46, wherein said growth factor receptor-binding compound comprises a peptide, a variant or analog thereof, or a peptidomimetic having the following general formula (IIa):

PEP(C)-PEP12-LINKER-PEP2-PEP(D) (IIa)

wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a

molecular weight (Mw) comprised between about 28 and about 2,000 Da; wherein one end of PEP(C) interacts covalently with PEP12; wherein one end of PEP(D) interacts covalently with one end of PEP2; wherein one end of LINKER interacts covalently with one end of PEP12; wherein another end of LINKER interacts covalently with another end of PEP2; wherein PEP(C) is a peptide with at least 5 amino acids comprising at least one peptide selected from the group consisting of PEP3, PEP5, PEP7 and PEP9; and wherein PEP(D) is a peptide with at least 5 amino acids comprising at least one peptide selected from the group consisting of PEP4, PEP6, PEP8 and PEP10.

50. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 46, wherein said growth factor receptor-binding compound has the following general formula (IIa):

PEP(C)-PEP12-LINKER-PEP2-PEP(D) (IIa)

wherein LINKER is a linear or branched organic divalent radical, moiety or compound having a molecular weight (Mw) comprised between about 28 and about 2,000 Da; wherein one end of PEP(C) interacts covalently with PEP12; wherein one end of PEP(D) interacts covalently with one end of PEP2; wherein one end of LINKER interacts covalently with one end of PEP12; wherein another end of LINKER interacts covalently with another end of PEP2; wherein PEP(C) is a peptide with at least 5 amino acids comprising at least one amino acid or peptide selected from the group consisting of PEP3, PEP5, PEP7 and PEP9; and wherein PEP(D) is a peptide with at least 5 amino acids comprising at least one amino acid or peptide selected from the group consisting of PEP4, PEP6, PEP8 and PEP10.

51. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP5 and PEP(D) is PEP6.

52. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP9; and PEP(D) is PEP10.

53. A pharmaceutical association for a use according to claim 50, wherein PEP(C) comprises PEP3 and PEP(D) is PEP6.

54. A pharmaceutical association for a use according to claim 50, wherein PEP(C) comprises PEP3 and PEP(D) is PEP10.

55. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP5 and PEP(D) comprises PEP4.

56. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP9 and PEP(D) comprises PEP4.

57. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP5 and PEP(D) is PEP10.

58. A pharmaceutical association for a use according to claim 50, wherein PEP(C) is PEP9 and PEP(D) is PEP6.

59. A pharmaceutical association for a use according to claim 50, wherein PEP(C) comprises PEP3 and PEP7, and PEP(D) is PEP6.

60. A pharmaceutical association for a use according to claim 50, wherein PEP(C) comprises PEP3 and PEP7, and PEP(D) is PEP10.

61. A pharmaceutical association for a use according to any one of claims 1 to 46, wherein said growth factor receptor-binding compound comprises a peptide, a variant or analog thereof, or a peptidomimetic having the following general formula (IIIa):

PEP7-PEP5-PEP12-LINKER-PEP2-PEP6-PEP8 (IIIa)

wherein LINKER is a linear or branched organic divalent radical having a molecular weight comprised between about 28 and about 2,000 Da; wherein one end of LINKER interacts covalently with one end of PEP12 via AA^{20}; wherein another end of LINKER interacts covalently with one end of PEP2 via AA^{21}; wherein one end of PEP5 interacts covalently with another end of PEP12 via AA^{12}; wherein another end of PEP5 interacts covalently with one end of PEP7 via AA^{8}; wherein one end of PEP6 interacts covalently with another end of PEP2 via AA^{26}; wherein another end of PEP6 interacts covalently with one end of PEP8 via AA^{32}.

62. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 46, wherein said growth factor receptor-binding compound has the following general formula (IIIa):

PEP7-PEP5-PEP12-LINKER-PEP2-PEP6-PEP8 (IIIa)

wherein LINKER is a linear or branched organic divalent radical having a molecular weight comprised between about 28 and about 2,000 Da; wherein one end of LINKER interacts covalently with one end of PEP12 via AA^{20}; wherein another end of LINKER interacts covalently with one end of PEP2 via AA^{21}; wherein one end of PEP5 interacts covalently with another end of PEP12 via AA^{12}; wherein another end of PEP5 interacts covalently with one end of PEP7 via AA^{8}; wherein one end of PEP6 interacts covalently with another end of PEP2 via AA^{26}; wherein another end of PEP6 interacts covalently with one end of PEP8 via AA^{32}.

63. A pharmaceutical association for a use according to any one of claims 1 to 46, wherein said growth factor receptor-binding compound comprises a peptide, a variant or analog thereof, or a peptidomimetic having the following general formula (IVa):

AA^1-AA^2-AA^3-AA^4-AA^5-AA^6-AA^7-AA^8-AA^9-AA^{10}-AA^{11}-AA^{12}-AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20}-LINKER-AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25}-AA^{26}-AA^{27}-AA^{28}-AA^{29}-AA^{30}-AA^{31}-AA^{32}-AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} (IVa)

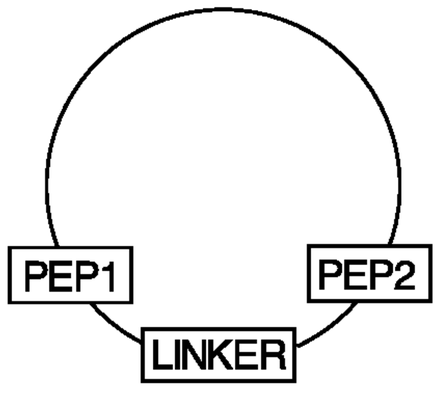
wherein LINKER is a linear or branched organic divalent radical having a molecular weight comprised between about 28 and about 2,000 Da; wherein AA^1-AA^2-AA^3-AA^4-AA^5-AA^6-AA^7 is PEP7 as defined herein; wherein AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20} is PEP12 as defined herein; wherein AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25} is PEP2 as already defined herein; wherein AA^8-AA^9-AA^{10} is PEP3 as defined herein; wherein AA^{30}-AA^{31}-AA^{32} is PEP4 as defined herein; wherein AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} is PEP8 as defined herein; wherein AA^{11}, AA^{12}, AA^{26}, AA^{27}, AA^{28}, and AA^{29} are as defined herein; wherein one end of LINKER interacts covalently with AA^{20}; wherein another end of LINKER interacts covalently with AA^{21}; wherein AA^1 and AA^{21} may be both N-terminal amino acids or both C-terminal amino acids; wherein AA^{38} and AA^{20} may be both N-terminal amino acids or both C-terminal amino acids.

64. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 46, comprising a peptide, a variant or analog thereof, or a peptidomimetic having the following general formula (IVa):

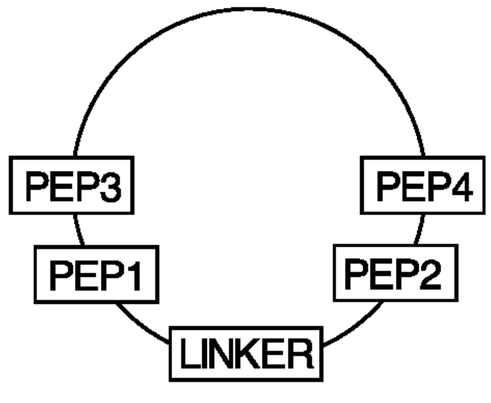
AA^1-AA^2-AA^3-AA^4-AA^5-AA^6-AA^7-AA^8-AA^9-AA^{10}-AA^{11}-AA^{12}-AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20}-LINKER-AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25}-AA^{26}-AA^{27}-AA^{28}-AA^{29}-AA^{30}-AA^{31}-AA^{32}-AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} (IVa)

wherein LINKER is a linear or branched organic divalent radical having a molecular weight (Mw) comprised between about 28 and about 2,000 Da; wherein AA^1-AA^2-AA^3-AA^4-AA^5-AA^6-AA^7 is PEP7 as defined herein; wherein AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20} is PEP12 as defined herein; wherein AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25} is PEP2 as already defined herein; wherein AA^8-AA^9-AA^{10} is PEP3 as defined herein; wherein AA^{30}-AA^{31}-AA^{32} is PEP4 as defined herein; wherein AA^{33}-AA^{34}-AA^{35}-AA^{36}-AA^{37}-AA^{38} is PEP8 as defined herein; wherein AA^{11}, AA^{12}, AA^{26}, AA^{27}, AA^{28}, and AA^{29} are as defined herein; wherein one end of LINKER interacts covalently with AA^{20}; wherein another end of LINKER interacts covalently with AA^{21}; wherein AA^1 and AA^{21} may be both N-terminal amino acids or both C-terminal amino acids; wherein AA^{38} and AA^{20} may be both N-terminal amino acids or both C-terminal amino acids.

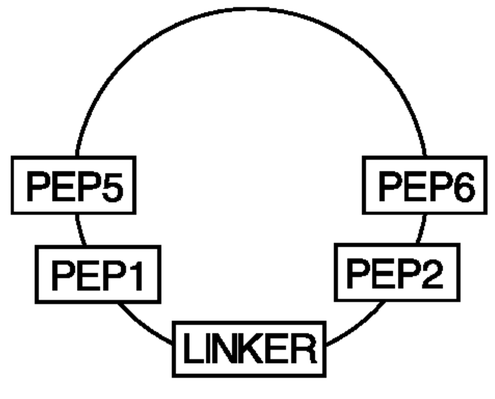
65. A pharmaceutical association for a use according to any one of claims 1 and 3 to 46, wherein said growth factor receptor-binding compound has any one of the following schematic general formulae (V) to (XXVIII):



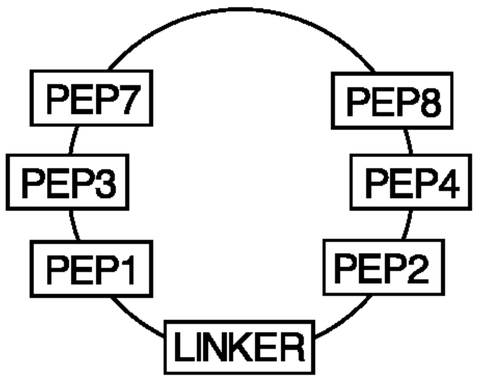
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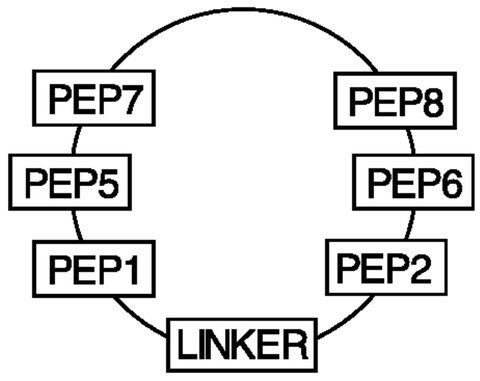
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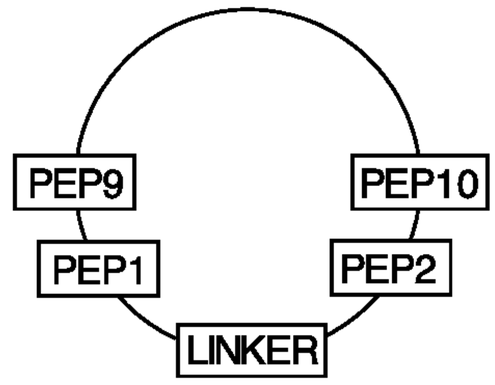
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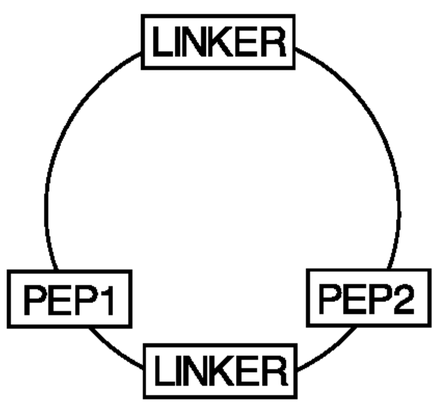
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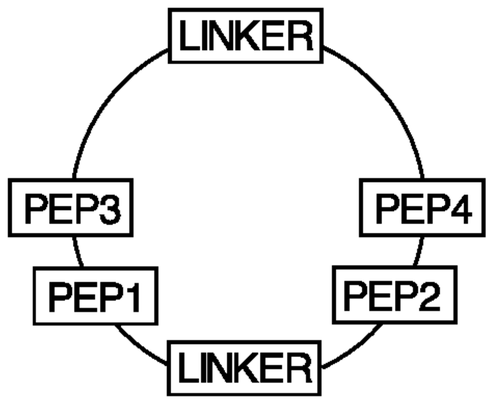
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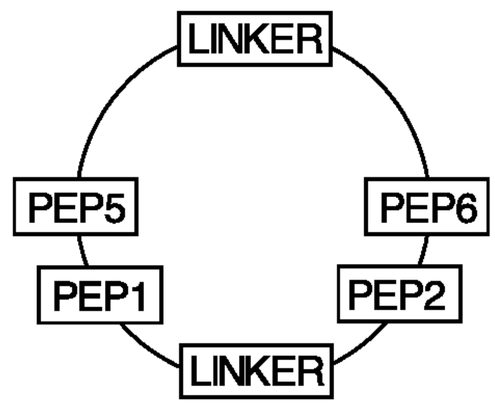
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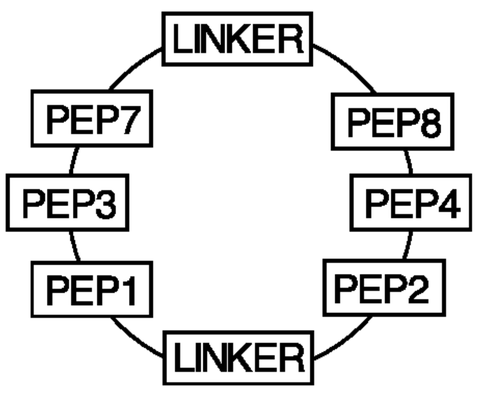
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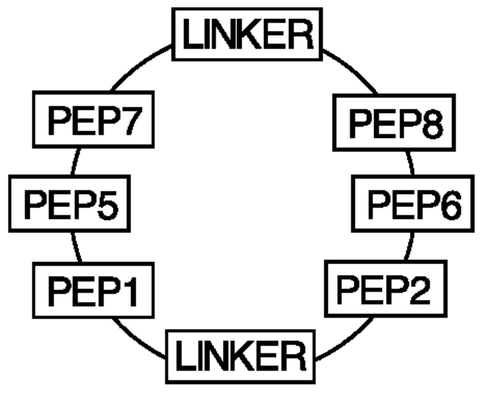
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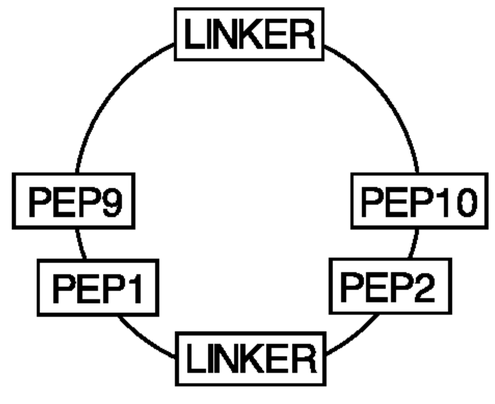
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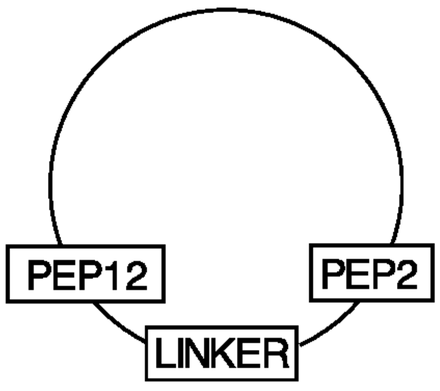
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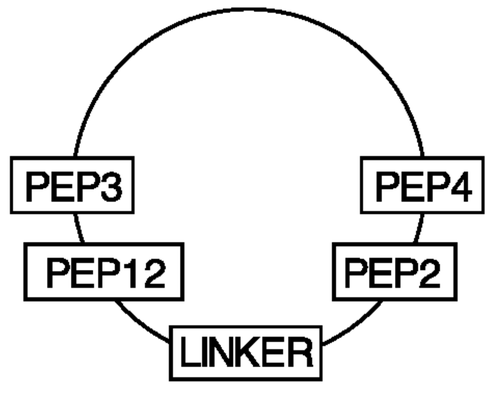
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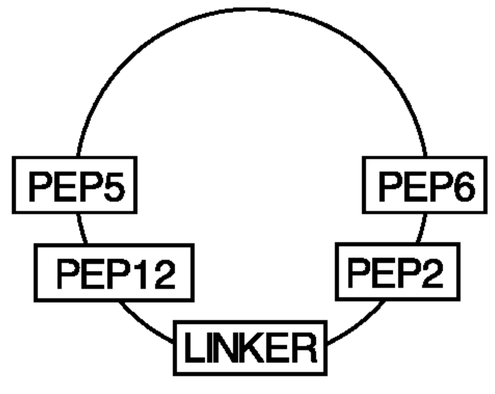
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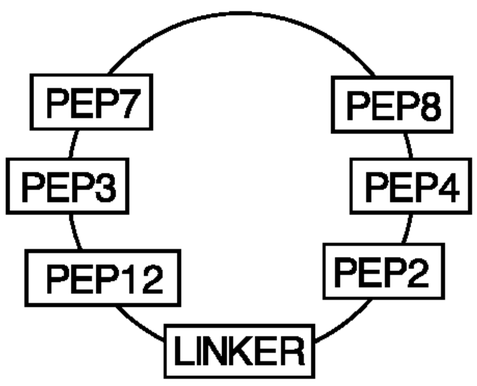
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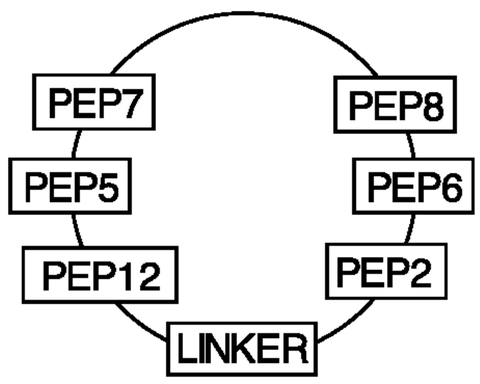
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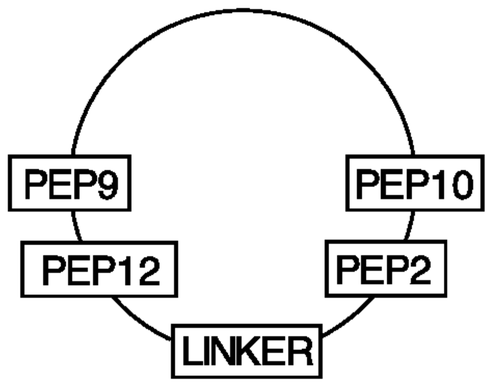
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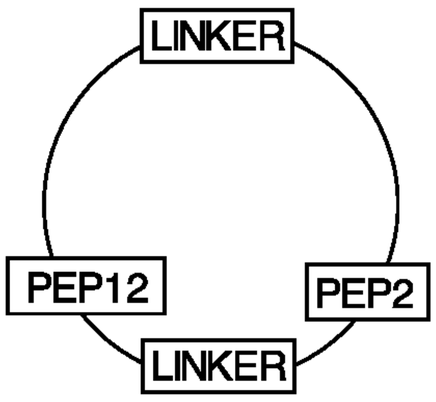
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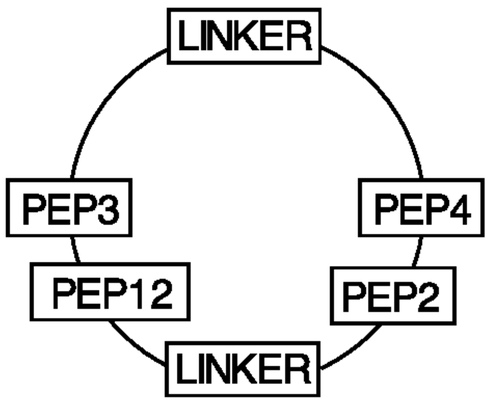
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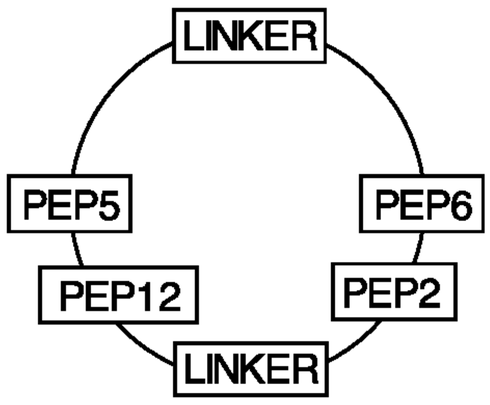
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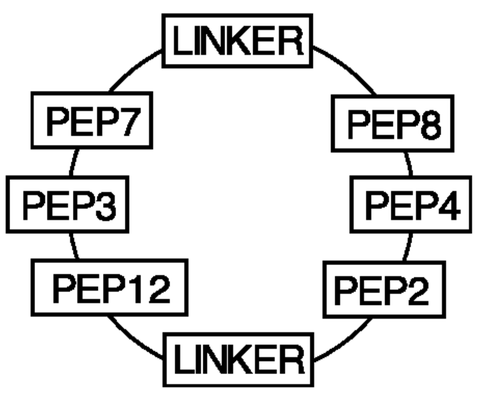
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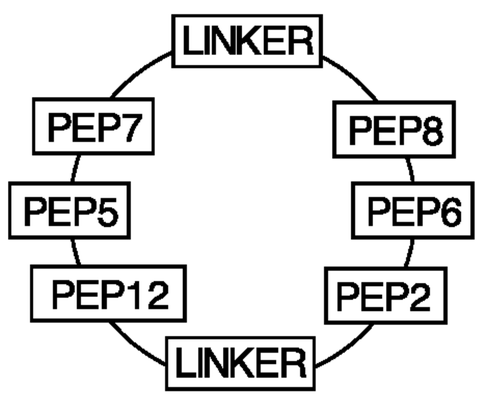
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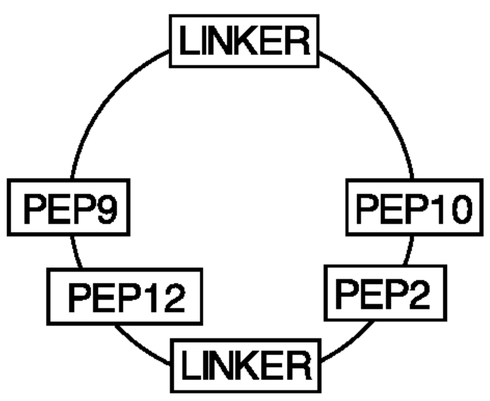
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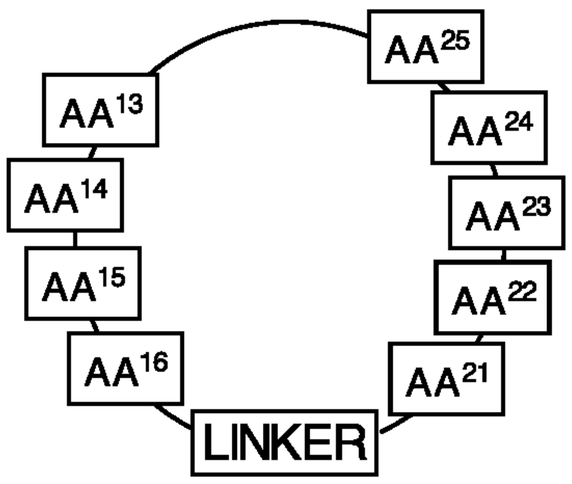
(XXVII)



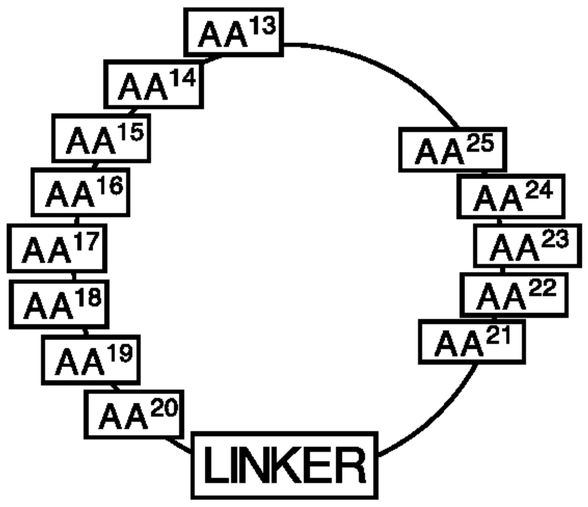
(XXVIII)

wherein LINKER is a linear or branched organic divalent radical having a molecular weight comprised between about 28 and about 2,000 Da; wherein PEP12 is a peptide with 8 amino acids of formula PEP1-AA^{17}-PEP11; wherein PEP2 is a peptide with five amino acids; wherein PEP5 is a peptide with five amino acids; wherein PEP6 is a peptide with between five and seven amino acids; wherein PEP7 an amino acid or a peptide with between two and seven amino acids; wherein PEP8 an amino acid or a peptide with between two and six amino acids; wherein PEP9 is a peptide with between six and twelve amino acids; wherein PEP10 is a peptide with between six and eleven amino acids; wherein curved lines represents covalent bonds between LINKERs and PEP1 to PEP12.

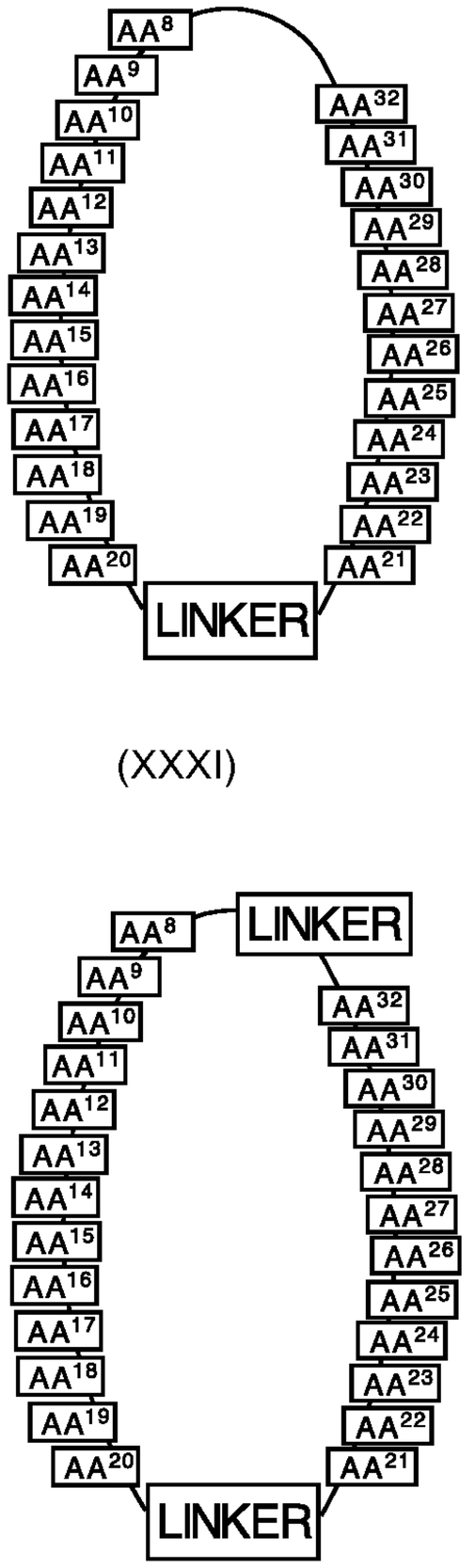
66. A pharmaceutical association for a use according to any one of claims 1 and 3 to 46, wherein said growth factor receptor-binding compound has any one of the following cyclic schematic general formulae (XXIX) to (XXXIV):



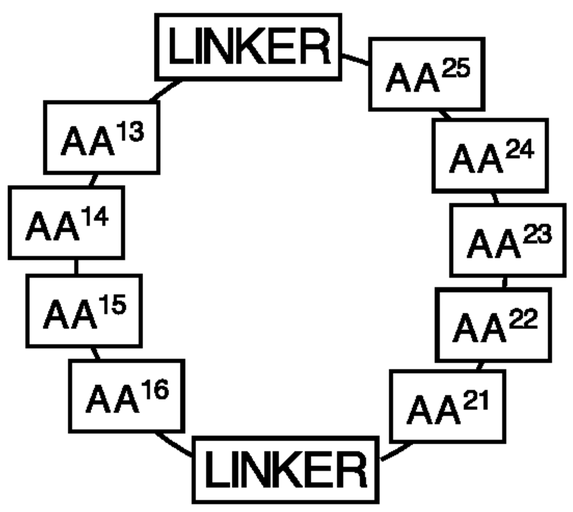
(XXIX)



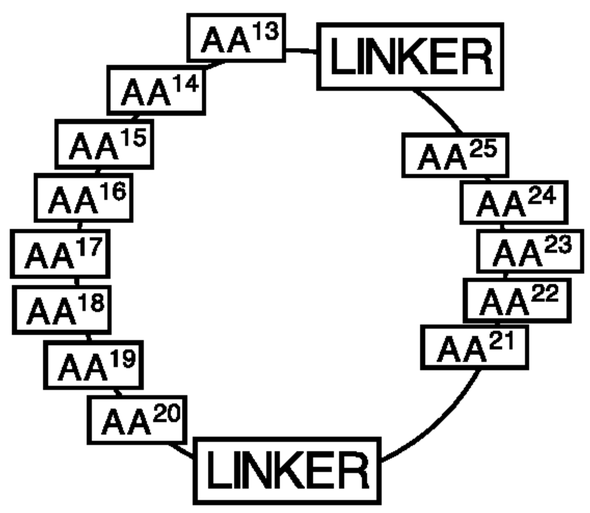
(XXX)



(XXXI)



(XXXII)



(XXXIII)

(XXXIV)

wherein LINKER is a linear or branched organic divalent radical having a molecular weight (Mw) comprised between about 28 and about 2,000 Da; wherein AA^{13}-AA^{14}-AA^{15}-AA^{16}-AA^{17}-AA^{18}-AA^{19}-AA^{20} is PEP12; wherein AA^{21}-AA^{22}-AA^{23}-AA^{24}-AA^{25} is PEP2; wherein AA^{8}-AA^{9}-AA^{10} is PEP3; wherein AA^{30}-AA^{31}-AA^{32} is PEP4; wherein one end of LINKER interacts covalently with AA^{16} or AA^{20}; and wherein another end of LINKER interacts covalently with AA^{21}.

67. A pharmaceutical association for a use according to any one of claims 47 to 66, wherein said LINKER is a peptide with 2 to 16 amino acids.

68. A pharmaceutical association for a use according to any one of claims 47 to 67, wherein said LINKER comprises a peptide of general formula (XXXV):

$$*AA^{201}\text{-}AA^{202}\text{-}AA^{203}\text{-}AA^{204}\text{-}AA^{205}\text{-}AA^{206}\text{-}AA^{207}\text{-}AA^{208}\text{-}AA^{209}** \qquad \text{(XXXV)}$$

wherein said peptide is selected from the group consisting of $*AA^{III}$-AA^{I}-AA^{I}-AA^{II}-AA^{VII}-AA^{XII}-AA^{XII}-AA^{XIII}-$AA^{XIII}**$, $*AA^{III}$-AA^{I}-AA^{VI}-AA^{II}-AA^{VII}-AA^{XII}-AA^{XII}-AA^{XIII}-$AA^{XIII}**$, $*AA^{III}$-AA^{I}-AA^{I}-AA^{II}-AA^{II}-AA^{XII}-

AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{III}-AA^{I}-AA^{II}-AA^{II}-AA^{VII}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{III}-AA^{I}-AA^{II}-AA^{IV}-AA^{IV}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{II}-AA^{I}-AA^{II}-AA^{II}-AA^{II}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{III}-AA^{III}-AA^{II}-AA^{VII}-AA^{II}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{III}-AA^{I}-AA^{I}-AA^{II}-AA^{II}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{V}-AA^{V}-AA^{VII}-AA^{VII}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**, *AA^{VIII}-AA^{V}-AA^{VII}-AA^{II}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}** and *AA^{V}-AA^{V}-AA^{VII}-AA^{II}-AA^{XII}-AA^{XII}-AA^{XIII}-AA^{XIII}**; wherein AA^{I} is an amino acid; wherein AA^{II} is a polar amino acid; wherein AA^{III} is an acidic amino acid; wherein AA^{IV} is a aliphatic amino acid; wherein AA^{V} is a apolar amino acid; wherein AA^{VI} is an aromatic amino acid; wherein AA^{VII} is a basic amino acid; wherein AA^{VIII} is L or I; wherein AA^{XII} is an amino acid selected from the group consisting of G, A, V, L, I, P, M, K, R, H, Y and E; wherein AA^{XIII} is absent, AA^{II} or AA^{VII}; wherein any one of AA^{201}, AA^{201}-AA^{202}, AA^{201}-AA^{202}-AA^{203}, AA^{201}-AA^{202}-AA^{203}-AA^{204}, AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}, AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}-AA^{206}, AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}-AA^{206}-AA^{207}, AA^{203}-AA^{204}-AA^{205}-AA^{206}-AA^{207}-AA^{208}-AA^{209}, AA^{204}-AA^{205}-AA^{206}-AA^{207}-AA^{208}-AA^{209}, AA^{205}-AA^{206}-AA^{207}-AA^{208}-AA^{209}, AA^{206}-AA^{207}-AA^{208}-AA^{209}, AA^{207}-AA^{208}-AA^{209}, AA^{208}-AA^{209} or AA^{209}, may be absent; and wherein the amino acids labelled "*" and "**" are either an N-terminal amino acid and a C-terminal amino acid.

69. A pharmaceutical association for a use according to claim 68, wherein said LINKER comprises a peptide selected from the group consisting of *AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}-AA^{206}-AA^{207}-AA^{208}-AA^{209}** (XXXV), *AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}-AA^{206}-AA^{207}** (XXXV-2) and *AA^{201}-AA^{202}-AA^{203}-AA^{204}-AA^{205}** (XXXV-4).

70. A pharmaceutical association for a use according to claim 68, wherein said LINKER comprises a peptide selected from the group consisting of DENEKVV, DENKNVV, DEYDKVV, DDSSNVI, DSSNNVI, DDMGVPT, DKGVVTY, NDKQQII, DAANNVV, DSANNVV, DDSSNVI, DNGRVLL, VGRKPKV, IGKTPKI, VGRTPKV, RIKPHQGQH, EYVRKKPKL, EIVRKKPIF, EYVRKKP, EIVRKKP, polyalanine (A_{1-9}) and polyglycine (G_{1-9}).

71. A pharmaceutical association for a use according to claim 68, wherein said LINKER is a peptide selected from the group consisting of DENEKVV, DENKNVV, DEYDKVV, DDSSNVI, DSSNNVI, DDMGVPT, DKGVVTY, NDKQQII, DAANNVV, DSANNVV, DDSSNVI, DNGRVLL, VGRKPKV, IGKTPKI, VGRTPKV, RIKPHQGQH, EYVRKKPKL, EIVRKKPIF, EYVRKKP, EIVRKKP, polyalanine (A_{1-9}) and polyglycine (G_{1-9}).

72. A pharmaceutical association for a use according to any one of claims 47 to 67, wherein said LINKER comprises a poly-alanine peptide $(A)_n$ and/or a poly-glycine $(G)_n$, n being an integer comprised between 2 and 16.

73. A pharmaceutical association for a use according to any one of claims 47 to 66, wherein said LINKER is a saturated or unsaturated hydrocarbon chain comprising between 1 and 22, wherein said hydrocarbon chain is optionally interrupted by one or more non-carbon atom, wherein said non-carbon atom is selected from the group consisting of -O-, -S-, -C(=O), -SO_2-, -N(Ri)(C=O)-, and -N(Ri)-, wherein Ri is selected from the group consisting of a hydrogen atom, a C1-C6 alkyl group and an aryl group, and wherein said hydrocarbon chain is non-substituted or substituted by

at least one radical selected from the group consisting of a halogen, a monosaccharide, a poly(1-6)saccharide, a nucleotide, a poly(1-6)nucleotide, a C1-C10 alkyl group and an aryl group.

74. A pharmaceutical association for a use according to any one of claims 4 to 73, wherein the pair PEP1:PEP2 is selected from the group consisting of SAIS:LKNYQ, SSLS:LKVYP, NAIS:LKKYR, SATS:LRKHR, SPIS:LKYHY, EPIS:KFKYE, SPIN:YGKIP, SPIS:YKQYE, KPLS:DHHKD, EPLP:EQLSN, EPLT:EQLSN, SNIT:IGEMS, SNIT:LGEMS, RSVK:KEVQV and RPVQ:KKATV.

75. A pharmaceutical association for a use according to any one of claims 4 to 74, wherein the pair PEP12:PEP2 is selected from the group consisting of SAIS-AA^{17}-LYL:LKNYQ, SSLS-AA^{17}-LFF:LKVYP, NAIS-AA^{17}-LYF:LKKYR, SATS-AA^{17}-LYY:LRKHR, SPIS-AA^{17}-LYK:LKYHY, EPIS-AA^{17}-LYL:KFKYE, SPIN-AA^{17}-LYF:YGKIP, SPIS-AA^{17}-LYI:YKQYE, SPIS-AA^{17}-LFI:YKQYE, KPLS-AA^{17}-LYV:DHHKD, EPLP-AA^{17}-VYY:EQLSN, EPLT-AA^{17}-LYY:EQLSN, SNIT-AA^{17}-QIM:IGEMS, SNIT-AA^{17}-QIM:LGEMS, RSVK-AA^{17}-AKV:KEVQV and RPVQ-AA^{17}-RKI:KKATV ; wherein AA^{17} is selected from the group consisting of G, A, V, L, I, P, F, M, W, T and S.

76. A pharmaceutical association for a use according to any one of claims 4 to 75, wherein the pair PEP3:PEP4 is selected from the group consisting of VPT:VVE, VPE:TVE, APT:VVR, APT:VVK, VPT:VAE, VPT:AVS, TPT:VVD, VPA:VVE, APV:VEE, VPQ:VRS, VSQ:VKS, VPQ:VKS, VPT:QHN, VPT:EHS, SRV:EEH and TQV:EDH.

77. A pharmaceutical association for a use according to any one of claims 4 to 76, wherein the pair PEP5:PEP6 is selected from the group consisting of VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVE, VPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVE, APT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVR, APT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVK, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAE, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVS, TPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVD, VPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVE, APV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEE, VPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRS, VSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKS, VPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKS, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHN, VPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHS, SRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEH and TQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDH.

78. A pharmaceutical association for a use according to any one of claims 4 to 77, wherein the pair PEP5:PEP6 is selected from the group consisting of VPTEL:DMVVE, VPEKM:NMTVE, VPTEL:EMVVE, APTKL:NMVVR, APTQL:NMVVR, APTKL:NMVVK, VPTKL:EGMSVAE, VPTKL:GMAVS, TPTKM:GMVVD, VPARL:DMVVE, VPTRL:DMVVE, APVKT:MIVEE, VPQAL:MIVRS, VSQDL:MIVKS, VPQDL:MVVKS, VPTEE:FLQHN, VPTGQ:LEEHS, SRVHH:RLEEH and TQVQL:TLEDH.

79. A pharmaceutical association for a use according to any one of claims 4 to 78, wherein the pair PEP7:PEP8 is selected from the group consisting of KIPKAXX:GXGXR, GIPEPXX:SXAXR, SIPKAXX:GXGXR, HVTKPTX:SXGXH, YVPKPXX:SXGXH, TVPKPXX:AXGXH, AVPKAXX:AXGXH, KVGKAXX:XGXR, KASKAXX:EXGXR, GSAGPXX:RXGXS,

AAPASXX:AXGXR, STPPTXX:SXGXR, HVPKPXX:SXGXH, RVPSTXX:XGXL, ASAAPXX:XKXS, ASASPXX:XKXS, NDEGLEX:KXEXR, NDEGLEX:QXEXR, SSVKXQP:LEXAXA and RNVQXRP:LAXKXE.

80. A pharmaceutical association for a use according to any one of claims 4 to 79, wherein the pair PEP9:PEP10 is selected from the group consisting of KIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, GIPEPXXVPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR, SIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR, HVTKPTXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, YVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, TVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH, AVPKAXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH, KVGKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR, KASKAXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR, GSAGPXXTPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS, AAPASXXVPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR, STPPTXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR, HVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH, RVPSTXXAPV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL, ASAAPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS, ASASPXXVSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, ASASPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR, NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR, SSVKXQPSRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EEHLEXAXA and RNVQXRPTQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE.

81. A pharmaceutical association for a use according to any one of claims 4 to 80, wherein the pair PEP9:PEP10 is selected from the group consisting of KIPKAXXVPTEL:DMVVEGXGXR, GIPEPXXVPEKM:NMTVESXAXR, SIPKAXXVPTEL:EMVVEGXGXR, HVTKPTXAPTKL:NMVVRSXGXH, YVPKPXXAPTKL:NMVVRSXGXH, TVPKPXXAPTQL:NMVVRAXGXH, AVPKAXXAPTKL:NMVVKAXGXH, KVGKAXXVPTKL:EGMSVAEXGXR, KASKAXXVPTKL:GMAVSEXGXR, GSAGPXXTPTKM:GMVVDRXGXS, AAPASXXVPARL:DMVVEAXGXR, STPPTXXVPTRL:DMVVESXGXR, HVPKPXXAPTKL:NMVVRSXGXH, RVPSTXXAPVKT:MIVEEXGXL, ASAAPXXVPQAL:MIVRSXKXS, ASASPXXVSQDL:MIVKSXKXS, ASASPXXVPQDL:MVVKSXKXS, NDEGLEXVPTEE:FLQHNKXEXR, NDEGLEXVPTGQ:LEEHSQXEXR, NDEGLEXVPTEE:FLQHNKXEXR, NDEGLEXVPTEE:FLQHNKXEXR, SSVKXQPSRVHH:RLEEHLEXAXA and RNVQXRPTQVQL:TLEDHLAXKXE.

82. A pharmaceutical association for a use according to any one of claims 4 to 81, wherein the pair PEP5:PEP6 is not VPTEL:DMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein the pair PEP5:PEP6 is not VPEKM:NMTVE when PEP1 is SSLS and PEP2 is LKVYP; wherein the pair PEP5:PEP6 is not VPTEL:EMVVE when PEP1 is SAIS and PEP2 is LKNYQ; wherein the pair PEP5:PEP6 is not APTKL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein the pair PEP5:PEP6 is not APTQL:NMVVR when PEP1 is NAIS and PEP2 is LKKYR; wherein the pair PEP5:PEP6 is not APTKL:NMVVK when PEP1 is SATS and PEP2 is LRKHR; wherein the pair

PEP5:PEP6 is not VPTKL:EGMSVAE when PEP1 is SPIS and PEP2 is LKYHY; wherein the pair PEP5:PEP6 is not VPTKL:GMAVS when PEP1 is EPIS and PEP2 is KFKYE; wherein the pair PEP5:PEP6 is not TPTKM:GMVVD when PEP1 is SPIN and PEP2 is YGKIP; wherein the pair PEP5:PEP6 is not VPARL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein the pair PEP5:PEP6 is not VPTRL:DMVVE when PEP1 is SPIS and PEP2 is YKQYE; wherein the pair PEP5:PEP6 is not APVKT:MIVEE when PEP1 is KPLS and PEP2 is DHHKD; wherein the pair PEP5:PEP6 is not VPQAL:MIVRS when PEP1 is EPLP and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VSQDL:MIVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VPQDL:MVVKS when PEP1 is EPLT and PEP2 is EQLSN; wherein the pair PEP5:PEP6 is not VPTEE:FLQHN when PEP1 is SNIT and PEP2 is IGEMS; wherein the pair PEP5:PEP6 is not VPTGQ:LEEHS when PEP1 is SNIT and PEP2 is LGEMS; wherein the pair PEP5:PEP6 is not SRVHH:RLEEH when PEP1 is RSVK and PEP2 is KEVQV; and wherein the pair PEP5:PEP6 is not TQVQL:TLEDH when PEP1 is RPVQ and PEP2 is KKATV.

83. A pharmaceutical association for a use according to any one of claims 4 to 82, wherein the pair PEP9:PEP10 is not KIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ ; wherein PEP9:PEP10 is not GIPEPXXVPE-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-TVESXAXR when PEP1 is SSLS and PEP2 is LKVYP; wherein PEP9:PEP10 is not SIPKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ; wherein PEP9:PEP10 is not HVTKPTXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not YVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not TVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRAXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not AVPKAXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVKAXGXH when PEP1 is SATS and PEP2 is LRKHR; wherein PEP9:PEP10 is not KVGKAXXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VAEXGXR when PEP1 is SPIS and PEP2 is LKYHY; wherein PEP9:PEP10 is not KASKAXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-AVSEXGXR when PEP1 is EPIS and PEP2 is KFKYE; wherein PEP9:PEP10 is not GSAGPXXTPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVDRXGXS when PEP1 is SPIN and PEP2 is YGKIP; wherein PEP9:PEP10 is not AAPASXXVPA-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVEAXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not STPPTXXVPT-AA^{11}-AA^{12}-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVESXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not HVPKPXXAPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not RVPSTXXAPV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VEEXGXL when PEP1 is KPLS and PEP2 is DHHKD; wherein PEP9:PEP10 is not ASAAPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VRSXKXS when PEP1 is EPLP and PEP2 is EQLSN; ASASPXXVSQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not ASASPXXVPQ-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-VKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-QHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPT-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EHSQXEXR when PEP1 is SNIT and PEP2 is LGEMS; wherein PEP9:PEP10 is not SSVKXQPSRV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-

AA^{28}-AA^{29}-EEHLEXAXA when PEP1 is RSVK and PEP2 is KEVQV; and wherein PEP9:PEP10 is not RNVQXRPTQV-AA^{11}-AA^{12}:AA^{26}-AA^{27}-AA^{28}-AA^{29}-EDHLAXKXE when PEP1 is RPVQ and PEP2 is KKATV.

84. A pharmaceutical association for a use according to any one of claims 4 to 83, wherein PEP9:PEP10 is not KIPKAXXVPTEL:DMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ ; wherein PEP9:PEP10 is not GIPEPXXVPEKM:NMTVESXAXR when PEP1 is SSLS and PEP2 is LKVYP; wherein PEP9:PEP10 is not SIPKAXXVPTEL:EMVVEGXGXR when PEP1 is SAIS and PEP2 is LKNYQ; wherein PEP9:PEP10 is not HVTKPTXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not YVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not TVPKPXXAPTQL:NMVVRAXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not AVPKAXXAPTKL:NMVVKAXGXH when PEP1 is SATS and PEP2 is LRKHR; wherein PEP9:PEP10 is not KVGKAXXVPTKL:EGMSVAEXGXR when PEP1 is SPIS and PEP2 is LKYHY; wherein PEP9:PEP10 is not KASKAXXVPTKL:GMAVSEXGXR when PEP1 is EPIS and PEP2 is KFKYE; wherein PEP9:PEP10 is not GSAGPXXTPTKM:GMVVDRXGXS when PEP1 is SPIN and PEP2 is YGKIP; wherein PEP9:PEP10 is not AAPASXXVPARL:DMVVEAXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not STPPTXXVPTRL:DMVVESXGXR when PEP1 is SPIS and PEP2 is YKQYE; wherein PEP9:PEP10 is not HVPKPXXAPTKL:NMVVRSXGXH when PEP1 is NAIS and PEP2 is LKKYR; wherein PEP9:PEP10 is not RVPSTXXAPVKT:MIVEEXGXL when PEP1 is KPLS and PEP2 is DHHKD; wherein PEP9:PEP10 is not ASAAPXXVPQAL:MIVRSXKXS when PEP1 is EPLP and PEP2 is EQLSN; ASASPXXVSQDL:MIVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not ASASPXXVPQDL:MVVKSXKXS when PEP1 is EPLT and PEP2 is EQLSN; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPTGQ:LEEHSQXEXR when PEP1 is SNIT and PEP2 is LGEMS ; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not NDEGLEXVPTEE:FLQHNKXEXR when PEP1 is SNIT and PEP2 is IGEMS; wherein PEP9:PEP10 is not SSVKXQPSRVHH:RLEEHLEXAXA when PEP1 is RSVK and PEP2 is KEVQV; and wherein PEP9:PEP10 is not RNVQXRPTQVQL:TLEDHLAXKXE when PEP1 is RPVQ and PEP2 is KKATV.

85. A pharmaceutical association for a use according to any one of claims 4 to 84, wherein the pair PEP1:PEP11 is selected from the group consisting of SAIS:LYL, SSLS:LFF, NAIS:LYF, SATS:LYY, SPIS:LYK, SPIS:LYI, SPIS:LFI, EPIS:LYL, SPIN:LYF, KPLS:LYV, EPLP:VYY, EPLT:LYY, SNIT:QIM, RSVK:AKV and RPVQ:RKI.

86. A pharmaceutical association for a use according to any one of claims 4 to 85, wherein the quadruplet PEP5:PEP1:PEP2:PEP6 is selected from the group consisting of VPTKM:SAIS:LKNYQ:NMVVE, VPTKL:SAIS:LKNYQ:NMVVE, VPTQL:SAIS:LKNYQ:NMVVE, VPTKL:SAIS:LKNYQ:EGMSVVE, VPTKL:SAIS:LKNYQ:GMVVE, VPTKM:SAIS:LKNYQ:GMVVE, VPTRL:SAIS:LKNYQ:DMVVE, VPTKT:SAIS:LKNYQ:MIVVE, VPTAL:SAIS:LKNYQ:MIVVE,

VPTDL:SAIS:LKNYQ:MIVVE, VPTDL:SAIS:LKNYQ:MVVVE, VPEKM:SAIS:LKNYQ:NMTVE,
APTKL:SAIS:LKNYQ:NMVVR, APTQL:SAIS:LKNYQ:NMVVR, APTKL:SAIS:LKNYQ:NMVVK,
VPTKL:SAIS:LKNYQ:EGMSVAE, VPTKL:SAIS:LKNYQ:GMAVS, TPTKM:SAIS:LKNYQ:GMVVD,
VPARL:SAIS:LKNYQ:DMVVE, APVKT:SAIS:LKNYQ:MIVEE, VPQAL:SAIS:LKNYQ:MIVRS,
VSQDL:SAIS:LKNYQ:MIVKS, VPQDL:SAIS:LKNYQ:MVVKS, VPTEE:SAIS:LKNYQ:FLQHN,
VPTGQ:SAIS:LKNYQ:LEEHS, SRVHH:SAIS:LKNYQ:RLEEH, TQVQL:SAIS:LKNYQ:TLEDH,
VPEEL:SSLS:LKVYP:DMTVE, VPEEL:SSLS:LKVYP:EMTVE, VPEKL:SSLS:LKVYP:NMTVE,
VPEQL:SSLS:LKVYP:NMTVE, VPEKL:SSLS:LKVYP:EGMSTVE, VPEKL:SSLS:LKVYP:GMTVE,
VPEKM:SSLS:LKVYP:GMTVE, VPERL:SSLS:LKVYP:DMTVE, VPEKT:SSLS:LKVYP:MITVE,
VPEAL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MITVE, VPEDL:SSLS:LKVYP:MVTVE,
VPTEL:SSLS:LKVYP:DMVVE, VPTEL:SSLS:LKVYP:EMVVE, APTKL:SSLS:LKVYP:NMVVR,
APTQL:SSLS:LKVYP:NMVVR, APTKL:SSLS:LKVYP:NMVVK, VPTKL:SSLS:LKVYP:EGMSVAE,
VPTKL:SSLS:LKVYP:GMAVS, TPTKM:SSLS:LKVYP:GMVVD, VPARL:SSLS:LKVYP:DMVVE,
VPTRL:SSLS:LKVYP:DMVVE, APVKT:SSLS:LKVYP:MIVEE, VPQAL:SSLS:LKVYP:MIVRS,
VSQDL:SSLS:LKVYP:MIVKS, VPQDL:SSLS:LKVYP:MVVKS, VPTEE:SSLS:LKVYP:FLQHN,
VPTGQ:SSLS:LKVYP:LEEHS, SRVHH:SSLS:LKVYP:RLEEH, TQVQL:SSLS:LKVYP:TLEDH,
APTEL:NAIS:LKKYR:DMVVR, APTKM:NAIS:LKKYR:NMVVR, APTEL:NAIS:LKKYR:EMVVR,
APTKL:NAIS:LKKYR:NMVVR, APTKL:NAIS:LKKYR:EGMSVVR, APTKL:NAIS:LKKYR:GMVVR,
APTKM:NAIS:LKKYR:GMVVR, APTRL:NAIS:LKKYR:DMVVR, APTKT:NAIS:LKKYR:MIVVR,
APTAL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MIVVR, APTDL:NAIS:LKKYR:MVVVR,
VPTEL:NAIS:LKKYR:DMVVE, VPEKM:NAIS:LKKYR:NMTVE, VPTEL:NAIS:LKKYR:EMVVE,
APTKL:NAIS:LKKYR:NMVVK, VPTKL:NAIS:LKKYR:EGMSVAE, VPTKL:NAIS:LKKYR:GMAVS,
TPTKM:NAIS:LKKYR:GMVVD, VPARL:NAIS:LKKYR:DMVVE, VPTRL:NAIS:LKKYR:DMVVE,
APVKT:NAIS:LKKYR:MIVEE, VPQAL:NAIS:LKKYR:MIVRS, VSQDL:NAIS:LKKYR:MIVKS,
VPQDL:NAIS:LKKYR:MVVKS, VPTEE:NAIS:LKKYR:FLQHN, VPTGQ:NAIS:LKKYR:LEEHS,
SRVHH:NAIS:LKKYR:RLEEH, TQVQL:NAIS:LKKYR:TLEDH, APTEL:SATS:LRKHR:DMVVK,
APTKM:SATS:LRKHR:NMVVK, APTEL:SATS:LRKHR:EMVVK, APTKL:SATS:LRKHR:NMVVK,
APTQL:SATS:LRKHR:NMVVK, APTKL:SATS:LRKHR:EGMSVVK, APTKL:SATS:LRKHR:GMVVK,
APTKM:SATS:LRKHR:GMVVK, APTRL:SATS:LRKHR:DMVVK, APTKT:SATS:LRKHR:MIVVK,
APTAL:SATS:LRKHR:MIVVK, APTDL:SATS:LRKHR:MIVVK, APTDL:SATS:LRKHR:MVVVK,
VPTEL:SATS:LRKHR:DMVVE, VPEKM:SATS:LRKHR:NMTVE, VPTEL:SATS:LRKHR:EMVVE,
APTKL:SATS:LRKHR:NMVVR, APTQL:SATS:LRKHR:NMVVR, VPTKL:SATS:LRKHR:EGMSVAE,
VPTKL:SATS:LRKHR:GMAVS, TPTKM:SATS:LRKHR:GMVVD, VPARL:SATS:LRKHR:DMVVE,
VPTRL:SATS:LRKHR:DMVVE, APVKT:SATS:LRKHR:MIVEE, VPQAL:SATS:LRKHR:MIVRS,
VSQDL:SATS:LRKHR:MIVKS, VPQDL:SATS:LRKHR:MVVKS, VPTEE:SATS:LRKHR:FLQHN,
VPTGQ:SATS:LRKHR:LEEHS, SRVHH:SATS:LRKHR:RLEEH, TQVQL:SATS:LRKHR:TLEDH,
VPTEL:SPIS:LKYHY:DMVAE, VPTKM:SPIS:LKYHY:NMVAE, VPTEL:SPIS:LKYHY:EMVAE,
VPTKL:SPIS:LKYHY:NMVAE, VPTQL:SPIS:LKYHY:NMVAE, VPTKL:SPIS:LKYHY:GMVAE,
VPTKM:SPIS:LKYHY:GMVAE, VPTRL:SPIS:LKYHY:DMVAE, VPTKT:SPIS:LKYHY:MIVAE,
VPTAL:SPIS:LKYHY:MIVAE, VPTDL:SPIS:LKYHY:MIVAE, VPTDL:SPIS:LKYHY:MVVAE,
VPTEL:SPIS:LKYHY:DMVVE, VPEKM:SPIS:LKYHY:NMTVE, VPTEL:SPIS:LKYHY:EMVVE,
APTKL:SPIS:LKYHY:NMVVR, APTQL:SPIS:LKYHY:NMVVR, APTKL:SPIS:LKYHY:NMVVK,

VPTKL:SPIS:LKYHY:GMAVS, TPTKM:SPIS:LKYHY:GMVVD, VPARL:SPIS:LKYHY:DMVVE,
VPTRL:SPIS:LKYHY:DMVVE, APVKT:SPIS:LKYHY:MIVEE, VPQAL:SPIS:LKYHY:MIVRS,
VSQDL:SPIS:LKYHY:MIVKS, VPQDL:SPIS:LKYHY:MVVKS, VPTEE:SPIS:LKYHY:FLQHN,
VPTGQ:SPIS:LKYHY:LEEHS, SRVHH:SPIS:LKYHY:RLEEH, TQVQL:SPIS:LKYHY:TLEDH,
VPTEL:EPIS:KFKYE:DMAVS, VPTKM:EPIS:KFKYE:NMAVS, VPTEL:EPIS:KFKYE:EMAVS,
VPTKL:EPIS:KFKYE:NMAVS, VPTQL:EPIS:KFKYE:NMAVS, VPTKL:EPIS:KFKYE:EGMSAVS,
VPTKM:EPIS:KFKYE:GMAVS, VPTRL:EPIS:KFKYE:DMAVS, VPTKT:EPIS:KFKYE:MIAVS,
VPTAL:EPIS:KFKYE:MIAVS, VPTDL:EPIS:KFKYE:MIAVS, VPTDL:EPIS:KFKYE:MVAVS,
VPTEL:EPIS:KFKYE:DMVVE, VPEKM:EPIS:KFKYE:NMTVE, VPTEL:EPIS:KFKYE:EMVVE,
APTKL:EPIS:KFKYE:NMVVR, APTQL:EPIS:KFKYE:NMVVR, APTKL:EPIS:KFKYE:NMVVK,
VPTKL:EPIS:KFKYE:EGMSVAE, TPTKM:EPIS:KFKYE:GMVVD, VPARL:EPIS:KFKYE:DMVVE,
VPTRL:EPIS:KFKYE:DMVVE, APVKT:EPIS:KFKYE:MIVEE, VPQAL:EPIS:KFKYE:MIVRS,
VSQDL:EPIS:KFKYE:MIVKS, VPQDL:EPIS:KFKYE:MVVKS, VPTEE:EPIS:KFKYE:FLQHN,
VPTGQ:EPIS:KFKYE:LEEHS, SRVHH:EPIS:KFKYE:RLEEH, TQVQL:EPIS:KFKYE:TLEDH,
TPTEL:SPIN:YGKIP:DMVVD, TPTKM:SPIN:YGKIP:NMVVD, TPTEL:SPIN:YGKIP:EMVVD,
TPTKL:SPIN:YGKIP:NMVVD, TPTQL:SPIN:YGKIP:NMVVD, TPTKL:SPIN:YGKIP:EGMSVVD,
TPTKL:SPIN:YGKIP:GMVVD, TPTRL:SPIN:YGKIP:DMVVD, TPTKT:SPIN:YGKIP:MIVVD,
TPTAL:SPIN:YGKIP:MIVVD, TPTDL:SPIN:YGKIP:MIVVD, TPTDL:SPIN:YGKIP:MVVVD,
VPTEL:SPIN:YGKIP:DMVVE, VPEKM:SPIN:YGKIP:NMTVE, VPTEL:SPIN:YGKIP:EMVVE,
APTKL:SPIN:YGKIP:NMVVR, APTQL:SPIN:YGKIP:NMVVR, APTKL:SPIN:YGKIP:NMVVK,
VPTKL:SPIN:YGKIP:EGMSVAE, VPTKL:SPIN:YGKIP:GMAVS, VPARL:SPIN:YGKIP:DMVVE,
VPTRL:SPIN:YGKIP:DMVVE, APVKT:SPIN:YGKIP:MIVEE, VPQAL:SPIN:YGKIP:MIVRS,
VSQDL:SPIN:YGKIP:MIVKS, VPQDL:SPIN:YGKIP:MVVKS, VPTEE:SPIN:YGKIP:FLQHN,
VPTGQ:SPIN:YGKIP:LEEHS, SRVHH:SPIN:YGKIP:RLEEH, TQVQL:SPIN:YGKIP:TLEDH,
VPAEL:SPIS:YKQYE:DMVVE, VPAKM:SPIS:YKQYE:NMVVE, VPAEL:SPIS:YKQYE:EMVVE,
VPAKL:SPIS:YKQYE:NMVVE, VPAQL:SPIS:YKQYE:NMVVE, VPAKL:SPIS:YKQYE:EGMSVVE,
VPAKL:SPIS:YKQYE:GMVVE, VPAKM:SPIS:YKQYE:GMVVE, VPARL:SPIS:YKQYE:DMVVE,
VPAKT:SPIS:YKQYE:MIVVE, VPAAL:SPIS:YKQYE:MIVVE, VPADL:SPIS:YKQYE:MIVVE,
VPADL:SPIS:YKQYE:MVVVE, VPTEL:SPIS:YKQYE:DMVVE, VPEKM:SPIS:YKQYE:NMTVE,
VPTEL:SPIS:YKQYE:EMVVE, APTKL:SPIS:YKQYE:NMVVR, APTQL:SPIS:YKQYE:NMVVR,
APTKL:SPIS:YKQYE:NMVVK, VPTKL:SPIS:YKQYE:EGMSVAE, VPTKL:SPIS:YKQYE:GMAVS,
TPTKM:SPIS:YKQYE:GMVVD, VPTRL:SPIS:YKQYE:DMVVE, APVKT:SPIS:YKQYE:MIVEE,
VPQAL:SPIS:YKQYE:MIVRS, VSQDL:SPIS:YKQYE:MIVKS, VPQDL:SPIS:YKQYE:MVVKS,
VPTEE:SPIS:YKQYE:FLQHN, VPTGQ:SPIS:YKQYE:LEEHS, SRVHH:SPIS:YKQYE:RLEEH,
TQVQL:SPIS:YKQYE:TLEDH, VPTKM:SPIS:YKQYE:NMVVE, VPTKL:SPIS:YKQYE:NMVVE,
VPTQL:SPIS:YKQYE:NMVVE, VPTKL:SPIS:YKQYE:EGMSVVE, VPTKL:SPIS:YKQYE:GMVVE,
VPTKM:SPIS:YKQYE:GMVVE, VPTKT:SPIS:YKQYE:MIVVE, VPTAL:SPIS:YKQYE:MIVVE,
VPTDL:SPIS:YKQYE:MIVVE, VPTDL:SPIS:YKQYE:MVVVE, APVEL:KPLS:DHHKD:DMVEE,
APVKM:KPLS:DHHKD:NMVEE, APVEL:KPLS:DHHKD:EMVEE, APVKL:KPLS:DHHKD:NMVEE,
APVQL:KPLS:DHHKD:NMVEE, APVKL:KPLS:DHHKD:EGMSVEE,
APVKL:KPLS:DHHKD:GMVEE, APVKM:KPLS:DHHKD:GMVEE, APVRL:KPLS:DHHKD:DMVEE,
APVAL:KPLS:DHHKD:MIVEE, APVDL:KPLS:DHHKD:MIVEE, APVDL:KPLS:DHHKD:MVVEE,

VPTEL:KPLS:DHHKD:DMVVE, VPEKM:KPLS:DHHKD:NMTVE, VPTEL:KPLS:DHHKD:EMVVE, APTKL:KPLS:DHHKD:NMVVR, APTQL:KPLS:DHHKD:NMVVR, APTKL:KPLS:DHHKD:NMVVK, VPTKL:KPLS:DHHKD:EGMSVAE, VPTKL:KPLS:DHHKD:GMAVS, TPTKM:KPLS:DHHKD:GMVVD, VPARL:KPLS:DHHKD:DMVVE, VPTRL:KPLS:DHHKD:DMVVE, VPQAL:KPLS:DHHKD:MIVRS, VSQDL:KPLS:DHHKD:MIVKS, VPQDL:KPLS:DHHKD:MVVKS, VPTEE:KPLS:DHHKD:FLQHN, VPTGQ:KPLS:DHHKD:LEEHS, SRVHH:KPLS:DHHKD:RLEEH, TQVQL:KPLS:DHHKD:TLEDH, VPQEL:EPLP:EQLSN:DMVRS, VPQKM:EPLP:EQLSN:NMVRS, VPQEL:EPLP:EQLSN:EMVRS, VPQKL:EPLP:EQLSN:NMVRS, VPQQL:EPLP:EQLSN:NMVRS, VPQKL:EPLP:EQLSN:EGMSVRS, VPQKL:EPLP:EQLSN:GMVRS, VPQKM:EPLP:EQLSN:GMVRS, VPQRL:EPLP:EQLSN:DMVRS, VPQKT:EPLP:EQLSN:MIVRS, VPQDL:EPLP:EQLSN:MIVRS, VPQDL:EPLP:EQLSN:MVVRS, VPTEL:EPLP:EQLSN:DMVVE, VPEKM:EPLP:EQLSN:NMTVE, VPTEL:EPLP:EQLSN:EMVVE, APTKL:EPLP:EQLSN:NMVVR, APTQL:EPLP:EQLSN:NMVVR, APTKL:EPLP:EQLSN:NMVVK, VPTKL:EPLP:EQLSN:EGMSVAE, VPTKL:EPLP:EQLSN:GMAVS, TPTKM:EPLP:EQLSN:GMVVD, VPARL:EPLP:EQLSN:DMVVE, VPTRL:EPLP:EQLSN:DMVVE, APVKT:EPLP:EQLSN:MIVEE, VSQDL:EPLP:EQLSN:MIVKS, VPQDL:EPLP:EQLSN:MVVKS, VPTEE:EPLP:EQLSN:FLQHN, VPTGQ:EPLP:EQLSN:LEEHS, SRVHH:EPLP:EQLSN:RLEEH, TQVQL:EPLP:EQLSN:TLEDH, VSQEL:EPLT:EQLSN:DMVKS, VSQKM:EPLT:EQLSN:NMVKS, VSQEL:EPLT:EQLSN:EMVKS, VSQKL:EPLT:EQLSN:NMVKS, VSQQL:EPLT:EQLSN:NMVKS, VSQKL:EPLT:EQLSN:EGMSVKS, VSQKL:EPLT:EQLSN:GMVKS, VSQKM:EPLT:EQLSN:GMVKS, VSQRL:EPLT:EQLSN:DMVKS, VSQKT:EPLT:EQLSN:MIVKS, VSQAL:EPLT:EQLSN:MIVKS, VSQDL:EPLT:EQLSN:MVVKS, VPTEL:EPLT:EQLSN:DMVVE, VPEKM:EPLT:EQLSN:NMTVE, VPTEL:EPLT:EQLSN:EMVVE, APTKL:EPLT:EQLSN:NMVVR, APTQL:EPLT:EQLSN:NMVVR, APTKL:EPLT:EQLSN:NMVVK, VPTKL:EPLT:EQLSN:EGMSVAE, VPTKL:EPLT:EQLSN:GMAVS, TPTKM:EPLT:EQLSN:GMVVD, VPARL:EPLT:EQLSN:DMVVE, VPTRL:EPLT:EQLSN:DMVVE, APVKT:EPLT:EQLSN:MIVEE, VPQAL:EPLT:EQLSN:MIVRS, VPTEE:EPLT:EQLSN:FLQHN, VPTGQ:EPLT:EQLSN:LEEHS, SRVHH:EPLT:EQLSN:RLEEH, TQVQL:EPLT:EQLSN:TLEDH, VPQEL:EPLT:EQLSN:DMVKS, VPQKM:EPLT:EQLSN:NMVKS, VPQEL:EPLT:EQLSN:EMVKS, VPQKL:EPLT:EQLSN:NMVKS, VPQQL:EPLT:EQLSN:NMVKS, VPQKL:EPLT:EQLSN:EGMSVKS, VPQKL:EPLT:EQLSN:GMVKS, VPQKM:EPLT:EQLSN:GMVKS, VPQRL:EPLT:EQLSN:DMVKS, VPQKT:EPLT:EQLSN:MIVKS, VPQAL:EPLT:EQLSN:MIVKS, VPQDL:EPLT:EQLSN:MIVKS, VPTGQ:SNIT:IGEMS:LEQHN, VPTEL:SNIT:IGEMS:DMVVE, VPEKM:SNIT:IGEMS:NMTVE, VPTEL:SNIT:IGEMS:EMVVE, APTKL:SNIT:IGEMS:NMVVR, APTQL:SNIT:IGEMS:NMVVR, APTKL:SNIT:IGEMS:NMVVK, VPTKL:SNIT:IGEMS:EGMSVAE, VPTKL:SNIT:IGEMS:GMAVS, TPTKM:SNIT:IGEMS:GMVVD, VPARL:SNIT:IGEMS:DMVVE, VPTRL:SNIT:IGEMS:DMVVE, APVKT:SNIT:IGEMS:MIVEE, VPQAL:SNIT:IGEMS:MIVRS, VSQDL:SNIT:IGEMS:MIVKS, VPQDL:SNIT:IGEMS:MVVKS, VPTGQ:SNIT:IGEMS:LEEHS, SRVHH:SNIT:IGEMS:RLEEH, TQVQL:SNIT:IGEMS:TLEDH, VPTEE:SNIT:LGEMS:FLEHS, VPTEL:SNIT:LGEMS:DMVVE, VPEKM:SNIT:LGEMS:NMTVE, VPTEL:SNIT:LGEMS:EMVVE, APTKL:SNIT:LGEMS:NMVVR, APTQL:SNIT:LGEMS:NMVVR, APTKL:SNIT:LGEMS:NMVVK, VPTKL:SNIT:LGEMS:EGMSVAE, VPTKL:SNIT:LGEMS:GMAVS, TPTKM:SNIT:LGEMS:GMVVD, VPARL:SNIT:LGEMS:DMVVE, VPTRL:SNIT:LGEMS:DMVVE, APVKT:SNIT:LGEMS:MIVEE, VPQAL:SNIT:LGEMS:MIVRS, VSQDL:SNIT:LGEMS:MIVKS,

VPQDL:SNIT:LGEMS:MVVKS, VPTEE:SNIT:LGEMS:FLQHN, SRVHH:SNIT:LGEMS:RLEEH, TQVQL:SNIT:LGEMS:TLEDH, SRVQL:RSVK:KEVQV:TLEEH, VPTEL:RSVK:KEVQV:DMVVE, VPEKM:RSVK:KEVQV:NMTVE, VPTEL:RSVK:KEVQV:EMVVE, APTKL:RSVK:KEVQV:NMVVR, APTQL:RSVK:KEVQV:NMVVR, APTKL:RSVK:KEVQV:NMVVK, VPTKL:RSVK:KEVQV:EGMSVAE, VPTKL:RSVK:KEVQV:GMAVS, TPTKM:RSVK:KEVQV:GMVVD, VPARL:RSVK:KEVQV:DMVVE, VPTRL:RSVK:KEVQV:DMVVE, APVKT:RSVK:KEVQV:MIVEE, VPQAL:RSVK:KEVQV:MIVRS, VSQDL:RSVK:KEVQV:MIVKS, VPQDL:RSVK:KEVQV:MVVKS, VPTEE:RSVK:KEVQV:FLQHN, VPTGQ:RSVK:KEVQV:LEEHS, TQVQL:RSVK:KEVQV:TLEDH, TQVHH:RPVQ:KKATV:RLEDH, VPTEL:RPVQ:KKATV:DMVVE, VPEKM:RPVQ:KKATV:NMTVE, VPTEL:RPVQ:KKATV:EMVVE, APTKL:RPVQ:KKATV:NMVVR, APTQL:RPVQ:KKATV:NMVVR, APTKL:RPVQ:KKATV:NMVVK, VPTKL:RPVQ:KKATV:EGMSVAE, VPTKL:RPVQ:KKATV:GMAVS, TPTKM:RPVQ:KKATV:GMVVD, VPARL:RPVQ:KKATV:DMVVE, VPTRL:RPVQ:KKATV:DMVVE, APVKT:RPVQ:KKATV:MIVEE, VPQAL:RPVQ:KKATV:MIVRS, VSQDL:RPVQ:KKATV:MIVKS, VPQDL:RPVQ:KKATV:MVVKS, VPTEE:RPVQ:KKATV:FLQHN, VPTGQ:RPVQ:KKATV:LEEHS and SRVHH:RPVQ:KKATV:RLEEH.

87. A pharmaceutical association for a use according to any one of claims 4 to 86, wherein the quadruplet PEP9:PEP1:PEP2:PEP10 is selected from the group consisting of GIPEPXXVPTKM:SAIS:LKNYQ:NMVVESXAXR, HVTKPTXVPTKL:SAIS:LKNYQ:NMVVESXGXH, YVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, TVPKPXXVPTQL:SAIS:LKNYQ:NMVVEAXGXH, AVPKAXXVPTKL:SAIS:LKNYQ:NMVVEAXGXH,
KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVVEXGXR,
KASKAXXVPTKL:SAIS:LKNYQ:GMVVEEXGXR,
GSAGPXXVPTKM:SAIS:LKNYQ:GMVVERXGXS,
AAPASXXVPTRL:SAIS:LKNYQ:DMVVEAXGXR, STPPTXXVPTRL:SAIS:LKNYQ:DMVVESXGXR,
HVPKPXXVPTKL:SAIS:LKNYQ:NMVVESXGXH, RVPSTXXVPTKT:SAIS:LKNYQ:MIVVEXGXL,
ASAAPXXVPTAL:SAIS:LKNYQ:MIVVEXKXS, ASASPXXVPTDL:SAIS:LKNYQ:MIVVEXKXS,
ASASPXXVPTDL:SAIS:LKNYQ:MVVVEXKXS, GIPEPXXVPEKM:SAIS:LKNYQ:NMTVESXAXR,
HVTKPTXAPTKL:SAIS:LKNYQ:NMVVRSXGXH, YVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH,
TVPKPXXAPTQL:SAIS:LKNYQ:NMVVRAXGXH, AVPKAXXAPTKL:SAIS:LKNYQ:NMVVKAXGXH,
KVGKAXXVPTKL:SAIS:LKNYQ:EGMSVAEXGXR,
KASKAXXVPTKL:SAIS:LKNYQ:GMAVSEXGXR,
GSAGPXXTPTKM:SAIS:LKNYQ:GMVVDRXGXS,
AAPASXXVPARL:SAIS:LKNYQ:DMVVEAXGXR, HVPKPXXAPTKL:SAIS:LKNYQ:NMVVRSXGXH,
RVPSTXXAPVKT:SAIS:LKNYQ:MIVEEXGXL, ASAAPXXVPQAL:SAIS:LKNYQ:MIVRSXKXS,
ASASPSSVSQDL:SAIS:LKNYQ:MIVKSXKXS, ASASPXXVPQDL:SAIS:LKNYQ:MVVKSXKXS,
NDEGLEXVPTEE:SAIS:LKNYQ:FLQHNKXEXR, NDEGLEXVPTGQ:SAIS:LKNYQ:LEEHSQXEXR,
SSVKXQPSRVHH:SAIS:LKNYQ:RLEEHLEXAXA,
RNVQXRPTQVQL:SAIS:LKNYQ:TLEDHLAXKXE,
KIPKAXXVPEEL:SSLS:LKVYP:DMTVEGXGXR, SIPKAXXVPEEL:SSLS:LKVYP:EMTVEGXGXR,
HVTKPTXVPEKL:SSLS:LKVYP:NMTVESXGXH, YVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH,

TVPKPXXVPEQL:SSLS:LKVYP:NMTVEAXGXH, AVPKAXXVPEKL:SSLS:LKVYP:NMTVEAXGXH,
KVGKAXXVPEKL:SSLS:LKVYP:EGMSTVEXGXR,
KASKAXXVPEKL:SSLS:LKVYP:GMTVEEXGXR,
GSAGPXXVPEKM:SSLS:LKVYP:GMTVERXGXS,
AAPASXXVPERL:SSLS:LKVYP:DMTVEAXGXR, STPPTXXVPERL:SSLS:LKVYP:DMTVESXGXR,
HVPKPXXVPEKL:SSLS:LKVYP:NMTVESXGXH, RVPSTXXVPEKT:SSLS:LKVYP:MITVEXGXL,
ASAAPXXVPEAL:SSLS:LKVYP:MITVEXKXS, ASASPXXVPEDL:SSLS:LKVYP:MITVEXKXS,
ASASPXXVPEDL:SSLS:LKVYP:MVTVEXKXS, KIPKAXXVPTEL:SSLS:LKVYP:DMVVEGXGXR,
SIPKAXXVPTEL:SSLS:LKVYP:EMVVEGXGXR, HVTKPTXAPTKL:SSLS:LKVYP:NMVVRSXGXH,
YVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH,
TVPKPXXAPTQL:SSLS:LKVYP:NMVVRAXGXH,
AVPKAXXAPTKL:SSLS:LKVYP:NMVVKAXGXH,
KVGKAXXVPTKL:SSLS:LKVYP:EGMSVAEXGXR,
KASKAXXVPTKL:SSLS:LKVYP:GMAVSEXGXR,
GSAGPXXTPTKM:SSLS:LKVYP:GMVVDRXGXS,
AAPASXXVPARL:SSLS:LKVYP:DMVVEAXGXR, STPPTXXVPTRL:SSLS:LKVYP:DMVVESXGXR,
HVPKPXXAPTKL:SSLS:LKVYP:NMVVRSXGXH, RVPSTXXAPVKT:SSLS:LKVYP:MIVEEXGXL,
ASAAPXXVPQAL:SSLS:LKVYP:MIVRSXKXS, ASASPSSVSQDL:SSLS:LKVYP:MIVKSXKXS,
ASASPXXVPQDL:SSLS:LKVYP:MVVKSXKXS, NDEGLEXVPTEE:SSLS:LKVYP:FLQHNKXEXR,
NDEGLEXVPTGQ:SSLS:LKVYP:LEEHSQXEXR,
SSVKXQPSRVHH:SSLS:LKVYP:RLEEHLEXAXA,
RNVQXRPTQVQL:SSLS:LKVYP:TLEDHLAXKXE,
KIPKAXXAPTEL:NAIS:LKKYR:DMVVRGXGXR, GIPEPXXAPTKM:NAIS:LKKYR:NMVVRSXAXR,
SIPKAXXAPTEL:NAIS:LKKYR:EMVVRGXGXR, AVPKAXXAPTKL:NAIS:LKKYR:NMVVRAXGXH,
KVGKAXXAPTKL:NAIS:LKKYR:EGMSVVRXGXR,
KASKAXXAPTKL:NAIS:LKKYR:GMVVREXGXR,
GSAGPXXAPTKM:NAIS:LKKYR:GMVVRRXGXS,
AAPASXXAPTRL:NAIS:LKKYR:DMVVRAXGXR, STPPTXXAPTRL:NAIS:LKKYR:DMVVRSXGXR,
RVPSTXXAPTKT:NAIS:LKKYR:MIVVRXGXL, ASAAPXXAPTAL:NAIS:LKKYR:MIVVRXKXS,
ASASPXXAPTDL:NAIS:LKKYR:MIVVRXKXS, ASASPXXAPTDL:NAIS:LKKYR:MVVVRXKXS,
KIPKAXXVPTEL:NAIS:LKKYR:DMVVEGXGXR, GIPEPXXVPEKM:NAIS:LKKYR:NMTVESXAXR,
SIPKAXXVPTEL:NAIS:LKKYR:EMVVEGXGXR, AVPKAXXAPTKL:NAIS:LKKYR:NMVVKAXGXH,
KVGKAXXVPTKL:NAIS:LKKYR:EGMSVAEXGXR,
KASKAXXVPTKL:NAIS:LKKYR:GMAVSEXGXR,
GSAGPXXTPTKM:NAIS:LKKYR:GMVVDRXGXS,
AAPASXXVPARL:NAIS:LKKYR:DMVVEAXGXR, STPPTXXVPTRL:NAIS:LKKYR:DMVVESXGXR,
RVPSTXXAPVKT:NAIS:LKKYR:MIVEEXGXL, ASAAPXXVPQAL:NAIS:LKKYR:MIVRSXKXS,
ASASPSSVSQDL:NAIS:LKKYR:MIVKSXKXS, ASASPXXVPQDL:NAIS:LKKYR:MVVKSXKXS,
NDEGLEXVPTEE:NAIS:LKKYR:FLQHNKXEXR, NDEGLEXVPTGQ:NAIS:LKKYR:LEEHSQXEXR,
SSVKXQPSRVHH:NAIS:LKKYR:RLEEHLEXAXA,
RNVQXRPTQVQL:NAIS:LKKYR:TLEDHLAXKXE,
KIPKAXXAPTEL:SATS:LRKHR:DMVVKGXGXR, GIPEPXXAPTKM:SATS:LRKHR:NMVVKSXAXR,

SIPKAXXAPTEL:SATS:LRKHR:EMVVKGXGXR, HVTKPTXAPTKL:SATS:LRKHR:NMVVKSXGXH,
YVPKPXXAPTKL:SATS:LRKHR:NMVVKSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVKAXGXH,
KVGKAXXAPTKL:SATS:LRKHR:EGMSVVKXGXR,
KASKAXXAPTKL:SATS:LRKHR:GMVVKEXGXR,
GSAGPXXAPTKM:SATS:LRKHR:GMVVKRXGXS,
AAPASXXAPTRL:SATS:LRKHR:DMVVKAXGXR,
STPPTXXAPTRL:SATS:LRKHR:DMVVKSXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVKSXGXH, RVPSTXXAPTKT:SATS:LRKHR:MIVVKXGXL,
ASAAPXXAPTAL:SATS:LRKHR:MIVVKXKXS, ASASPXXAPTDL:SATS:LRKHR:MIVVKXKXS,
ASASPXXAPTDL:SATS:LRKHR:MVVVKXKXS, KIPKAXXVPTEL:SATS:LRKHR:DMVVEGXGXR,
GIPEPXXVPEKM:SATS:LRKHR:NMTVESXAXR, SIPKAXXVPTEL:SATS:LRKHR:EMVVEGXGXR,
HVTKPTXAPTKL:SATS:LRKHR:NMVVRSXGXH,
YVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH,
TVPKPXXAPTQL:SATS:LRKHR:NMVVRAXGXH,
KVGKAXXVPTKL:SATS:LRKHR:EGMSVAEXGXR,
KASKAXXVPTKL:SATS:LRKHR:GMAVSEXGXR,
GSAGPXXTPTKM:SATS:LRKHR:GMVVDRXGXS,
AAPASXXVPARL:SATS:LRKHR:DMVVEAXGXR,
STPPTXXVPTRL:SATS:LRKHR:DMVVESXGXR,
HVPKPXXAPTKL:SATS:LRKHR:NMVVRSXGXH, RVPSTXXAPVKT:SATS:LRKHR:MIVEEXGXL,
ASAAPXXVPQAL:SATS:LRKHR:MIVRSXKXS, ASASPSSVSQDL:SATS:LRKHR:MIVKSXKXS,
ASASPXXVPQDL:SATS:LRKHR:MVVKSXKXS, NDEGLEXVPTEE:SATS:LRKHR:FLQHNKXEXR,
NDEGLEXVPTGQ:SATS:LRKHR:LEEHSQXEXR,
SSVKXQPSRVHH:SATS:LRKHR:RLEEHLEXAXA,
RNVQXRPTQVQL:SATS:LRKHR:TLEDHLAXKXE,
KIPKAXXVPTEL:SPIS:LKYHY:DMVAEGXGXR, GIPEPXXVPTKM:SPIS:LKYHY:NMVAESXAXR,
SIPKAXXVPTEL:SPIS:LKYHY:EMVAEGXGXR, HVTKPTXVPTKL:SPIS:LKYHY:NMVAESXGXH,
YVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH, TVPKPXXVPTQL:SPIS:LKYHY:NMVAEAXGXH,
AVPKAXXVPTKL:SPIS:LKYHY:NMVAEAXGXH, KASKAXXVPTKL:SPIS:LKYHY:GMVAEEXGXR,
GSAGPXXVPTKM:SPIS:LKYHY:GMVAERXGXS,
AAPASXXVPTRL:SPIS:LKYHY:DMVAEAXGXR, STPPTXXVPTRL:SPIS:LKYHY:DMVAESXGXR,
HVPKPXXVPTKL:SPIS:LKYHY:NMVAESXGXH, RVPSTXXVPTKT:SPIS:LKYHY:MIVAEXGXL,
ASAAPXXVPTAL:SPIS:LKYHY:MIVAEXKXS, ASASPXXVPTDL:SPIS:LKYHY:MIVAEXKXS,
ASASPXXVPTDL:SPIS:LKYHY:MVVAEXKXS, KIPKAXXVPTEL:SPIS:LKYHY:DMVVEGXGXR,
GIPEPXXVPEKM:SPIS:LKYHY:NMTVESXAXR, SIPKAXXVPTEL:SPIS:LKYHY:EMVVEGXGXR,
HVTKPTXAPTKL:SPIS:LKYHY:NMVVRSXGXH, YVPKPXXAPTKL:SPIS:LKYHY:NMVVRSXGXH,
TVPKPXXAPTQL:SPIS:LKYHY:NMVVRAXGXH, AVPKAXXAPTKL:SPIS:LKYHY:NMVVKAXGXH,
KASKAXXVPTKL:SPIS:LKYHY:GMAVSEXGXR,
GSAGPXXTPTKM:SPIS:LKYHY:GMVVDRXGXS,
AAPASXXVPARL:SPIS:LKYHY:DMVVEAXGXR, STPPTXXVPTRL:SPIS:LKYHY:DMVVESXGXR,
HVPKPXXAPTKL:SPIS:LKYHY:NMVVRSXGXH, RVPSTXXAPVKT:SPIS:LKYHY:MIVEEXGXL,

ASAAPXXVPQAL:SPIS:LKYHY:MIVRSXKXS, ASASPSSVSQDL:SPIS:LKYHY:MIVKSXKXS,
ASASPXXVPQDL:SPIS:LKYHY:MVVKSXKXS, NDEGLEXVPTEE:SPIS:LKYHY:FLQHNKXEXR,
NDEGLEXVPTGQ:SPIS:LKYHY:LEEHSQXEXR,
SSVKXQPSRVHH:SPIS:LKYHY:RLEEHLEXAXA,
RNVQXRPTQVQL:SPIS:LKYHY:TLEDHLAXKXE, KIPKAXXVPTEL:EPIS:KFKYE:DMAVXGXGSR,
GIPEPXXVPTKM:EPIS:KFKYE:NMAVSSXAXR, SIPKAXXVPTEL:EPIS:KFKYE:EMAVXGXGSR,
HVTKPTXVPTKL:EPIS:KFKYE:NMAVSSXGXH, YVPKPXXVPTKL:EPIS:KFKYE:NMAVSSXGXH,
TVPKPXXVPTQL:EPIS:KFKYE:NMAVSAXGXH, AVPKAXXVPTKL:EPIS:KFKYE:NMAVSAXGXH,
KVGKAXXVPTKL:EPIS:KFKYE:EGMSAVSXGXR,
GSAGPXXVPTKM:EPIS:KFKYE:GMAVSRXGXS,
AAPASXXVPTRL:EPIS:KFKYE:DMAVSAXGXR, STPPTXXVPTRL:EPIS:KFKYE:DMAVSSXGXR,
HVPKPXXVPTKL:EPIS:KFKYE:NMAVSSXGXH, RVPSTXXVPTKT:EPIS:KFKYE:MIAVSXGXL,
ASAAPXXVPTAL:EPIS:KFKYE:MIAVSXKXS, ASASPXXVPTDL:EPIS:KFKYE:MIAVSXKXS,
ASASPXXVPTDL:EPIS:KFKYE:MVAVSXKXS, KIPKAXXVPTEL:EPIS:KFKYE:DMVVEGXGXR,
GIPEPXXVPEKM:EPIS:KFKYE:NMTVESXAXR, SIPKAXXVPTEL:EPIS:KFKYE:EMVVEGXGXR,
HVTKPTXAPTKL:EPIS:KFKYE:NMVVRSXGXH, YVPKPXXAPTKL:EPIS:KFKYE:NMVVRSXGXH,
TVPKPXXAPTQL:EPIS:KFKYE:NMVVRAXGXH, AVPKAXXAPTKL:EPIS:KFKYE:NMVVKAXGXH,
KVGKAXXVPTKL:EPIS:KFKYE:EGMSVAEXGXR,
GSAGPXXTPTKM:EPIS:KFKYE:GMVVDRXGXS,
AAPASXXVPARL:EPIS:KFKYE:DMVVEAXGXR, STPPTXXVPTRL:EPIS:KFKYE:DMVVESXGXR,
HVPKPXXAPTKL:EPIS:KFKYE:NMVVRSXGXH, RVPSTXXAPVKT:EPIS:KFKYE:MIVEEXGXL,
ASAAPXXVPQAL:EPIS:KFKYE:MIVRSXKXS, ASASPSSVSQDL:EPIS:KFKYE:MIVKSXKXS,
ASASPXXVPQDL:EPIS:KFKYE:MVVKSXKXS, NDEGLEXVPTEE:EPIS:KFKYE:FLQHNKXEXR,
NDEGLEXVPTGQ:EPIS:KFKYE:LEEHSQXEXR,
SSVKXQPSRVHH:EPIS:KFKYE:RLEEHLEXAXA,
RNVQXRPTQVQL:EPIS:KFKYE:TLEDHLAXKXE, KIPKAXXTPTEL:SPIN:YGKIP:DMVVDGXGXR,
GIPEPXXTPTKM:SPIN:YGKIP:NMVVDSXAXR, SIPKAXXTPTEL:SPIN:YGKIP:EMVVDGXGXR,
HVTKPTXTPTKL:SPIN:YGKIP:NMVVDSXGXH, YVPKPXXTPTKL:SPIN:YGKIP:NMVVDSXGXH,
TVPKPXXTPTQL:SPIN:YGKIP:NMVVDAXGXH, AVPKAXXTPTKL:SPIN:YGKIP:NMVVDAXGXH,
KVGKAXXTPTKL:SPIN:YGKIP:EGMSVVDXGXR,
KASKAXXTPTKL:SPIN:YGKIP:GMVVDEXGXR, AAPASXXTPTRL:SPIN:YGKIP:DMVVDAXGXR,
STPPTXXTPTRL:SPIN:YGKIP:DMVVDSXGXR, HVPKPXXTPTKL:SPIN:YGKIP:NMVVDSXGXH,
RVPSTXXTPTKT:SPIN:YGKIP:MIVVDXGXL, ASAAPXXTPTAL:SPIN:YGKIP:MIVVDXKXS,
ASASPXXTPTDL:SPIN:YGKIP:MIVVDXKXS, ASASPXXTPTDL:SPIN:YGKIP:MVVVDXKXS,
KIPKAXXVPTEL:SPIN:YGKIP:DMVVEGXGXR, GIPEPXXVPEKM:SPIN:YGKIP:NMTVESXAXR,
SIPKAXXVPTEL:SPIN:YGKIP:EMVVEGXGXR, HVTKPTXAPTKL:SPIN:YGKIP:NMVVRSXGXH,
YVPKPXXAPTKL:SPIN:YGKIP:NMVVRSXGXH, TVPKPXXAPTQL:SPIN:YGKIP:NMVVRAXGXH,
AVPKAXXAPTKL:SPIN:YGKIP:NMVVKAXGXH, KVGKAXXVPTKL:SPIN:YGKIP:EGMSVAEXGXR,
KASKAXXVPTKL:SPIN:YGKIP:GMAVSEXGXR, AAPASXXVPARL:SPIN:YGKIP:DMVVEAXGXR,
STPPTXXVPTRL:SPIN:YGKIP:DMVVESXGXR, HVPKPXXAPTKL:SPIN:YGKIP:NMVVRSXGXH,
RVPSTXXAPVKT:SPIN:YGKIP:MIVEEXGXL, ASAAPXXVPQAL:SPIN:YGKIP:MIVRSXKXS,
ASASPSSVSQDL:SPIN:YGKIP:MIVKSXKXS, ASASPXXVPQDL:SPIN:YGKIP:MVVKSXKXS,

NDEGLEXVPTEE:SPIN:YGKIP:FLQHNKXEXR, NDEGLEXVPTGQ:SPIN:YGKIP:LEEHSQXEXR,
SSVKXQPSRVHH:SPIN:YGKIP:RLEEHLEXAXA,
RNVQXRPTQVQL:SPIN:YGKIP:TLEDHLAXKXE, KIPKAXXVPAEL:SPIS:YKQYE:DMVVEGXGXR,
GIPEPXXVPAKM:SPIS:YKQYE:NMVVESXAXR, SIPKAXXVPAEL:SPIS:YKQYE:EMVVEGXGXR,
HVTKPTXVPAKL:SPIS:YKQYE:NMVVESXGXH, YVPKPXXVPAKL:SPIS:YKQYE:NMVVESXGXH,
TVPKPXXVPAQL:SPIS:YKQYE:NMVVEAXGXH, AVPKAXXVPAKL:SPIS:YKQYE:NMVVEAXGXH,
KVGKAXXVPAKL:SPIS:YKQYE:EGMSVVEXGXR,
KASKAXXVPAKL:SPIS:YKQYE:GMVVEEXGXR,
GSAGPXXVPAKM:SPIS:YKQYE:GMVVERXGXS,
STPPTXXVPARL:SPIS:YKQYE:DMVVESXGXR, HVPKPXXVPAKL:SPIS:YKQYE:NMVVESXGXH,
RVPSTXXVPAKT:SPIS:YKQYE:MIVVEXGXL, ASAAPXXVPAAL:SPIS:YKQYE:MIVVEXKXS,
ASASPXXVPADL:SPIS:YKQYE:MIVVEXKXS, ASASPXXVPADL:SPIS:YKQYE:MVVVEXKXS,
KIPKAXXVPTEL:SPIS:YKQYE:DMVVEGXGXR, GIPEPXXVPEKM:SPIS:YKQYE:NMTVESXAXR,
SIPKAXXVPTEL:SPIS:YKQYE:EMVVEGXGXR, HVTKPTXAPTKL:SPIS:YKQYE:NMVVRSXGXH,
YVPKPXXAPTKL:SPIS:YKQYE:NMVVRSXGXH, TVPKPXXAPTQL:SPIS:YKQYE:NMVVRAXGXH,
AVPKAXXAPTKL:SPIS:YKQYE:NMVVKAXGXH,
KVGKAXXVPTKL:SPIS:YKQYE:EGMSVAEXGXR,
KASKAXXVPTKL:SPIS:YKQYE:GMAVSEXGXR,
GSAGPXXTPTKM:SPIS:YKQYE:GMVVDRXGXS,
STPPTXXVPTRL:SPIS:YKQYE:DMVVESXGXR, HVPKPXXAPTKL:SPIS:YKQYE:NMVVRSXGXH,
RVPSTXXAPVKT:SPIS:YKQYE:MIVEEXGXL, ASAAPXXVPQAL:SPIS:YKQYE:MIVRSXKXS,
ASASPSSVSQDL:SPIS:YKQYE:MIVKSXKXS, ASASPXXVPQDL:SPIS:YKQYE:MVVKSXKXS,
NDEGLEXVPTEE:SPIS:YKQYE:FLQHNKXEXR, NDEGLEXVPTGQ:SPIS:YKQYE:LEEHSQXEXR,
SSVKXQPSRVHH:SPIS:YKQYE:RLEEHLEXAXA,
RNVQXRPTQVQL:SPIS:YKQYE:TLEDHLAXKXE,
GIPEPXXVPTKM:SPIS:YKQYE:NMVVESXAXR, HVTKPTXVPTKL:SPIS:YKQYE:NMVVESXGXH,
YVPKPXXVPTKL:SPIS:YKQYE:NMVVESXGXH, TVPKPXXVPTQL:SPIS:YKQYE:NMVVEAXGXH,
AVPKAXXVPTKL:SPIS:YKQYE:NMVVEAXGXH,
KVGKAXXVPTKL:SPIS:YKQYE:EGMSVVEXGXR,
KASKAXXVPTKL:SPIS:YKQYE:GMVVEEXGXR,
GSAGPXXVPTKM:SPIS:YKQYE:GMVVERXGXS,
AAPASXXVPTRL:SPIS:YKQYE:DMVVEAXGXR, HVPKPXXVPTKL:SPIS:YKQYE:NMVVESXGXH,
RVPSTXXVPTKT:SPIS:YKQYE:MIVVEXGXL, ASAAPXXVPTAL:SPIS:YKQYE:MIVVEXKXS,
ASASPXXVPTDL:SPIS:YKQYE:MIVVEXKXS, ASASPXXVPTDL:SPIS:YKQYE:MVVVEXKXS,
AAPASXXVPARL:SPIS:YKQYE:DMVVEAXGXR,
KIPKAXXAPVEL:KPLS:DHHKD:DMVEEGXGXR,
GIPEPXXAPVKM:KPLS:DHHKD:NMVEESXAXR,
SIPKAXXAPVEL:KPLS:DHHKD:EMVEEGXGXR,
HVTKPTXAPVKL:KPLS:DHHKD:NMVEESXGXH,
YVPKPXXAPVKL:KPLS:DHHKD:NMVEESXGXH,
TVPKPXXAPVQL:KPLS:DHHKD:NMVEEAXGXH,
AVPKAXXAPVKL:KPLS:DHHKD:NMVEEAXGXH,

KVGKAXXAPVKL:KPLS:DHHKD:EGMSVEEXGXR,

KASKAXXAPVKL:KPLS:DHHKD:GMVEEEXGXR,

GSAGPXXAPVKM:KPLS:DHHKD:GMVEERXGXS,

AAPASXXAPVRL:KPLS:DHHKD:DMVEEAXGXR,

STPPTXXAPVRL:KPLS:DHHKD:DMVEESXGXR,

HVPKPXXAPVKL:KPLS:DHHKD:NMVEESXGXH, ASAAPXXAPVAL:KPLS:DHHKD:MIVEEXKXS,

ASASPXXAPVDL:KPLS:DHHKD:MIVEEXKXS, ASASPXXAPVDL:KPLS:DHHKD:MVVEEXKXS,

KIPKAXXVPTEL:KPLS:DHHKD:DMVVEGXGXR,

GIPEPXXVPEKM:KPLS:DHHKD:NMTVESXAXR,

SIPKAXXVPTEL:KPLS:DHHKD:EMVVEGXGXR,

HVTKPTXAPTKL:KPLS:DHHKD:NMVVRSXGXH,

YVPKPXXAPTKL:KPLS:DHHKD:NMVVRSXGXH,

TVPKPXXAPTQL:KPLS:DHHKD:NMVVRAXGXH,

AVPKAXXAPTKL:KPLS:DHHKD:NMVVKAXGXH,

KVGKAXXVPTKL:KPLS:DHHKD:EGMSVAEXGXR,

KASKAXXVPTKL:KPLS:DHHKD:GMAVSEXGXR,

GSAGPXXTPTKM:KPLS:DHHKD:GMVVDRXGXS,

AAPASXXVPARL:KPLS:DHHKD:DMVVEAXGXR,

STPPTXXVPTRL:KPLS:DHHKD:DMVVESXGXR,

HVPKPXXAPTKL:KPLS:DHHKD:NMVVRSXGXH, ASAAPXXVPQAL:KPLS:DHHKD:MIVRSXKXS,

ASASPSSVSQDL:KPLS:DHHKD:MIVKSXKXS, ASASPXXVPQDL:KPLS:DHHKD:MVVKSXKXS,

NDEGLEXVPTEE:KPLS:DHHKD:FLQHNKXEXR,

NDEGLEXVPTGQ:KPLS:DHHKD:LEEHSQXEXR,

SSVKXQPSRVHH:KPLS:DHHKD:RLEEHLEXAXA,

RNVQXRPTQVQL:KPLS:DHHKD:TLEDHLAXKXE,

KIPKAXXVPQEL:EPLP:EQLSN:DMVRXGXGSR,

GIPEPXXVPQKM:EPLP:EQLSN:NMVRSSXAXR,

SIPKAXXVPQEL:EPLP:EQLSN:EMVRXGXGSR,

HVTKPTXVPQKL:EPLP:EQLSN:NMVRSSXGXH,

YVPKPXXVPQKL:EPLP:EQLSN:NMVRSSXGXH,

TVPKPXXVPQQL:EPLP:EQLSN:NMVRSAXGXH,

AVPKAXXVPQKL:EPLP:EQLSN:NMVRSAXGXH,

KVGKAXXVPQKL:EPLP:EQLSN:EGMSVRSXGXR,

KASKAXXVPQKL:EPLP:EQLSN:GMVRSEXGXR,

GSAGPXXVPQKM:EPLP:EQLSN:GMVRSRXGXS,

AAPASXXVPQRL:EPLP:EQLSN:DMVRSAXGXR,

STPPTXXVPQRL:EPLP:EQLSN:DMVRSSXGXR,

HVPKPXXVPQKL:EPLP:EQLSN:NMVRSSXGXH, RVPSTXXVPQKT:EPLP:EQLSN:MIVRSXGXL,

ASASPXXVPQDL:EPLP:EQLSN:MIVRSXKXS, ASASPXXVPQDL:EPLP:EQLSN:MVVRSXKXS,

KIPKAXXVPTEL:EPLP:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLP:EQLSN:NMTVESXAXR,

SIPKAXXVPTEL:EPLP:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLP:EQLSN:NMVVRSXGXH,

YVPKPXXAPTKL:EPLP:EQLSN:NMVVRSXGXH,

TVPKPXXAPTQL:EPLP:EQLSN:NMVVRAXGXH,
AVPKAXXAPTKL:EPLP:EQLSN:NMVVKAXGXH,
KVGKAXXVPTKL:EPLP:EQLSN:EGMSVAEXGXR,
KASKAXXVPTKL:EPLP:EQLSN:GMAVSEXGXR,
GSAGPXXTPTKM:EPLP:EQLSN:GMVVDRXGXS,
AAPASXXVPARL:EPLP:EQLSN:DMVVEAXGXR,
STPPTXXVPTRL:EPLP:EQLSN:DMVVESXGXR,
HVPKPXXAPTKL:EPLP:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLP:EQLSN:MIVEEXGXL,
ASASPSSVSQDL:EPLP:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLP:EQLSN:MVVKSXKXS,
NDEGLEXVPTEE:EPLP:EQLSN:FLQHNKXEXR,
NDEGLEXVPTGQ:EPLP:EQLSN:LEEHSQXEXR,
SSVKXQPSRVHH:EPLP:EQLSN:RLEEHLEXAXA,
RNVQXRPTQVQL:EPLP:EQLSN:TLEDHLAXKXE,
KIPKASSVSQEL:EPLT:EQLSN:DMVKXGXGSR,
GIPEPSSVSQKM:EPLT:EQLSN:NMVKSSXAXR,
SIPKASSVSQEL:EPLT:EQLSN:EMVKXGXGSR,
HVTKPTXVSQKL:EPLT:EQLSN:NMVKSSXGXH,
YVPKPSSVSQKL:EPLT:EQLSN:NMVKSSXGXH,
TVPKPSSVSQQL:EPLT:EQLSN:NMVKSAXGXH,
AVPKASSVSQKL:EPLT:EQLSN:NMVKSAXGXH,
KVGKASSVSQKL:EPLT:EQLSN:EGMSVKSXGXR,
KASKASSVSQKL:EPLT:EQLSN:GMVKSEXGXR,
GSAGPSSVSQKM:EPLT:EQLSN:GMVKSRXGXS,
AAPASSSVSQRL:EPLT:EQLSN:DMVKSAXGXR,
STPPTSSVSQRL:EPLT:EQLSN:DMVKSSXGXR,
HVPKPSSVSQKL:EPLT:EQLSN:NMVKSSXGXH, RVPSTSSVSQKT:EPLT:EQLSN:MIVKSXGXL,
ASAAPSSVSQAL:EPLT:EQLSN:MIVKSXKXS, ASASPSSVSQDL:EPLT:EQLSN:MVVKSXKXS,
KIPKAXXVPTEL:EPLT:EQLSN:DMVVEGXGXR, GIPEPXXVPEKM:EPLT:EQLSN:NMTVESXAXR,
SIPKAXXVPTEL:EPLT:EQLSN:EMVVEGXGXR, HVTKPTXAPTKL:EPLT:EQLSN:NMVVRSXGXH,
YVPKPXXAPTKL:EPLT:EQLSN:NMVVRSXGXH,
TVPKPXXAPTQL:EPLT:EQLSN:NMVVRAXGXH,
AVPKAXXAPTKL:EPLT:EQLSN:NMVVKAXGXH,
KVGKAXXVPTKL:EPLT:EQLSN:EGMSVAEXGXR,
KASKAXXVPTKL:EPLT:EQLSN:GMAVSEXGXR,
GSAGPXXTPTKM:EPLT:EQLSN:GMVVDRXGXS,
AAPASXXVPARL:EPLT:EQLSN:DMVVEAXGXR,
STPPTXXVPTRL:EPLT:EQLSN:DMVVESXGXR,
HVPKPXXAPTKL:EPLT:EQLSN:NMVVRSXGXH, RVPSTXXAPVKT:EPLT:EQLSN:MIVEEXGXL,
ASAAPXXVPQAL:EPLT:EQLSN:MIVRSXKXS, NDEGLEXVPTEE:EPLT:EQLSN:FLQHNKXEXR,
NDEGLEXVPTGQ:EPLT:EQLSN:LEEHSQXEXR,
SSVKXQPSRVHH:EPLT:EQLSN:RLEEHLEXAXA,
RNVQXRPTQVQL:EPLT:EQLSN:TLEDHLAXKXE,

KIPKAXXVPQEL:EPLT:EQLSN:DMVKXGXGSR,

GIPEPXXVPQKM:EPLT:EQLSN:NMVKSSXAXR,

SIPKAXXVPQEL:EPLT:EQLSN:EMVKXGXGSR,

HVTKPTXVPQKL:EPLT:EQLSN:NMVKSSXGXH,

YVPKPXXVPQKL:EPLT:EQLSN:NMVKSSXGXH,

TVPKPXXVPQQL:EPLT:EQLSN:NMVKSAXGXH,

AVPKAXXVPQKL:EPLT:EQLSN:NMVKSAXGXH,

KVGKAXXVPQKL:EPLT:EQLSN:EGMSVKSXGXR,

KASKAXXVPQKL:EPLT:EQLSN:GMVKSEXGXR,

GSAGPXXVPQKM:EPLT:EQLSN:GMVKSRXGXS,

AAPASXXVPQRL:EPLT:EQLSN:DMVKSAXGXR,

STPPTXXVPQRL:EPLT:EQLSN:DMVKSSXGXR,

HVPKPXXVPQKL:EPLT:EQLSN:NMVKSSXGXH, RVPSTXXVPQKT:EPLT:EQLSN:MIVKSXGXL,

ASAAPXXVPQAL:EPLT:EQLSN:MIVKSXKXS, ASASPXXVPQDL:EPLT:EQLSN:MIVKSXKXS,

NDEGLEXVPTGQ:SNIT:IGEMS:LEQHNQXEXR, KIPKAXXVPTEL:SNIT:IGEMS:DMVVEGXGXR,

GIPEPXXVPEKM:SNIT:IGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT:IGEMS:EMVVEGXGXR,

HVTKPTXAPTKL:SNIT:IGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT:IGEMS:NMVVRSXGXH,

TVPKPXXAPTQL:SNIT:IGEMS:NMVVRAXGXH, AVPKAXXAPTKL:SNIT:IGEMS:NMVVKAXGXH,

KVGKAXXVPTKL:SNIT:IGEMS:EGMSVAEXGXR,

KASKAXXVPTKL:SNIT:IGEMS:GMAVSEXGXR, GSAGPXXTPTKM:SNIT:IGEMS:GMVVDRXGXS,

AAPASXXVPARL:SNIT:IGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT:IGEMS:DMVVESXGXR,

HVPKPXXAPTKL:SNIT:IGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT:IGEMS:MIVEEXGXL,

ASAAPXXVPQAL:SNIT:IGEMS:MIVRSXKXS, ASASPSSVSQDL:SNIT:IGEMS:MIVKSXKXS,

ASASPXXVPQDL:SNIT:IGEMS:MVVKSXKXS, NDEGLEXVPTGQ:SNIT:IGEMS:LEEHSQXEXR,

SSVKXQPSRVHH:SNIT:IGEMS:RLEEHLEXAXA,

RNVQXRPTQVQL:SNIT:IGEMS:TLEDHLAXKXE,

NDEGLEXVPTEE:SNIT:LGEMS:FLEHXKXESR, KIPKAXXVPTEL:SNIT:LGEMS:DMVVEGXGXR,

GIPEPXXVPEKM:SNIT:LGEMS:NMTVESXAXR, SIPKAXXVPTEL:SNIT:LGEMS:EMVVEGXGXR,

HVTKPTXAPTKL:SNIT:LGEMS:NMVVRSXGXH, YVPKPXXAPTKL:SNIT:LGEMS:NMVVRSXGXH,

TVPKPXXAPTQL:SNIT:LGEMS:NMVVRAXGXH,

AVPKAXXAPTKL:SNIT:LGEMS:NMVVKAXGXH,

KVGKAXXVPTKL:SNIT:LGEMS:EGMSVAEXGXR,

KASKAXXVPTKL:SNIT:LGEMS:GMAVSEXGXR,

GSAGPXXTPTKM:SNIT:LGEMS:GMVVDRXGXS,

AAPASXXVPARL:SNIT:LGEMS:DMVVEAXGXR, STPPTXXVPTRL:SNIT:LGEMS:DMVVESXGXR,

HVPKPXXAPTKL:SNIT:LGEMS:NMVVRSXGXH, RVPSTXXAPVKT:SNIT:LGEMS:MIVEEXGXL,

ASAAPXXVPQAL:SNIT:LGEMS:MIVRSXKXS, ASASPSSVSQDL:SNIT:LGEMS:MIVKSXKXS,

ASASPXXVPQDL:SNIT:LGEMS:MVVKSXKXS, NDEGLEXVPTEE:SNIT:LGEMS:FLQHNKXEXR,

SSVKXQPSRVHH:SNIT:LGEMS:RLEEHLEXAXA,

RNVQXRPTQVQL:SNIT:LGEMS:TLEDHLAXKXE,

RNVQXRPSRVQL:RSVK:KEVQV:TLEEHLAXKXE,

KIPKAXXVPTEL:RSVK:KEVQV:DMVVEGXGXR,

GIPEPXXVPEKM:RSVK:KEVQV:NMTVESXAXR,
SIPKAXXVPTEL:RSVK:KEVQV:EMVVEGXGXR,
HVTKPTXAPTKL:RSVK:KEVQV:NMVVRSXGXH,
YVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH,
TVPKPXXAPTQL:RSVK:KEVQV:NMVVRAXGXH,
AVPKAXXAPTKL:RSVK:KEVQV:NMVVKAXGXH,
KVGKAXXVPTKL:RSVK:KEVQV:EGMSVAEXGXR,
KASKAXXVPTKL:RSVK:KEVQV:GMAVSEXGXR,
GSAGPXXTPTKM:RSVK:KEVQV:GMVVDRXGXS,
AAPASXXVPARL:RSVK:KEVQV:DMVVEAXGXR,
STPPTXXVPTRL:RSVK:KEVQV:DMVVESXGXR,
HVPKPXXAPTKL:RSVK:KEVQV:NMVVRSXGXH, RVPSTXXAPVKT:RSVK:KEVQV:MIVEEXGXL,
ASAAPXXVPQAL:RSVK:KEVQV:MIVRSXKXS, ASASPSSVSQDL:RSVK:KEVQV:MIVKSXKXS,
ASASPXXVPQDL:RSVK:KEVQV:MVVKSXKXS, NDEGLEXVPTEE:RSVK:KEVQV:FLQHNKXEXR,
NDEGLEXVPTGQ:RSVK:KEVQV:LEEHSQXEXR,
RNVQXRPTQVQL:RSVK:KEVQV:TLEDHLAXKXE,
SSVKXQPTQVHH:RPVQ:KKATV:RLEDHLEXAXA,
KIPKAXXVPTEL:RPVQ:KKATV:DMVVEGXGXR,
GIPEPXXVPEKM:RPVQ:KKATV:NMTVESXAXR,
SIPKAXXVPTEL:RPVQ:KKATV:EMVVEGXGXR,
HVTKPTXAPTKL:RPVQ:KKATV:NMVVRSXGXH,
YVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH,
TVPKPXXAPTQL:RPVQ:KKATV:NMVVRAXGXH,
AVPKAXXAPTKL:RPVQ:KKATV:NMVVKAXGXH,
KVGKAXXVPTKL:RPVQ:KKATV:EGMSVAEXGXR,
KASKAXXVPTKL:RPVQ:KKATV:GMAVSEXGXR,
GSAGPXXTPTKM:RPVQ:KKATV:GMVVDRXGXS,
AAPASXXVPARL:RPVQ:KKATV:DMVVEAXGXR,
STPPTXXVPTRL:RPVQ:KKATV:DMVVESXGXR,
HVPKPXXAPTKL:RPVQ:KKATV:NMVVRSXGXH, RVPSTXXAPVKT:RPVQ:KKATV:MIVEEXGXL,
ASAAPXXVPQAL:RPVQ:KKATV:MIVRSXKXS, ASASPSSVSQDL:RPVQ:KKATV:MIVKSXKXS,
ASASPXXVPQDL:RPVQ:KKATV:MVVKSXKXS, NDEGLEXVPTEE:RPVQ:KKATV:FLQHNKXEXR,
NDEGLEXVPTGQ:RPVQ:KKATV:LEEHSQXEXR and
SSVKXQPSRVHH:RPVQ:KKATV:RLEEHLEXAXA.

88. A pharmaceutical association for a use according to any one of claims 4 to 87, wherein the hexaplet PEP7:PEP3:PEP1:PEP2:PEP4:PEP8 is selected from the group consisting of
GIPEPXX:VPT:SAIS:LKNYQ:VVE:SXAXR, HVTKPTX:VPT:SAIS:LKNYQ:VVE:SXGXH,
YVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH, TVPKPXX:VPT:SAIS:LKNYQ:VVE:AXGXH,
AVPKAXX:VPT:SAIS:LKNYQ:VVE:AXGXH, KVGKAXX:VPT:SAIS:LKNYQ:VVE:XGXR,
KASKAXX:VPT:SAIS:LKNYQ:VVE:EXGXR, GSAGPXX:VPT:SAIS:LKNYQ:VVE:RXGXS,
AAPASXX:VPT:SAIS:LKNYQ:VVE:AXGXR, STPPTXX:VPT:SAIS:LKNYQ:VVE:SXGXR,

HVPKPXX:VPT:SAIS:LKNYQ:VVE:SXGXH,
ASAAPXX:VPT:SAIS:LKNYQ:VVE:XKXS,
GIPEPXX:VPE:SAIS:LKNYQ:TVE:SXAXR,
YVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH,
AVPKAXX:APT:SAIS:LKNYQ:VVK:AXGXH,
KASKAXX:VPT:SAIS:LKNYQ:AVS:EXGXR,
AAPASXX:VPA:SAIS:LKNYQ:VVE:AXGXR,
RVPSTXX:APV:SAIS:LKNYQ:VEE:XGXL,
ASASPXX:VSQ:SAIS:LKNYQ:VKS:XKXS,
NDEGLEX:VPT:SAIS:LKNYQ:QHN:KXEXR,
SSVKXQP:SRV:SAIS:LKNYQ:EEH:LEXAXA,
KIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR,
HVTKPTX:VPE:SSLS:LKVYP:TVE:SXGXH,
TVPKPXX:VPE:SSLS:LKVYP:TVE:AXGXH,
KVGKAXX:VPE:SSLS:LKVYP:TVE:XGXR,
GSAGPXX:VPE:SSLS:LKVYP:TVE:RXGXS,
STPPTXX:VPE:SSLS:LKVYP:TVE:SXGXR,
RVPSTXX:VPE:SSLS:LKVYP:TVE:XGXL,
ASASPXX:VPE:SSLS:LKVYP:TVE:XKXS,
SIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR,
YVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH,
AVPKAXX:APT:SSLS:LKVYP:VVK:AXGXH,
KASKAXX:VPT:SSLS:LKVYP:AVS:EXGXR,
AAPASXX:VPA:SSLS:LKVYP:VVE:AXGXR,
HVPKPXX:APT:SSLS:LKVYP:VVR:SXGXH,
ASAAPXX:VPQ:SSLS:LKVYP:VRS:XKXS,
ASASPXX:VPQ:SSLS:LKVYP:VKS:XKXS,
NDEGLEX:VPT:SSLS:LKVYP:EHS:QXEXR,
RNVQXRP:TQV:SSLS:LKVYP:EDH:LAXKXE,
GIPEPXX:APT:NAIS:LKKYR:VVR:SXAXR,
AVPKAXX:APT:NAIS:LKKYR:VVR:AXGXH,
KASKAXX:APT:NAIS:LKKYR:VVR:EXGXR,
AAPASXX:APT:NAIS:LKKYR:VVR:AXGXR,
RVPSTXX:APT:NAIS:LKKYR:VVR:XGXL,
ASASPXX:APT:NAIS:LKKYR:VVR:XKXS,
GIPEPXX:VPE:NAIS:LKKYR:TVE:SXAXR,
AVPKAXX:APT:NAIS:LKKYR:VVK:AXGXH,
KASKAXX:VPT:NAIS:LKKYR:AVS:EXGXR,
AAPASXX:VPA:NAIS:LKKYR:VVE:AXGXR,
RVPSTXX:APV:NAIS:LKKYR:VEE:XGXL,
ASASPXX:VSQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:QHN:KXEXR,

RVPSTXX:VPT:SAIS:LKNYQ:VVE:XGXL,
ASASPXX:VPT:SAIS:LKNYQ:VVE:XKXS,
HVTKPTX:APT:SAIS:LKNYQ:VVR:SXGXH,
TVPKPXX:APT:SAIS:LKNYQ:VVR:AXGXH,
KVGKAXX:VPT:SAIS:LKNYQ:VAE:XGXR,
GSAGPXX:TPT:SAIS:LKNYQ:VVD:RXGXS,
HVPKPXX:APT:SAIS:LKNYQ:VVR:SXGXH,
ASAAPXX:VPQ:SAIS:LKNYQ:VRS:XKXS,
ASASPXX:VPQ:SAIS:LKNYQ:VKS:XKXS,
NDEGLEX:VPT:SAIS:LKNYQ:EHS:QXEXR,
RNVQXRP:TQV:SAIS:LKNYQ:EDH:LAXKXE,
SIPKAXX:VPE:SSLS:LKVYP:TVE:GXGXR,
YVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
AVPKAXX:VPE:SSLS:LKVYP:TVE:AXGXH,
KASKAXX:VPE:SSLS:LKVYP:TVE:EXGXR,
AAPASXX:VPE:SSLS:LKVYP:TVE:AXGXR,
HVPKPXX:VPE:SSLS:LKVYP:TVE:SXGXH,
ASAAPXX:VPE:SSLS:LKVYP:TVE:XKXS,
KIPKAXX:VPT:SSLS:LKVYP:VVE:GXGXR,
HVTKPTX:APT:SSLS:LKVYP:VVR:SXGXH,
TVPKPXX:APT:SSLS:LKVYP:VVR:AXGXH,
KVGKAXX:VPT:SSLS:LKVYP:VAE:XGXR,
GSAGPXX:TPT:SSLS:LKVYP:VVD:RXGXS,
STPPTXX:VPT:SSLS:LKVYP:VVE:SXGXR,
RVPSTXX:APV:SSLS:LKVYP:VEE:XGXL,
ASASPXX:VSQ:SSLS:LKVYP:VKS:XKXS,
NDEGLEX:VPT:SSLS:LKVYP:QHN:KXEXR,
SSVKXQP:SRV:SSLS:LKVYP:EEH:LEXAXA,
KIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
SIPKAXX:APT:NAIS:LKKYR:VVR:GXGXR,
KVGKAXX:APT:NAIS:LKKYR:VVR:XGXR,
GSAGPXX:APT:NAIS:LKKYR:VVR:RXGXS,
STPPTXX:APT:NAIS:LKKYR:VVR:SXGXR,
ASAAPXX:APT:NAIS:LKKYR:VVR:XKXS,
KIPKAXX:VPT:NAIS:LKKYR:VVE:GXGXR,
SIPKAXX:VPT:NAIS:LKKYR:VVE:GXGXR,
KVGKAXX:VPT:NAIS:LKKYR:VAE:XGXR,
GSAGPXX:TPT:NAIS:LKKYR:VVD:RXGXS,
STPPTXX:VPT:NAIS:LKKYR:VVE:SXGXR,
ASAAPXX:VPQ:NAIS:LKKYR:VRS:XKXS,
ASASPXX:VPQ:NAIS:LKKYR:VKS:XKXS,
NDEGLEX:VPT:NAIS:LKKYR:EHS:QXEXR,

SSVKXQP:SRV:NAIS:LKKYR:EEH:LEXAXA,
KIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
SIPKAXX:APT:SATS:LRKHR:VVK:GXGXR,
YVPKPXX:APT:SATS:LRKHR:VVK:SXGXH,
KVGKAXX:APT:SATS:LRKHR:VVK:XGXR,
GSAGPXX:APT:SATS:LRKHR:VVK:RXGXS,
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ASASPXX:APT:SATS:LRKHR:VVK:XKXS,
GIPEPXX:VPE:SATS:LRKHR:TVE:SXAXR,
HVTKPTX:APT:SATS:LRKHR:VVR:SXGXH,
TVPKPXX:APT:SATS:LRKHR:VVR:AXGXH,
KASKAXX:VPT:SATS:LRKHR:AVS:EXGXR,
AAPASXX:VPA:SATS:LRKHR:VVE:AXGXR,
HVPKPXX:APT:SATS:LRKHR:VVR:SXGXH,
ASAAPXX:VPQ:SATS:LRKHR:VRS:XKXS,
ASASPXX:VPQ:SATS:LRKHR:VKS:XKXS,
NDEGLEX:VPT:SATS:LRKHR:EHS:QXEXR,
RNVQXRP:TQV:SATS:LRKHR:EDH:LAXKXE,
GIPEPXX:VPT:SPIS:LKYHY:VAE:SXAXR,
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TVPKPXX:VPT:SPIS:LKYHY:VAE:AXGXH,
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HVPKPXX:VPT:SPIS:LKYHY:VAE:SXGXH,
ASAAPXX:VPT:SPIS:LKYHY:VAE:XKXS,
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SIPKAXX:VPT:SPIS:LKYHY:VVE:GXGXR,
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RVPSTXX:APV:SPIS:LKYHY:VEE:XGXL,
ASASPXX:VSQ:SPIS:LKYHY:VKS:XKXS,
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SSVKXQP:SRV:SPIS:LKYHY:EEH:LEXAXA,
KIPKAXX:VPT:EPIS:KFKYE:AVS:GXGXR,
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GSAGPXX:VPT:EPIS:KFKYE:AVS:RXGXS,
STPPTXX:VPT:EPIS:KFKYE:AVS:SXGXR,

RNVQXRP:TQV:NAIS:LKKYR:EDH:LAXKXE,
GIPEPXX:APT:SATS:LRKHR:VVK:SXAXR,
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TVPKPXX:APT:SATS:LRKHR:VVK:AXGXH,
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AAPASXX:APT:SATS:LRKHR:VVK:AXGXR,
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SIPKAXX:VPT:SATS:LRKHR:VVE:GXGXR,
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KASKAXX:TPT:SPIN:YGKIP:VVD:EXGXR,
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ASASPXX:VPQ:SPIN:YGKIP:VKS:XKXS,
NDEGLEX:VPT:SPIN:YGKIP:EHS:QXEXR,
RNVQXRP:TQV:SPIN:YGKIP:EDH:LAXKXE,
GIPEPXX:VPA:SPIS:YKQYE:VVE:SXAXR,
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ASAAPXX:VPA:SPIS:YKQYE:VVE:XKXS,
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SIPKAXX:VPT:SPIS:YKQYE:VVE:GXGXR,
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AVPKAXX:APT:SPIS:YKQYE:VVK:AXGXH,
KASKAXX:VPT:SPIS:YKQYE:AVS:EXGXR,
STPPTXX:VPT:SPIS:YKQYE:VVE:SXGXR,

HVPKPXX:APT:SPIS:YKQYE:VVR:SXGXH,
ASAAPXX:VPQ:SPIS:YKQYE:VRS:XKXS,
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NDEGLEX:VPT:SPIS:YKQYE:EHS:QXEXR,
RNVQXRP:TQV:SPIS:YKQYE:EDH:LAXKXE,
HVTKPTX:VPT:SPIS:YKQYE:VVE:SXGXH,
TVPKPXX:VPT:SPIS:YKQYE:VVE:AXGXH,
KVGKAXX:VPT:SPIS:YKQYE:VVE:XGXR,
GSAGPXX:VPT:SPIS:YKQYE:VVE:RXGXS,
HVPKPXX:VPT:SPIS:YKQYE:VVE:SXGXH,
ASAAPXX:VPT:SPIS:YKQYE:VVE:XKXS,
AAPASXX:VPA:SPIS:YKQYE:VVE:AXGXR,
GIPEPXX:APV:KPLS:DHHKD:VEE:SXAXR,
HVTKPTX:APV:KPLS:DHHKD:VEE:SXGXH,
TVPKPXX:APV:KPLS:DHHKD:VEE:AXGXH,
KVGKAXX:APV:KPLS:DHHKD:VEE:XGXR,
GSAGPXX:APV:KPLS:DHHKD:VEE:RXGXS,
STPPTXX:APV:KPLS:DHHKD:VEE:SXGXR,
ASAAPXX:APV:KPLS:DHHKD:VEE:XKXS,
KIPKAXX:VPT:KPLS:DHHKD:VVE:GXGXR,
SIPKAXX:VPT:KPLS:DHHKD:VVE:GXGXR,
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AAPASXX:VPA:KPLS:DHHKD:VVE:AXGXR,
HVPKPXX:APT:KPLS:DHHKD:VVR:SXGXH,
ASASPXX:VSQ:KPLS:DHHKD:VKS:XKXS,
NDEGLEX:VPT:KPLS:DHHKD:QHN:KXEXR,
SSVKXQP:SRV:KPLS:DHHKD:EEH:LEXAXA,
KIPKAXX:VPQ:EPLP:EQLSN:VRS:GXGXR,
SIPKAXX:VPQ:EPLP:EQLSN:VRS:GXGXR,
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AAPASXX:VPQ:EPLP:EQLSN:VRS:AXGXR,
HVPKPXX:VPQ:EPLP:EQLSN:VRS:SXGXH,
ASASPXX:VPQ:EPLP:EQLSN:VRS:XKXS,
GIPEPXX:VPE:EPLP:EQLSN:TVE:SXAXR,
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TVPKPXX:APT:EPLP:EQLSN:VVR:AXGXH,
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ASASPXX:VSQ:SPIS:YKQYE:VKS:XKXS,
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SSVKXQP:SRV:SPIS:YKQYE:EEH:LEXAXA,
GIPEPXX:VPT:SPIS:YKQYE:VVE:SXAXR,
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AAPASXX:VPT:SPIS:YKQYE:VVE:AXGXR,
RVPSTXX:VPT:SPIS:YKQYE:VVE:XGXL,
ASASPXX:VPT:SPIS:YKQYE:VVE:XKXS,
KIPKAXX:APV:KPLS:DHHKD:VEE:GXGXR,
SIPKAXX:APV:KPLS:DHHKD:VEE:GXGXR,
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KASKAXX:APV:KPLS:DHHKD:VEE:EXGXR,
AAPASXX:APV:KPLS:DHHKD:VEE:AXGXR,
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ASASPXX:APV:KPLS:DHHKD:VEE:XKXS,
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ASASPXX:VPQ:KPLS:DHHKD:VKS:XKXS,
NDEGLEX:VPT:KPLS:DHHKD:EHS:QXEXR,
RNVQXRP:TQV:KPLS:DHHKD:EDH:LAXKXE,
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STPPTXX:VSQ:EPLT:EQLSN:VKS:SXGXR,
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GIPEPXX:VPE:EPLT:EQLSN:TVE:SXAXR,
HVTKPTX:APT:EPLT:EQLSN:VVR:SXGXH,
TVPKPXX:APT:EPLT:EQLSN:VVR:AXGXH,
KVGKAXX:VPT:EPLT:EQLSN:VAE:XGXR,
GSAGPXX:TPT:EPLT:EQLSN:VVD:RXGXS,
STPPTXX:VPT:EPLT:EQLSN:VVE:SXGXR,
RVPSTXX:APV:EPLT:EQLSN:VEE:XGXL,
NDEGLEX:VPT:EPLT:EQLSN:QHN:KXEXR,
SSVKXQP:SRV:EPLT:EQLSN:EEH:LEXAXA,
KIPKAXX:VPQ:EPLT:EQLSN:VKS:GXGXR,
SIPKAXX:VPQ:EPLT:EQLSN:VKS:GXGXR,
YVPKPXX:VPQ:EPLT:EQLSN:VKS:SXGXH,
AVPKAXX:VPQ:EPLT:EQLSN:VKS:AXGXH,
KASKAXX:VPQ:EPLT:EQLSN:VKS:EXGXR,
AAPASXX:VPQ:EPLT:EQLSN:VKS:AXGXR,
HVPKPXX:VPQ:EPLT:EQLSN:VKS:SXGXH,
ASAAPXX:VPQ:EPLT:EQLSN:VKS:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:QHN:QXEXR,
GIPEPXX:VPE:SNIT:IGEMS:TVE:SXAXR,
HVTKPTX:APT:SNIT:IGEMS:VVR:SXGXH,
TVPKPXX:APT:SNIT:IGEMS:VVR:AXGXH,
KVGKAXX:VPT:SNIT:IGEMS:VAE:XGXR,
GSAGPXX:TPT:SNIT:IGEMS:VVD:RXGXS,
STPPTXX:VPT:SNIT:IGEMS:VVE:SXGXR,
RVPSTXX:APV:SNIT:IGEMS:VEE:XGXL,
ASASPXX:VSQ:SNIT:IGEMS:VKS:XKXS,
NDEGLEX:VPT:SNIT:IGEMS:EHS:QXEXR,
RNVQXRP:TQV:SNIT:IGEMS:EDH:LAXKXE,
KIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR,

HVPKPXX:APT:EPLP:EQLSN:VVR:SXGXH,
ASASPXX:VSQ:EPLP:EQLSN:VKS:XKXS,
NDEGLEX:VPT:EPLP:EQLSN:QHN:KXEXR,
SSVKXQP:SRV:EPLP:EQLSN:EEH:LEXAXA,
KIPKAXX:VSQ:EPLT:EQLSN:VKS:GXGXR,
SIPKAXX:VSQ:EPLT:EQLSN:VKS:GXGXR,
YVPKPXX:VSQ:EPLT:EQLSN:VKS:SXGXH,
AVPKAXX:VSQ:EPLT:EQLSN:VKS:AXGXH,
KASKAXX:VSQ:EPLT:EQLSN:VKS:EXGXR,
AAPASXX:VSQ:EPLT:EQLSN:VKS:AXGXR,
HVPKPXX:VSQ:EPLT:EQLSN:VKS:SXGXH,
ASAAPXX:VSQ:EPLT:EQLSN:VKS:XKXS,
KIPKAXX:VPT:EPLT:EQLSN:VVE:GXGXR,
SIPKAXX:VPT:EPLT:EQLSN:VVE:GXGXR,
YVPKPXX:APT:EPLT:EQLSN:VVR:SXGXH,
AVPKAXX:APT:EPLT:EQLSN:VVK:AXGXH,
KASKAXX:VPT:EPLT:EQLSN:AVS:EXGXR,
AAPASXX:VPA:EPLT:EQLSN:VVE:AXGXR,
HVPKPXX:APT:EPLT:EQLSN:VVR:SXGXH,
ASAAPXX:VPQ:EPLT:EQLSN:VRS:XKXS,
NDEGLEX:VPT:EPLT:EQLSN:EHS:QXEXR,
RNVQXRP:TQV:EPLT:EQLSN:EDH:LAXKXE,
GIPEPXX:VPQ:EPLT:EQLSN:VKS:SXAXR,
HVTKPTX:VPQ:EPLT:EQLSN:VKS:SXGXH,
TVPKPXX:VPQ:EPLT:EQLSN:VKS:AXGXH,
KVGKAXX:VPQ:EPLT:EQLSN:VKS:XGXR,
GSAGPXX:VPQ:EPLT:EQLSN:VKS:RXGXS,
STPPTXX:VPQ:EPLT:EQLSN:VKS:SXGXR,
RVPSTXX:VPQ:EPLT:EQLSN:VKS:XGXL,
ASASPXX:VPQ:EPLT:EQLSN:VKS:XKXS,
KIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
SIPKAXX:VPT:SNIT:IGEMS:VVE:GXGXR,
YVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
AVPKAXX:APT:SNIT:IGEMS:VVK:AXGXH,
KASKAXX:VPT:SNIT:IGEMS:AVS:EXGXR,
AAPASXX:VPA:SNIT:IGEMS:VVE:AXGXR,
HVPKPXX:APT:SNIT:IGEMS:VVR:SXGXH,
ASAAPXX:VPQ:SNIT:IGEMS:VRS:XKXS,
ASASPXX:VPQ:SNIT:IGEMS:VKS:XKXS,
SSVKXQP:SRV:SNIT:IGEMS:EEH:LEXAXA,
NDEGLEX:VPT:SNIT:LGEMS:EHS:KXEXR,
GIPEPXX:VPE:SNIT:LGEMS:TVE:SXAXR,

SIPKAXX:VPT:SNIT:LGEMS:VVE:GXGXR, HVTKPTX:APT:SNIT:LGEMS:VVR:SXGXH,
YVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH, TVPKPXX:APT:SNIT:LGEMS:VVR:AXGXH,
AVPKAXX:APT:SNIT:LGEMS:VVK:AXGXH, KVGKAXX:VPT:SNIT:LGEMS:VAE:XGXR,
KASKAXX:VPT:SNIT:LGEMS:AVS:EXGXR, GSAGPXX:TPT:SNIT:LGEMS:VVD:RXGXS,
AAPASXX:VPA:SNIT:LGEMS:VVE:AXGXR, STPPTXX:VPT:SNIT:LGEMS:VVE:SXGXR,
HVPKPXX:APT:SNIT:LGEMS:VVR:SXGXH, RVPSTXX:APV:SNIT:LGEMS:VEE:XGXL,
ASAAPXX:VPQ:SNIT:LGEMS:VRS:XKXS, ASASPXX:VSQ:SNIT:LGEMS:VKS:XKXS,
ASASPXX:VPQ:SNIT:LGEMS:VKS:XKXS, NDEGLEX:VPT:SNIT:LGEMS:QHN:KXEXR,
SSVKXQP:SRV:SNIT:LGEMS:EEH:LEXAXA, RNVQXRP:TQV:SNIT:LGEMS:EDH:LAXKXE,
RNVQXRP:SRV:RSVK:KEVQV:EEH:LAXKXE, KIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
GIPEPXX:VPE:RSVK:KEVQV:TVE:SXAXR, SIPKAXX:VPT:RSVK:KEVQV:VVE:GXGXR,
HVTKPTX:APT:RSVK:KEVQV:VVR:SXGXH, YVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
TVPKPXX:APT:RSVK:KEVQV:VVR:AXGXH, AVPKAXX:APT:RSVK:KEVQV:VVK:AXGXH,
KVGKAXX:VPT:RSVK:KEVQV:VAE:XGXR, KASKAXX:VPT:RSVK:KEVQV:AVS:EXGXR,
GSAGPXX:TPT:RSVK:KEVQV:VVD:RXGXS, AAPASXX:VPA:RSVK:KEVQV:VVE:AXGXR,
STPPTXX:VPT:RSVK:KEVQV:VVE:SXGXR, HVPKPXX:APT:RSVK:KEVQV:VVR:SXGXH,
RVPSTXX:APV:RSVK:KEVQV:VEE:XGXL, ASAAPXX:VPQ:RSVK:KEVQV:VRS:XKXS,
ASASPXX:VSQ:RSVK:KEVQV:VKS:XKXS, ASASPXX:VPQ:RSVK:KEVQV:VKS:XKXS,
NDEGLEX:VPT:RSVK:KEVQV:QHN:KXEXR, NDEGLEX:VPT:RSVK:KEVQV:EHS:QXEXR,
RNVQXRP:TQV:RSVK:KEVQV:EDH:LAXKXE, SSVKXQP:TQV:RPVQ:KKATV:EDH:LEXAXA,
KIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, GIPEPXX:VPE:RPVQ:KKATV:TVE:SXAXR,
SIPKAXX:VPT:RPVQ:KKATV:VVE:GXGXR, HVTKPTX:APT:RPVQ:KKATV:VVR:SXGXH,
YVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, TVPKPXX:APT:RPVQ:KKATV:VVR:AXGXH,
AVPKAXX:APT:RPVQ:KKATV:VVK:AXGXH, KVGKAXX:VPT:RPVQ:KKATV:VAE:XGXR,
KASKAXX:VPT:RPVQ:KKATV:AVS:EXGXR, GSAGPXX:TPT:RPVQ:KKATV:VVD:RXGXS,
AAPASXX:VPA:RPVQ:KKATV:VVE:AXGXR, STPPTXX:VPT:RPVQ:KKATV:VVE:SXGXR,
HVPKPXX:APT:RPVQ:KKATV:VVR:SXGXH, RVPSTXX:APV:RPVQ:KKATV:VEE:XGXL,
ASAAPXX:VPQ:RPVQ:KKATV:VRS:XKXS, ASASPXX:VSQ:RPVQ:KKATV:VKS:XKXS,
ASASPXX:VPQ:RPVQ:KKATV:VKS:XKXS, NDEGLEX:VPT:RPVQ:KKATV:QHN:KXEXR,
NDEGLEX:VPT:RPVQ:KKATV:EHS:QXEXR and SSVKXQP:SRV:RPVQ:KKATV:EEH:LEXAXA.

89. A pharmaceutical association for a use according to any one of claims 4 to 88, wherein the hexaplet PEP7:PEP5:PEP1:PEP2:PEP6:PEP8 is selected from the group consisting of

GIPEPXX:VPTKM:SAIS:LKNYQ:NMVVE:SXAXR,
HVTKPTX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH,
YVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH,
TVPKPXX:VPTQL:SAIS:LKNYQ:NMVVE:AXGXH,
AVPKAXX:VPTKL:SAIS:LKNYQ:NMVVE:AXGXH,
KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVVE:XGXR,
KASKAXX:VPTKL:SAIS:LKNYQ:GMVVE:EXGXR,
GSAGPXX:VPTKM:SAIS:LKNYQ:GMVVE:RXGXS,
AAPASXX:VPTRL:SAIS:LKNYQ:DMVVE:AXGXR,

STPPTXX:VPTRL:SAIS:LKNYQ:DMVVE:SXGXR,

HVPKPXX:VPTKL:SAIS:LKNYQ:NMVVE:SXGXH, RVPSTXX:VPTKT:SAIS:LKNYQ:MIVVE:XGXL,

ASAAPXX:VPTAL:SAIS:LKNYQ:MIVVE:XKXS, ASASPXX:VPTDL:SAIS:LKNYQ:MIVVE:XKXS,

ASASPXX:VPTDL:SAIS:LKNYQ:MVVVE:XKXS, GIPEPXX:VPEKM:SAIS:LKNYQ:NMTVE:SXAXR,

HVTKPTX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH,

YVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH,

TVPKPXX:APTQL:SAIS:LKNYQ:NMVVR:AXGXH,

AVPKAXX:APTKL:SAIS:LKNYQ:NMVVK:AXGXH,

KVGKAXX:VPTKL:SAIS:LKNYQ:EGMSVAE:XGXR,

KASKAXX:VPTKL:SAIS:LKNYQ:GMAVS:EXGXR,

GSAGPXX:TPTKM:SAIS:LKNYQ:GMVVD:RXGXS,

AAPASXX:VPARL:SAIS:LKNYQ:DMVVE:AXGXR,

HVPKPXX:APTKL:SAIS:LKNYQ:NMVVR:SXGXH, RVPSTXX:APVKT:SAIS:LKNYQ:MIVEE:XGXL,

ASAAPXX:VPQAL:SAIS:LKNYQ:MIVRS:XKXS, ASASPXX:VSQDL:SAIS:LKNYQ:MIVKS:XKXS,

ASASPXX:VPQDL:SAIS:LKNYQ:MVVKS:XKXS, NDEGLEX:VPTEE:SAIS:LKNYQ:FLQHN:KXEXR,

NDEGLEX:VPTGQ:SAIS:LKNYQ:LEEHS:QXEXR,

SSVKXQP:SRVHH:SAIS:LKNYQ:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SAIS:LKNYQ:TLEDH:LAXKXE,

KIPKAXX:VPEEL:SSLS:LKVYP:DMTVE:GXGXR,

SIPKAXX:VPEEL:SSLS:LKVYP:EMTVE:GXGXR,

HVTKPTX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH,

YVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH,

TVPKPXX:VPEQL:SSLS:LKVYP:NMTVE:AXGXH,

AVPKAXX:VPEKL:SSLS:LKVYP:NMTVE:AXGXH,

KVGKAXX:VPEKL:SSLS:LKVYP:EGMSTVE:XGXR,

KASKAXX:VPEKL:SSLS:LKVYP:GMTVE:EXGXR,

GSAGPXX:VPEKM:SSLS:LKVYP:GMTVE:RXGXS,

AAPASXX:VPERL:SSLS:LKVYP:DMTVE:AXGXR,

STPPTXX:VPERL:SSLS:LKVYP:DMTVE:SXGXR,

HVPKPXX:VPEKL:SSLS:LKVYP:NMTVE:SXGXH, RVPSTXX:VPEKT:SSLS:LKVYP:MITVE:XGXL,

ASAAPXX:VPEAL:SSLS:LKVYP:MITVE:XKXS, ASASPXX:VPEDL:SSLS:LKVYP:MITVE:XKXS,

ASASPXX:VPEDL:SSLS:LKVYP:MVTVE:XKXS, KIPKAXX:VPTEL:SSLS:LKVYP:DMVVE:GXGXR,

SIPKAXX:VPTEL:SSLS:LKVYP:EMVVE:GXGXR,

HVTKPTX:APTKL:SSLS:LKVYP:NMVVR:SXGXH,

YVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH,

TVPKPXX:APTQL:SSLS:LKVYP:NMVVR:AXGXH,

AVPKAXX:APTKL:SSLS:LKVYP:NMVVK:AXGXH,

KVGKAXX:VPTKL:SSLS:LKVYP:EGMSVAE:XGXR,

KASKAXX:VPTKL:SSLS:LKVYP:GMAVS:EXGXR,

GSAGPXX:TPTKM:SSLS:LKVYP:GMVVD:RXGXS,

AAPASXX:VPARL:SSLS:LKVYP:DMVVE:AXGXR,

STPPTXX:VPTRL:SSLS:LKVYP:DMVVE:SXGXR,

HVPKPXX:APTKL:SSLS:LKVYP:NMVVR:SXGXH, RVPSTXX:APVKT:SSLS:LKVYP:MIVEE:XGXL,
ASAAPXX:VPQAL:SSLS:LKVYP:MIVRS:XKXS, ASASPXX:VSQDL:SSLS:LKVYP:MIVKS:XKXS,
ASASPXX:VPQDL:SSLS:LKVYP:MVVKS:XKXS,
NDEGLEX:VPTEE:SSLS:LKVYP:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SSLS:LKVYP:LEEHS:QXEXR,
SSVKXQP:SRVHH:SSLS:LKVYP:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SSLS:LKVYP:TLEDH:LAXKXE,
KIPKAXX:APTEL:NAIS:LKKYR:DMVVR:GXGXR,
GIPEPXX:APTKM:NAIS:LKKYR:NMVVR:SXAXR,
SIPKAXX:APTEL:NAIS:LKKYR:EMVVR:GXGXR,
AVPKAXX:APTKL:NAIS:LKKYR:NMVVR:AXGXH,
KVGKAXX:APTKL:NAIS:LKKYR:EGMSVVR:XGXR,
KASKAXX:APTKL:NAIS:LKKYR:GMVVR:EXGXR,
GSAGPXX:APTKM:NAIS:LKKYR:GMVVR:RXGXS,
AAPASXX:APTRL:NAIS:LKKYR:DMVVR:AXGXR,
STPPTXX:APTRL:NAIS:LKKYR:DMVVR:SXGXR, RVPSTXX:APTKT:NAIS:LKKYR:MIVVR:XGXL,
ASAAPXX:APTAL:NAIS:LKKYR:MIVVR:XKXS, ASASPXX:APTDL:NAIS:LKKYR:MIVVR:XKXS,
ASASPXX:APTDL:NAIS:LKKYR:MVVVR:XKXS, KIPKAXX:VPTEL:NAIS:LKKYR:DMVVE:GXGXR,
GIPEPXX:VPEKM:NAIS:LKKYR:NMTVE:SXAXR,
SIPKAXX:VPTEL:NAIS:LKKYR:EMVVE:GXGXR,
AVPKAXX:APTKL:NAIS:LKKYR:NMVVK:AXGXH,
KVGKAXX:VPTKL:NAIS:LKKYR:EGMSVAE:XGXR,
KASKAXX:VPTKL:NAIS:LKKYR:GMAVS:EXGXR,
GSAGPXX:TPTKM:NAIS:LKKYR:GMVVD:RXGXS,
AAPASXX:VPARL:NAIS:LKKYR:DMVVE:AXGXR,
STPPTXX:VPTRL:NAIS:LKKYR:DMVVE:SXGXR, RVPSTXX:APVKT:NAIS:LKKYR:MIVEE:XGXL,
ASAAPXX:VPQAL:NAIS:LKKYR:MIVRS:XKXS, ASASPXX:VSQDL:NAIS:LKKYR:MIVKS:XKXS,
ASASPXX:VPQDL:NAIS:LKKYR:MVVKS:XKXS, NDEGLEX:VPTEE:NAIS:LKKYR:FLQHN:KXEXR,
NDEGLEX:VPTGQ:NAIS:LKKYR:LEEHS:QXEXR,
SSVKXQP:SRVHH:NAIS:LKKYR:RLEEH:LEXAXA,
RNVQXRP:TQVQL:NAIS:LKKYR:TLEDH:LAXKXE,
KIPKAXX:APTEL:SATS:LRKHR:DMVVK:GXGXR,
GIPEPXX:APTKM:SATS:LRKHR:NMVVK:SXAXR,
SIPKAXX:APTEL:SATS:LRKHR:EMVVK:GXGXR,
HVTKPTX:APTKL:SATS:LRKHR:NMVVK:SXGXH,
YVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH,
TVPKPXX:APTQL:SATS:LRKHR:NMVVK:AXGXH,
KVGKAXX:APTKL:SATS:LRKHR:EGMSVVK:XGXR,
KASKAXX:APTKL:SATS:LRKHR:GMVVK:EXGXR,
GSAGPXX:APTKM:SATS:LRKHR:GMVVK:RXGXS,
AAPASXX:APTRL:SATS:LRKHR:DMVVK:AXGXR,
STPPTXX:APTRL:SATS:LRKHR:DMVVK:SXGXR,

HVPKPXX:APTKL:SATS:LRKHR:NMVVK:SXGXH,

RVPSTXX:APTKT:SATS:LRKHR:MIVVK:XGXL, ASAAPXX:APTAL:SATS:LRKHR:MIVVK:XKXS,

ASASPXX:APTDL:SATS:LRKHR:MIVVK:XKXS, ASASPXX:APTDL:SATS:LRKHR:MVVVK:XKXS,

KIPKAXX:VPTEL:SATS:LRKHR:DMVVE:GXGXR,

GIPEPXX:VPEKM:SATS:LRKHR:NMTVE:SXAXR,

SIPKAXX:VPTEL:SATS:LRKHR:EMVVE:GXGXR,

HVTKPTX:APTKL:SATS:LRKHR:NMVVR:SXGXH,

YVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH,

TVPKPXX:APTQL:SATS:LRKHR:NMVVR:AXGXH,

KVGKAXX:VPTKL:SATS:LRKHR:EGMSVAE:XGXR,

KASKAXX:VPTKL:SATS:LRKHR:GMAVS:EXGXR,

GSAGPXX:TPTKM:SATS:LRKHR:GMVVD:RXGXS,

AAPASXX:VPARL:SATS:LRKHR:DMVVE:AXGXR,

STPPTXX:VPTRL:SATS:LRKHR:DMVVE:SXGXR,

HVPKPXX:APTKL:SATS:LRKHR:NMVVR:SXGXH,

RVPSTXX:APVKT:SATS:LRKHR:MIVEE:XGXL, ASAAPXX:VPQAL:SATS:LRKHR:MIVRS:XKXS,

ASASPXX:VSQDL:SATS:LRKHR:MIVKS:XKXS, ASASPXX:VPQDL:SATS:LRKHR:MVVKS:XKXS,

NDEGLEX:VPTEE:SATS:LRKHR:FLQHN:KXEXR,

NDEGLEX:VPTGQ:SATS:LRKHR:LEEHS:QXEXR,

SSVKXQP:SRVHH:SATS:LRKHR:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SATS:LRKHR:TLEDH:LAXKXE,

KIPKAXX:VPTEL:SPIS:LKYHY:DMVAE:GXGXR,

GIPEPXX:VPTKM:SPIS:LKYHY:NMVAE:SXAXR,

SIPKAXX:VPTEL:SPIS:LKYHY:EMVAE:GXGXR,

HVTKPTX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH,

YVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH,

TVPKPXX:VPTQL:SPIS:LKYHY:NMVAE:AXGXH,

AVPKAXX:VPTKL:SPIS:LKYHY:NMVAE:AXGXH,

KASKAXX:VPTKL:SPIS:LKYHY:GMVAE:EXGXR,

GSAGPXX:VPTKM:SPIS:LKYHY:GMVAE:RXGXS,

AAPASXX:VPTRL:SPIS:LKYHY:DMVAE:AXGXR,

STPPTXX:VPTRL:SPIS:LKYHY:DMVAE:SXGXR,

HVPKPXX:VPTKL:SPIS:LKYHY:NMVAE:SXGXH, RVPSTXX:VPTKT:SPIS:LKYHY:MIVAE:XGXL,

ASAAPXX:VPTAL:SPIS:LKYHY:MIVAE:XKXS, ASASPXX:VPTDL:SPIS:LKYHY:MIVAE:XKXS,

ASASPXX:VPTDL:SPIS:LKYHY:MVVAE:XKXS, KIPKAXX:VPTEL:SPIS:LKYHY:DMVVE:GXGXR,

GIPEPXX:VPEKM:SPIS:LKYHY:NMTVE:SXAXR,

SIPKAXX:VPTEL:SPIS:LKYHY:EMVVE:GXGXR,

HVTKPTX:APTKL:SPIS:LKYHY:NMVVR:SXGXH,

YVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH,

TVPKPXX:APTQL:SPIS:LKYHY:NMVVR:AXGXH,

AVPKAXX:APTKL:SPIS:LKYHY:NMVVK:AXGXH,

KASKAXX:VPTKL:SPIS:LKYHY:GMAVS:EXGXR,

GSAGPXX:TPTKM:SPIS:LKYHY:GMVVD:RXGXS,

AAPASXX:VPARL:SPIS:LKYHY:DMVVE:AXGXR,

STPPTXX:VPTRL:SPIS:LKYHY:DMVVE:SXGXR,

HVPKPXX:APTKL:SPIS:LKYHY:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS:LKYHY:MIVEE:XGXL,

ASAAPXX:VPQAL:SPIS:LKYHY:MIVRS:XKXS, ASASPXX:VSQDL:SPIS:LKYHY:MIVKS:XKXS,

ASASPXX:VPQDL:SPIS:LKYHY:MVVKS:XKXS, NDEGLEX:VPTEE:SPIS:LKYHY:FLQHN:KXEXR,

NDEGLEX:VPTGQ:SPIS:LKYHY:LEEHS:QXEXR,

SSVKXQP:SRVHH:SPIS:LKYHY:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SPIS:LKYHY:TLEDH:LAXKXE,

KIPKAXX:VPTEL:EPIS:KFKYE:DMAVS:GXGXR,

GIPEPXX:VPTKM:EPIS:KFKYE:NMAVS:SXAXR,

SIPKAXX:VPTEL:EPIS:KFKYE:EMAVS:GXGXR,

HVTKPTX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH,

YVPKPXX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH,

TVPKPXX:VPTQL:EPIS:KFKYE:NMAVS:AXGXH,

AVPKAXX:VPTKL:EPIS:KFKYE:NMAVS:AXGXH,

KVGKAXX:VPTKL:EPIS:KFKYE:EGMSAVS:XGXR,

GSAGPXX:VPTKM:EPIS:KFKYE:GMAVS:RXGXS,

AAPASXX:VPTRL:EPIS:KFKYE:DMAVS:AXGXR,

STPPTXX:VPTRL:EPIS:KFKYE:DMAVS:SXGXR,

HVPKPXX:VPTKL:EPIS:KFKYE:NMAVS:SXGXH, RVPSTXX:VPTKT:EPIS:KFKYE:MIAVS:XGXL,

ASAAPXX:VPTAL:EPIS:KFKYE:MIAVS:XKXS, ASASPXX:VPTDL:EPIS:KFKYE:MIAVS:XKXS,

ASASPXX:VPTDL:EPIS:KFKYE:MVAVS:XKXS, KIPKAXX:VPTEL:EPIS:KFKYE:DMVVE:GXGXR,

GIPEPXX:VPEKM:EPIS:KFKYE:NMTVE:SXAXR,

SIPKAXX:VPTEL:EPIS:KFKYE:EMVVE:GXGXR,

HVTKPTX:APTKL:EPIS:KFKYE:NMVVR:SXGXH,

YVPKPXX:APTKL:EPIS:KFKYE:NMVVR:SXGXH,

TVPKPXX:APTQL:EPIS:KFKYE:NMVVR:AXGXH,

AVPKAXX:APTKL:EPIS:KFKYE:NMVVK:AXGXH,

KVGKAXX:VPTKL:EPIS:KFKYE:EGMSVAE:XGXR,

GSAGPXX:TPTKM:EPIS:KFKYE:GMVVD:RXGXS,

AAPASXX:VPARL:EPIS:KFKYE:DMVVE:AXGXR,

STPPTXX:VPTRL:EPIS:KFKYE:DMVVE:SXGXR,

HVPKPXX:APTKL:EPIS:KFKYE:NMVVR:SXGXH, RVPSTXX:APVKT:EPIS:KFKYE:MIVEE:XGXL,

ASAAPXX:VPQAL:EPIS:KFKYE:MIVRS:XKXS, ASASPXX:VSQDL:EPIS:KFKYE:MIVKS:XKXS,

ASASPXX:VPQDL:EPIS:KFKYE:MVVKS:XKXS, NDEGLEX:VPTEE:EPIS:KFKYE:FLQHN:KXEXR,

NDEGLEX:VPTGQ:EPIS:KFKYE:LEEHS:QXEXR,

SSVKXQP:SRVHH:EPIS:KFKYE:RLEEH:LEXAXA,

RNVQXRP:TQVQL:EPIS:KFKYE:TLEDH:LAXKXE,

KIPKAXX:TPTEL:SPIN:YGKIP:DMVVD:GXGXR, GIPEPXX:TPTKM:SPIN:YGKIP:NMVVD:SXAXR,

SIPKAXX:TPTEL:SPIN:YGKIP:EMVVD:GXGXR, HVTKPTX:TPTKL:SPIN:YGKIP:NMVVD:SXGXH,

YVPKPXX:TPTKL:SPIN:YGKIP:NMVVD:SXGXH,

TVPKPXX:TPTQL:SPIN:YGKIP:NMVVD:AXGXH,
AVPKAXX:TPTKL:SPIN:YGKIP:NMVVD:AXGXH,
KVGKAXX:TPTKL:SPIN:YGKIP:EGMSVVD:XGXR,
KASKAXX:TPTKL:SPIN:YGKIP:GMVVD:EXGXR,
AAPASXX:TPTRL:SPIN:YGKIP:DMVVD:AXGXR,
STPPTXX:TPTRL:SPIN:YGKIP:DMVVD:SXGXR,
HVPKPXX:TPTKL:SPIN:YGKIP:NMVVD:SXGXH, RVPSTXX:TPTKT:SPIN:YGKIP:MIVVD:XGXL,
ASAAPXX:TPTAL:SPIN:YGKIP:MIVVD:XKXS, ASASPXX:TPTDL:SPIN:YGKIP:MIVVD:XKXS,
ASASPXX:TPTDL:SPIN:YGKIP:MVVVD:XKXS, KIPKAXX:VPTEL:SPIN:YGKIP:DMVVE:GXGXR,
GIPEPXX:VPEKM:SPIN:YGKIP:NMTVE:SXAXR, SIPKAXX:VPTEL:SPIN:YGKIP:EMVVE:GXGXR,
HVTKPTX:APTKL:SPIN:YGKIP:NMVVR:SXGXH,
YVPKPXX:APTKL:SPIN:YGKIP:NMVVR:SXGXH,
TVPKPXX:APTQL:SPIN:YGKIP:NMVVR:AXGXH,
AVPKAXX:APTKL:SPIN:YGKIP:NMVVK:AXGXH,
KVGKAXX:VPTKL:SPIN:YGKIP:EGMSVAE:XGXR,
KASKAXX:VPTKL:SPIN:YGKIP:GMAVS:EXGXR,
AAPASXX:VPARL:SPIN:YGKIP:DMVVE:AXGXR,
STPPTXX:VPTRL:SPIN:YGKIP:DMVVE:SXGXR,
HVPKPXX:APTKL:SPIN:YGKIP:NMVVR:SXGXH, RVPSTXX:APVKT:SPIN:YGKIP:MIVEE:XGXL,
ASAAPXX:VPQAL:SPIN:YGKIP:MIVRS:XKXS, ASASPXX:VSQDL:SPIN:YGKIP:MIVKS:XKXS,
ASASPXX:VPQDL:SPIN:YGKIP:MVVKS:XKXS, NDEGLEX:VPTEE:SPIN:YGKIP:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SPIN:YGKIP:LEEHS:QXEXR,
SSVKXQP:SRVHH:SPIN:YGKIP:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SPIN:YGKIP:TLEDH:LAXKXE,
KIPKAXX:VPAEL:SPIS:YKQYE:DMVVE:GXGXR,
GIPEPXX:VPAKM:SPIS:YKQYE:NMVVE:SXAXR,
SIPKAXX:VPAEL:SPIS:YKQYE:EMVVE:GXGXR,
HVTKPTX:VPAKL:SPIS:YKQYE:NMVVE:SXGXH,
YVPKPXX:VPAKL:SPIS:YKQYE:NMVVE:SXGXH,
TVPKPXX:VPAQL:SPIS:YKQYE:NMVVE:AXGXH,
AVPKAXX:VPAKL:SPIS:YKQYE:NMVVE:AXGXH,
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KASKAXX:VPAKL:SPIS:YKQYE:GMVVE:EXGXR,
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HVPKPXX:VPAKL:SPIS:YKQYE:NMVVE:SXGXH, RVPSTXX:VPAKT:SPIS:YKQYE:MIVVE:XGXL,
ASAAPXX:VPAAL:SPIS:YKQYE:MIVVE:XKXS, ASASPXX:VPADL:SPIS:YKQYE:MIVVE:XKXS,
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GIPEPXX:VPEKM:SPIS:YKQYE:NMTVE:SXAXR,
SIPKAXX:VPTEL:SPIS:YKQYE:EMVVE:GXGXR,
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YVPKPXX:APTKL:SPIS:YKQYE:NMVVR:SXGXH,

TVPKPXX:APTQL:SPIS:YKQYE:NMVVR:AXGXH,
AVPKAXX:APTKL:SPIS:YKQYE:NMVVK:AXGXH,
KVGKAXX:VPTKL:SPIS:YKQYE:EGMSVAE:XGXR,
KASKAXX:VPTKL:SPIS:YKQYE:GMAVS:EXGXR,
GSAGPXX:TPTKM:SPIS:YKQYE:GMVVD:RXGXS,
STPPTXX:VPTRL:SPIS:YKQYE:DMVVE:SXGXR,
HVPKPXX:APTKL:SPIS:YKQYE:NMVVR:SXGXH, RVPSTXX:APVKT:SPIS:YKQYE:MIVEE:XGXL,
ASAAPXX:VPQAL:SPIS:YKQYE:MIVRS:XKXS, ASASPXX:VSQDL:SPIS:YKQYE:MIVKS:XKXS,
ASASPXX:VPQDL:SPIS:YKQYE:MVVKS:XKXS,
NDEGLEX:VPTEE:SPIS:YKQYE:FLQHN:KXEXR,
NDEGLEX:VPTGQ:SPIS:YKQYE:LEEHS:QXEXR,
SSVKXQP:SRVHH:SPIS:YKQYE:RLEEH:LEXAXA,
RNVQXRP:TQVQL:SPIS:YKQYE:TLEDH:LAXKXE,
GIPEPXX:VPTKM:SPIS:YKQYE:NMVVE:SXAXR,
HVTKPTX:VPTKL:SPIS:YKQYE:NMVVE:SXGXH,
YVPKPXX:VPTKL:SPIS:YKQYE:NMVVE:SXGXH,
TVPKPXX:VPTQL:SPIS:YKQYE:NMVVE:AXGXH,
AVPKAXX:VPTKL:SPIS:YKQYE:NMVVE:AXGXH,
KVGKAXX:VPTKL:SPIS:YKQYE:EGMSVVE:XGXR,
KASKAXX:VPTKL:SPIS:YKQYE:GMVVE:EXGXR,
GSAGPXX:VPTKM:SPIS:YKQYE:GMVVE:RXGXS,
AAPASXX:VPTRL:SPIS:YKQYE:DMVVE:AXGXR,
HVPKPXX:VPTKL:SPIS:YKQYE:NMVVE:SXGXH, RVPSTXX:VPTKT:SPIS:YKQYE:MIVVE:XGXL,
ASAAPXX:VPTAL:SPIS:YKQYE:MIVVE:XKXS, ASASPXX:VPTDL:SPIS:YKQYE:MIVVE:XKXS,
ASASPXX:VPTDL:SPIS:YKQYE:MVVVE:XKXS,
AAPASXX:VPARL:SPIS:YKQYE:DMVVE:AXGXR,
KIPKAXX:APVEL:KPLS:DHHKD:DMVEE:GXGXR,
GIPEPXX:APVKM:KPLS:DHHKD:NMVEE:SXAXR,
SIPKAXX:APVEL:KPLS:DHHKD:EMVEE:GXGXR,
HVTKPTX:APVKL:KPLS:DHHKD:NMVEE:SXGXH,
YVPKPXX:APVKL:KPLS:DHHKD:NMVEE:SXGXH,
TVPKPXX:APVQL:KPLS:DHHKD:NMVEE:AXGXH,
AVPKAXX:APVKL:KPLS:DHHKD:NMVEE:AXGXH,
KVGKAXX:APVKL:KPLS:DHHKD:EGMSVEE:XGXR,
KASKAXX:APVKL:KPLS:DHHKD:GMVEE:EXGXR,
GSAGPXX:APVKM:KPLS:DHHKD:GMVEE:RXGXS,
AAPASXX:APVRL:KPLS:DHHKD:DMVEE:AXGXR,
STPPTXX:APVRL:KPLS:DHHKD:DMVEE:SXGXR,
HVPKPXX:APVKL:KPLS:DHHKD:NMVEE:SXGXH,
ASAAPXX:APVAL:KPLS:DHHKD:MIVEE:XKXS, ASASPXX:APVDL:KPLS:DHHKD:MIVEE:XKXS,
ASASPXX:APVDL:KPLS:DHHKD:MVVEE:XKXS,
KIPKAXX:VPTEL:KPLS:DHHKD:DMVVE:GXGXR,

GIPEPXX:VPEKM:KPLS:DHHKD:NMTVE:SXAXR,

SIPKAXX:VPTEL:KPLS:DHHKD:EMVVE:GXGXR,

HVTKPTX:APTKL:KPLS:DHHKD:NMVVR:SXGXH,

YVPKPXX:APTKL:KPLS:DHHKD:NMVVR:SXGXH,

TVPKPXX:APTQL:KPLS:DHHKD:NMVVR:AXGXH,

AVPKAXX:APTKL:KPLS:DHHKD:NMVVK:AXGXH,

KVGKAXX:VPTKL:KPLS:DHHKD:EGMSVAE:XGXR,

KASKAXX:VPTKL:KPLS:DHHKD:GMAVS:EXGXR,

GSAGPXX:TPTKM:KPLS:DHHKD:GMVVD:RXGXS,

AAPASXX:VPARL:KPLS:DHHKD:DMVVE:AXGXR,

STPPTXX:VPTRL:KPLS:DHHKD:DMVVE:SXGXR,

HVPKPXX:APTKL:KPLS:DHHKD:NMVVR:SXGXH,

ASAAPXX:VPQAL:KPLS:DHHKD:MIVRS:XKXS, ASASPXX:VSQDL:KPLS:DHHKD:MIVKS:XKXS,

ASASPXX:VPQDL:KPLS:DHHKD:MVVKS:XKXS,

NDEGLEX:VPTEE:KPLS:DHHKD:FLQHN:KXEXR,

NDEGLEX:VPTGQ:KPLS:DHHKD:LEEHS:QXEXR,

SSVKXQP:SRVHH:KPLS:DHHKD:RLEEH:LEXAXA,

RNVQXRP:TQVQL:KPLS:DHHKD:TLEDH:LAXKXE,

KIPKAXX:VPQEL:EPLP:EQLSN:DMVRS:GXGXR,

GIPEPXX:VPQKM:EPLP:EQLSN:NMVRS:SXAXR,

SIPKAXX:VPQEL:EPLP:EQLSN:EMVRS:GXGXR,

HVTKPTX:VPQKL:EPLP:EQLSN:NMVRS:SXGXH,

YVPKPXX:VPQKL:EPLP:EQLSN:NMVRS:SXGXH,

TVPKPXX:VPQQL:EPLP:EQLSN:NMVRS:AXGXH,

AVPKAXX:VPQKL:EPLP:EQLSN:NMVRS:AXGXH,

KVGKAXX:VPQKL:EPLP:EQLSN:EGMSVRS:XGXR,

KASKAXX:VPQKL:EPLP:EQLSN:GMVRS:EXGXR,

GSAGPXX:VPQKM:EPLP:EQLSN:GMVRS:RXGXS,

AAPASXX:VPQRL:EPLP:EQLSN:DMVRS:AXGXR,

STPPTXX:VPQRL:EPLP:EQLSN:DMVRS:SXGXR,

HVPKPXX:VPQKL:EPLP:EQLSN:NMVRS:SXGXH,

RVPSTXX:VPQKT:EPLP:EQLSN:MIVRS:XGXL, ASASPXX:VPQDL:EPLP:EQLSN:MIVRS:XKXS,

ASASPXX:VPQDL:EPLP:EQLSN:MVVRS:XKXS,

KIPKAXX:VPTEL:EPLP:EQLSN:DMVVE:GXGXR,

GIPEPXX:VPEKM:EPLP:EQLSN:NMTVE:SXAXR,

SIPKAXX:VPTEL:EPLP:EQLSN:EMVVE:GXGXR,

HVTKPTX:APTKL:EPLP:EQLSN:NMVVR:SXGXH,

YVPKPXX:APTKL:EPLP:EQLSN:NMVVR:SXGXH,

TVPKPXX:APTQL:EPLP:EQLSN:NMVVR:AXGXH,

AVPKAXX:APTKL:EPLP:EQLSN:NMVVK:AXGXH,

KVGKAXX:VPTKL:EPLP:EQLSN:EGMSVAE:XGXR,

KASKAXX:VPTKL:EPLP:EQLSN:GMAVS:EXGXR,

GSAGPXX:TPTKM:EPLP:EQLSN:GMVVD:RXGXS,

AAPASXX:VPARL:EPLP:EQLSN:DMVVE:AXGXR,

STPPTXX:VPTRL:EPLP:EQLSN:DMVVE:SXGXR,

HVPKPXX:APTKL:EPLP:EQLSN:NMVVR:SXGXH,

RVPSTXX:APVKT:EPLP:EQLSN:MIVEE:XGXL, ASASPXX:VSQDL:EPLP:EQLSN:MIVKS:XKXS,

ASASPXX:VPQDL:EPLP:EQLSN:MVVKS:XKXS,

NDEGLEX:VPTEE:EPLP:EQLSN:FLQHN:KXEXR,

NDEGLEX:VPTGQ:EPLP:EQLSN:LEEHS:QXEXR,

SSVKXQP:SRVHH:EPLP:EQLSN:RLEEH:LEXAXA,

RNVQXRP:TQVQL:EPLP:EQLSN:TLEDH:LAXKXE,

KIPKAXX:VSQEL:EPLT:EQLSN:DMVKS:GXGXR,

GIPEPXX:VSQKM:EPLT:EQLSN:NMVKS:SXAXR,

SIPKAXX:VSQEL:EPLT:EQLSN:EMVKS:GXGXR,

HVTKPTX:VSQKL:EPLT:EQLSN:NMVKS:SXGXH,

YVPKPXX:VSQKL:EPLT:EQLSN:NMVKS:SXGXH,

TVPKPXX:VSQQL:EPLT:EQLSN:NMVKS:AXGXH,

AVPKAXX:VSQKL:EPLT:EQLSN:NMVKS:AXGXH,

KVGKAXX:VSQKL:EPLT:EQLSN:EGMSVKS:XGXR,

KASKAXX:VSQKL:EPLT:EQLSN:GMVKS:EXGXR,

GSAGPXX:VSQKM:EPLT:EQLSN:GMVKS:RXGXS,

AAPASXX:VSQRL:EPLT:EQLSN:DMVKS:AXGXR,

STPPTXX:VSQRL:EPLT:EQLSN:DMVKS:SXGXR,

HVPKPXX:VSQKL:EPLT:EQLSN:NMVKS:SXGXH,

RVPSTXX:VSQKT:EPLT:EQLSN:MIVKS:XGXL, ASAAPXX:VSQAL:EPLT:EQLSN:MIVKS:XKXS,

ASASPXX:VSQDL:EPLT:EQLSN:MVVKS:XKXS,

KIPKAXX:VPTEL:EPLT:EQLSN:DMVVE:GXGXR,

GIPEPXX:VPEKM:EPLT:EQLSN:NMTVE:SXAXR,

SIPKAXX:VPTEL:EPLT:EQLSN:EMVVE:GXGXR,

HVTKPTX:APTKL:EPLT:EQLSN:NMVVR:SXGXH,

YVPKPXX:APTKL:EPLT:EQLSN:NMVVR:SXGXH,

TVPKPXX:APTQL:EPLT:EQLSN:NMVVR:AXGXH,

AVPKAXX:APTKL:EPLT:EQLSN:NMVVK:AXGXH,

KVGKAXX:VPTKL:EPLT:EQLSN:EGMSVAE:XGXR,

KASKAXX:VPTKL:EPLT:EQLSN:GMAVS:EXGXR,

GSAGPXX:TPTKM:EPLT:EQLSN:GMVVD:RXGXS,

AAPASXX:VPARL:EPLT:EQLSN:DMVVE:AXGXR,

STPPTXX:VPTRL:EPLT:EQLSN:DMVVE:SXGXR,

HVPKPXX:APTKL:EPLT:EQLSN:NMVVR:SXGXH,

RVPSTXX:APVKT:EPLT:EQLSN:MIVEE:XGXL, ASAAPXX:VPQAL:EPLT:EQLSN:MIVRS:XKXS,

NDEGLEX:VPTEE:EPLT:EQLSN:FLQHN:KXEXR,

NDEGLEX:VPTGQ:EPLT:EQLSN:LEEHS:QXEXR,

SSVKXQP:SRVHH:EPLT:EQLSN:RLEEH:LEXAXA,

RNVQXRP:TQVQL:EPLT:EQLSN:TLEDH:LAXKXE,

KIPKAXX:VPQEL:EPLT:EQLSN:DMVKS:GXGXR,

GIPEPXX:VPQKM:EPLT:EQLSN:NMVKS:SXAXR,

SIPKAXX:VPQEL:EPLT:EQLSN:EMVKS:GXGXR,

HVTKPTX:VPQKL:EPLT:EQLSN:NMVKS:SXGXH,

YVPKPXX:VPQKL:EPLT:EQLSN:NMVKS:SXGXH,

TVPKPXX:VPQQL:EPLT:EQLSN:NMVKS:AXGXH,

AVPKAXX:VPQKL:EPLT:EQLSN:NMVKS:AXGXH,

KVGKAXX:VPQKL:EPLT:EQLSN:EGMSVKS:XGXR,

KASKAXX:VPQKL:EPLT:EQLSN:GMVKS:EXGXR,

GSAGPXX:VPQKM:EPLT:EQLSN:GMVKS:RXGXS,

AAPASXX:VPQRL:EPLT:EQLSN:DMVKS:AXGXR,

STPPTXX:VPQRL:EPLT:EQLSN:DMVKS:SXGXR,

HVPKPXX:VPQKL:EPLT:EQLSN:NMVKS:SXGXH,

RVPSTXX:VPQKT:EPLT:EQLSN:MIVKS:XGXL, ASAAPXX:VPQAL:EPLT:EQLSN:MIVKS:XKXS,

ASASPXX:VPQDL:EPLT:EQLSN:MIVKS:XKXS,

NDEGLEX:VPTGQ:SNIT:IGEMS:LEQHN:QXEXR,

KIPKAXX:VPTEL:SNIT:IGEMS:DMVVE:GXGXR, GIPEPXX:VPEKM:SNIT:IGEMS:NMTVE:SXAXR,

SIPKAXX:VPTEL:SNIT:IGEMS:EMVVE:GXGXR,

HVTKPTX:APTKL:SNIT:IGEMS:NMVVR:SXGXH,

YVPKPXX:APTKL:SNIT:IGEMS:NMVVR:SXGXH,

TVPKPXX:APTQL:SNIT:IGEMS:NMVVR:AXGXH,

AVPKAXX:APTKL:SNIT:IGEMS:NMVVK:AXGXH,

KVGKAXX:VPTKL:SNIT:IGEMS:EGMSVAE:XGXR,

KASKAXX:VPTKL:SNIT:IGEMS:GMAVS:EXGXR,

GSAGPXX:TPTKM:SNIT:IGEMS:GMVVD:RXGXS,

AAPASXX:VPARL:SNIT:IGEMS:DMVVE:AXGXR,

STPPTXX:VPTRL:SNIT:IGEMS:DMVVE:SXGXR,

HVPKPXX:APTKL:SNIT:IGEMS:NMVVR:SXGXH, RVPSTXX:APVKT:SNIT:IGEMS:MIVEE:XGXL,

ASAAPXX:VPQAL:SNIT:IGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT:IGEMS:MIVKS:XKXS,

ASASPXX:VPQDL:SNIT:IGEMS:MVVKS:XKXS, NDEGLEX:VPTGQ:SNIT:IGEMS:LEEHS:QXEXR,

SSVKXQP:SRVHH:SNIT:IGEMS:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SNIT:IGEMS:TLEDH:LAXKXE,

NDEGLEX:VPTEE:SNIT:LGEMS:FLEHS:KXEXR,

KIPKAXX:VPTEL:SNIT:LGEMS:DMVVE:GXGXR,

GIPEPXX:VPEKM:SNIT:LGEMS:NMTVE:SXAXR,

SIPKAXX:VPTEL:SNIT:LGEMS:EMVVE:GXGXR,

HVTKPTX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,

YVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH,

TVPKPXX:APTQL:SNIT:LGEMS:NMVVR:AXGXH,

AVPKAXX:APTKL:SNIT:LGEMS:NMVVK:AXGXH,

KVGKAXX:VPTKL:SNIT:LGEMS:EGMSVAE:XGXR,

KASKAXX:VPTKL:SNIT:LGEMS:GMAVS:EXGXR,

GSAGPXX:TPTKM:SNIT:LGEMS:GMVVD:RXGXS,

AAPASXX:VPARL:SNIT:LGEMS:DMVVE:AXGXR,

STPPTXX:VPTRL:SNIT:LGEMS:DMVVE:SXGXR,

HVPKPXX:APTKL:SNIT:LGEMS:NMVVR:SXGXH, RVPSTXX:APVKT:SNIT:LGEMS:MIVEE:XGXL,

ASAAPXX:VPQAL:SNIT:LGEMS:MIVRS:XKXS, ASASPXX:VSQDL:SNIT:LGEMS:MIVKS:XKXS,

ASASPXX:VPQDL:SNIT:LGEMS:MVVKS:XKXS,

NDEGLEX:VPTEE:SNIT:LGEMS:FLQHN:KXEXR,

SSVKXQP:SRVHH:SNIT:LGEMS:RLEEH:LEXAXA,

RNVQXRP:TQVQL:SNIT:LGEMS:TLEDH:LAXKXE,

RNVQXRP:SRVQL:RSVK:KEVQV:TLEEH:LAXKXE,

KIPKAXX:VPTEL:RSVK:KEVQV:DMVVE:GXGXR,

GIPEPXX:VPEKM:RSVK:KEVQV:NMTVE:SXAXR,

SIPKAXX:VPTEL:RSVK:KEVQV:EMVVE:GXGXR,

HVTKPTX:APTKL:RSVK:KEVQV:NMVVR:SXGXH,

YVPKPXX:APTKL:RSVK:KEVQV:NMVVR:SXGXH,

TVPKPXX:APTQL:RSVK:KEVQV:NMVVR:AXGXH,

AVPKAXX:APTKL:RSVK:KEVQV:NMVVK:AXGXH,

KVGKAXX:VPTKL:RSVK:KEVQV:EGMSVAE:XGXR,

KASKAXX:VPTKL:RSVK:KEVQV:GMAVS:EXGXR,

GSAGPXX:TPTKM:RSVK:KEVQV:GMVVD:RXGXS,

AAPASXX:VPARL:RSVK:KEVQV:DMVVE:AXGXR,

STPPTXX:VPTRL:RSVK:KEVQV:DMVVE:SXGXR,

HVPKPXX:APTKL:RSVK:KEVQV:NMVVR:SXGXH,

RVPSTXX:APVKT:RSVK:KEVQV:MIVEE:XGXL, ASAAPXX:VPQAL:RSVK:KEVQV:MIVRS:XKXS,

ASASPXX:VSQDL:RSVK:KEVQV:MIVKS:XKXS, ASASPXX:VPQDL:RSVK:KEVQV:MVVKS:XKXS,

NDEGLEX:VPTEE:RSVK:KEVQV:FLQHN:KXEXR,

NDEGLEX:VPTGQ:RSVK:KEVQV:LEEHS:QXEXR,

RNVQXRP:TQVQL:RSVK:KEVQV:TLEDH:LAXKXE,

SSVKXQP:TQVHH:RPVQ:KKATV:RLEDH:LEXAXA,

KIPKAXX:VPTEL:RPVQ:KKATV:DMVVE:GXGXR,

GIPEPXX:VPEKM:RPVQ:KKATV:NMTVE:SXAXR,

SIPKAXX:VPTEL:RPVQ:KKATV:EMVVE:GXGXR,

HVTKPTX:APTKL:RPVQ:KKATV:NMVVR:SXGXH,

YVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH,

TVPKPXX:APTQL:RPVQ:KKATV:NMVVR:AXGXH,

AVPKAXX:APTKL:RPVQ:KKATV:NMVVK:AXGXH,

KVGKAXX:VPTKL:RPVQ:KKATV:EGMSVAE:XGXR,

KASKAXX:VPTKL:RPVQ:KKATV:GMAVS:EXGXR,

GSAGPXX:TPTKM:RPVQ:KKATV:GMVVD:RXGXS,

AAPASXX:VPARL:RPVQ:KKATV:DMVVE:AXGXR,

STPPTXX:VPTRL:RPVQ:KKATV:DMVVE:SXGXR,

HVPKPXX:APTKL:RPVQ:KKATV:NMVVR:SXGXH,
RVPSTXX:APVKT:RPVQ:KKATV:MIVEE:XGXL, ASAAPXX:VPQAL:RPVQ:KKATV:MIVRS:XKXS,
ASASPXX:VSQDL:RPVQ:KKATV:MIVKS:XKXS, ASASPXX:VPQDL:RPVQ:KKATV:MVVKS:XKXS,
NDEGLEX:VPTEE:RPVQ:KKATV:FLQHN:KXEXR,
NDEGLEX:VPTGQ:RPVQ:KKATV:LEEHS:QXEXR and
SSVKXQP:SRVHH:RPVQ:KKATV:RLEEH:LEXAXA.

90. A pharmaceutical association for a use according to any one of claims 1 to 89, wherein said growth factor receptor-binding compound comprises at least one bioactive carrier-affinity-containing group, wherein said at least one bioactive carrier-affinity-containing group provides said growth factor receptor-binding compound with the ability to covalently or non-covalently interact with a bioactive carrier.

91. A pharmaceutical association for a use according to claim 90, wherein said bioactive carrier-affinity-containing group is a biomaterial affinity-containing group.

92. A pharmaceutical association for a use according to claim 91, wherein said biomaterial affinity-containing group is adapted for forming at least one covalent bond with a biomaterial.

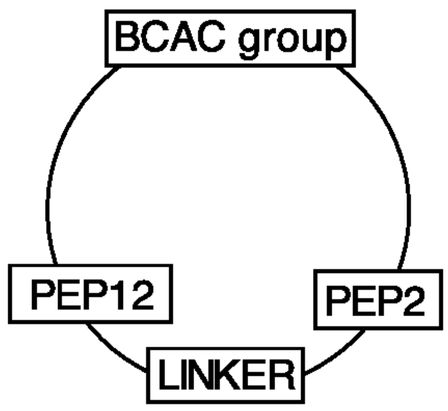
93. A pharmaceutical association for a use according to claim 91, wherein said biomaterial affinity-containing group is adapted for forming at least one non-covalent bond with a biomaterial.

94. A pharmaceutical association for a use according to claim 92, wherein said biomaterial affinity-containing group is a thiol-containing group.

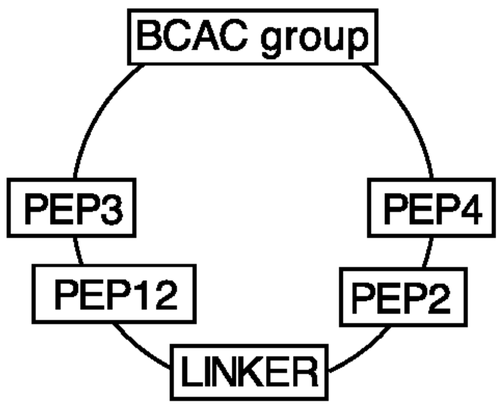
95. A pharmaceutical association for a use according to claim 94, wherein said thiol-containing group is a cysteine-containing group.

96. A pharmaceutical association for a use according to claim 93, wherein said biomaterial affinity-containing group is a peptide with 3 to 25 amino acids comprising one or more of Phe, Trp or Tyr.

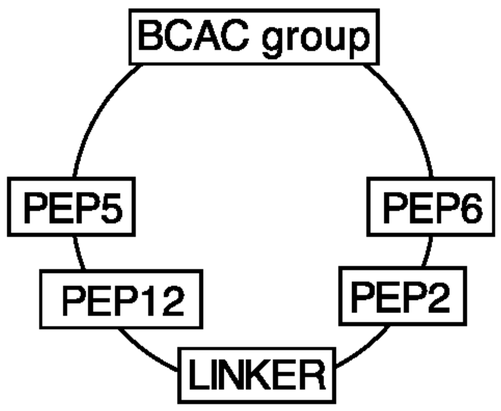
97. A pharmaceutical association for a use according to any one of claims 1 and 3 to 96, wherein said growth factor receptor-binding compound has any one of the following cyclic schematic general formulae:



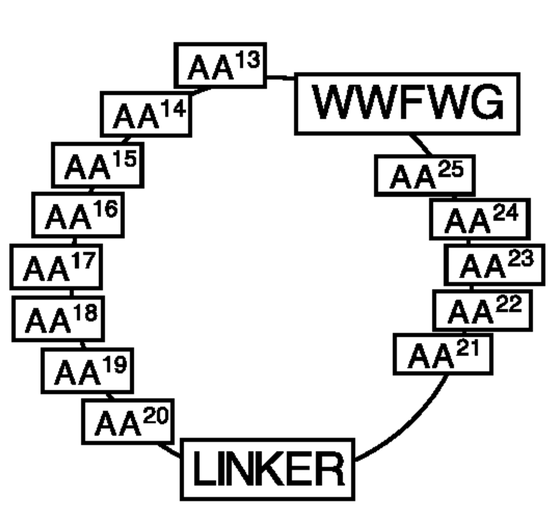
(XXXVI)



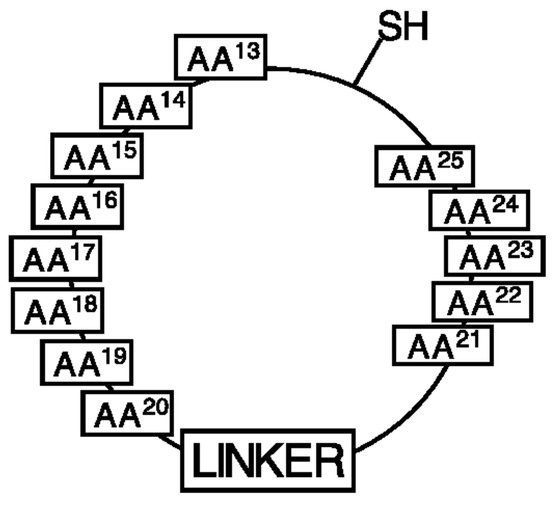
(XXXVII)



(XXXVIII)



(XXXIX)



(XXXX)

98. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 97, wherein said growth factor receptor-binding compound is a peptide, or a variant or analog thereof, with between 25 and 60 amino acids having growth factor receptor-binding capability.

99. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 97, wherein said growth factor receptor-binding compound is a peptide, or a variant or analog thereof with between 25 and 50 amino acids.

100. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 97, wherein said growth factor receptor-binding compound is a peptide, or a variant or analog thereof with between 25 and 45 amino acids.

101. A pharmaceutical association for a use according to any one of claims 98 to 100, wherein the RMSD value of the structure coordinates of said peptide, variant or analog thereof with respect to PEPREF is 2.45Å (Angstroms) or less, and wherein PEPREF is

ATOM	511	N	LYS	A	1	-14.570	46.437	27.424
ATOM	512	CA	LYS	A	1	-13.512	45.748	28.151
ATOM	513	C	LYS	A	1	-13.655	44.259	27.884
ATOM	514	O	LYS	A	1	-12.769	43.463	28.197
ATOM	515	CB	LYS	A	1	-13.605	46.029	29.652
ATOM	516	CG	LYS	A	1	-13.640	47.509	29.991
ATOM	517	CD	LYS	A	1	-12.615	48.297	29.183
ATOM	518	CE	LYS	A	1	-12.625	49.768	29.575
ATOM	519	NZ	LYS	A	1	-13.994	50.369	29.497
ATOM	520	N	ILE	A	2	-14.792	43.890	27.309
ATOM	521	CA	ILE	A	2	-15.051	42.499	26.967
ATOM	522	C	ILE	A	2	-14.911	42.370	25.444
ATOM	523	O	ILE	A	2	-15.531	43.125	24.683
ATOM	524	CB	ILE	A	2	-16.466	42.065	27.401
ATOM	525	CG1	ILE	A	2	-16.630	42.238	28.915
ATOM	526	CG2	ILE	A	2	-16.710	40.629	26.985
ATOM	527	CD1	ILE	A	2	-15.631	41.478	29.30
ATOM	528	N	PRO	A	3	-14.085	41.411	24.989
ATOM	529	CA	PRO	A	3	-13.789	41.109	23.588
ATOM	530	C	PRO	A	3	-14.998	40.695	22.768
ATOM	531	O	PRO	A	3	-15.969	40.164	23.305

ATOM	532	CB	PRO	A	3	-12.785	39.968	23.688
ATOM	533	CG	PRO	A	3	-12.156	40.166	25.007
ATOM	534	CD	PRO	A	3	-13.330	40.506	25.867
ATOM	535	N	LYS	A	4	-14.937	40.937	21.463
ATOM	536	CA	LYS	A	4	-16.023	40.529	20.590
ATOM	537	C	LYS	A	4	-15.886	39.015	20.391
ATOM	538	O	LYS	A	4	-14.903	38.415	20.831
ATOM	539	CB	LYS	A	4	-15.926	41.244	19.245
ATOM	540	CG	LYS	A	4	-15.802	42.751	19.355
ATOM	541	CD	LYS	A	4	-16.292	43.433	18.083
ATOM	542	CE	LYS	A	4	-16.162	44.943	18.177
ATOM	543	NZ	LYS	A	4	-16.825	45.628	17.019
ATOM	544	N	ALA	A	5	-16.85	38.393	19.759
ATOM	545	CA	ALA	A	5	-16.811	36.955	19.507
ATOM	546	C	ALA	A	5	-15.772	36.771	18.416
ATOM	547	O	ALA	A	5	-15.727	37.534	17.455
ATOM	548	CB	ALA	A	5	-18.168	36.419	19.043
ATOM	549	N	CYS	A	6	-14.935	35.756	18.562
ATOM	550	CA	CYS	A	6	-13.887	35.518	17.584
ATOM	551	C	CYS	A	6	-14.347	34.765	16.338
ATOM	552	O	CYS	A	6	-15.327	34.018	16.368
ATOM	553	CB	CYS	A	6	-12.743	34.768	18.241
ATOM	554	SG	CYS	A	6	-11.198	34.959	17.353
ATOM	555	N	CYS	A	7	-13.623	34.973	15.243
ATOM	556	CA	CYS	A	7	-13.931	34.328	13.969
ATOM	557	C	CYS	A	7	-13.091	33.071	13.798
ATOM	558	O	CYS	A	7	-11.961	33.123	13.302
ATOM	559	CB	CYS	A	7	-13.653	35.290	12.824
ATOM	560	SG	CYS	A	7	-13.930	34.633	11.154
ATOM	561	N	VAL	A	8	-13.654	31.941	14.209
ATOM	562	CA	VAL	A	8	-12.949	30.684	14.110
ATOM	563	C	VAL	A	8	-13.653	29.733	13.157
ATOM	564	O	VAL	A	8	-14.759	30.016	12.687
ATOM	565	CB	VAL	A	8	-12.814	30.038	15.492
ATOM	566	CG1	VAL	A	8	-11.807	30.825	16.337
ATOM	567	CG2	VAL	A	8	-14.161	30.006	16.170
ATOM	568	N	PRO	A	9	-13.003	28.601	12.828
ATOM	569	CA	PRO	A	9	-13.593	27.615	11.918
ATOM	570	C	PRO	A	9	-14.726	26.886	12.631
ATOM	571	O	PRO	A	9	-14.581	26.476	13.780
ATOM	572	CB	PRO	A	9	-12.423	26.676	11.601
ATOM	573	CG	PRO	A	9	-11.204	27.487	11.925
ATOM	574	CD	PRO	A	9	-11.620	28.226	13.163
ATOM	575	N	THR	A	10	-15.847	26.721	11.942
ATOM	576	CA	THR	A	10	-16.999	26.060	12.527
ATOM	577	C	THR	A	10	-17.334	24.767	11.804
ATOM	578	O	THR	A	10	-18.097	23.943	12.303
ATOM	579	CB	THR	A	10	-18.211	27.010	12.523
ATOM	580	OG1	THR	A	10	-18.491	27.445	11.185
ATOM	581	CG2	THR	A	10	-17.902	28.230	13.375
ATOM	582	N	GLU	A	11	-16.750	24.586	10.627
ATOM	583	CA	GLU	A	11	-16.980	23.377	9.848
ATOM	584	C	GLU	A	11	-15.643	22.935	9.246
ATOM	585	O	GLU	A	11	-15.029	23.666	8.464
ATOM	586	CB	GLU	A	11	-17.981	23.624	8.715
ATOM	587	CG	GLU	A	11	-19.421	23.807	9.163
ATOM	588	CD	GLU	A	11	-19.686	25.166	9.770
ATOM	589	OE1	GLU	A	11	-19.478	26.175	9.073
ATOM	590	OE2	GLU	A	11	-20.111	25.227	10.939
ATOM	591	N	LEU	A	12	-15.183	21.749	9.622

ATOM	592	CA	LEU	A	12	-13.923	21.254	9.104
ATOM	593	C	LEU	A	12	-14.062	19.912	8.386
ATOM	594	O	LEU	A	12	-15.136	19.299	8.359
ATOM	595	CB	LEU	A	12	-12.893	21.144	10.230
ATOM	596	CG	LEU	A	12	-12.660	22.422	11.054
ATOM	597	CD1	LEU	A	12	-13.475	22.350	12.337
ATOM	598	CD2	LEU	A	12	-11.181	22.586	11.399
ATOM	599	N	SER	A	13	-12.971	19.476	7.771
ATOM	600	CA	SER	A	13	-12.964	18.218	7.046
ATOM	601	C	SER	A	13	-11.568	17.628	7.164
ATOM	602	O	SER	A	13	-10.613	18.320	7.550
ATOM	603	CB	SER	A	13	-13.346	18.435	5.578
ATOM	604	OG	SER	A	13	-12.404	19.261	4.923
ATOM	605	N	ALA	A	13	-11.449	16.352	6.818
ATOM	606	CA	ALA	A	13	-10.179	15.665	6.949
ATOM	607	C	ALA	A	13	-9.421	15.471	5.652
ATOM	608	O	ALA	A	13	-9.941	15.720	4.563
ATOM	609	CB	ALA	A	13	-10.413	14.306	7.626
ATOM	610	N	ILE	A	14	-8.171	15.046	5.783
ATOM	611	CA	ILE	A	14	-7.343	14.746	4.623
ATOM	612	C	ILE	A	14	-6.475	13.559	5.004
ATOM	613	O	ILE	A	14	-6.212	13.316	6.183
ATOM	614	CB	ILE	A	14	-6.401	15.916	4.183
ATOM	615	CG1	ILE	A	14	-5.284	16.106	5.200
ATOM	616	CG2	ILE	A	14	-7.188	17.211	3.982
ATOM	617	CD1	ILE	A	14	-4.173	16.973	4.696
ATOM	618	N	SER	A	15	-6.045	12.806	3.999
ATOM	619	CA	SER	A	15	-5.187	11.662	4.242
ATOM	620	C	SER	A	15	-3.740	12.089	4.217
ATOM	621	O	SER	A	15	-3.360	13.020	3.508
ATOM	622	CB	SER	A	15	-5.416	10.584	3.185
ATOM	623	OG	SER	A	15	-6.667	9.971	3.401
ATOM	624	N	MET	A	16	-2.933	11.409	5.012
ATOM	625	CA	MET	A	16	-1.518	11.700	5.047
ATOM	626	C	MET	A	16	-0.778	10.414	5.244
ATOM	627	O	MET	A	16	-1.137	9.594	6.078
ATOM	628	CB	MET	A	16	-1.170	12.694	6.164
ATOM	629	CG	MET	A	16	-1.848	14.042	5.974
ATOM	630	SD	MET	A	16	-1.017	15.431	6.760
ATOM	631	CE	MET	A	16	-0.799	14.823	8.475
ATOM	632	N	LEU	A	17	0.238	10.231	4.426
ATOM	633	CA	LEU	A	17	1.077	9.065	4.508
ATOM	634	C	LEU	A	17	2.289	9.610	5.264
ATOM	635	O	LEU	A	17	2.939	10.565	4.818
ATOM	636	CB	LEU	A	17	1.461	8.608	3.100
ATOM	637	CG	LEU	A	17	2.324	7.355	2.955
ATOM	638	CD1	LEU	A	17	1.553	6.145	3.445
ATOM	639	CD2	LEU	A	17	2.723	7.190	1.492
ATOM	640	N	TYR	A	18	2.581	9.029	6.418
ATOM	641	CA	TYR	A	18	3.706	9.501	7.196
ATOM	642	C	TYR	A	18	4.434	8.333	7.835
ATOM	643	O	TYR	A	18	4.081	7.186	7.603
ATOM	644	CB	TYR	A	18	3.222	10.458	8.281
ATOM	645	CG	TYR	A	18	2.386	9.782	9.346
ATOM	646	CD1	TYR	A	18	1.029	9.527	9.147
ATOM	647	CD2	TYR	A	18	2.961	9.379	10.550
ATOM	648	CE1	TYR	A	18	0.273	8.894	10.128
ATOM	649	CE2	TYR	A	18	2.218	8.745	11.526
ATOM	650	CZ	TYR	A	18	0.877	8.508	11.317
ATOM	651	OH	TYR	A	18	0.134	7.922	12.318

ATOM	652	N	LEU	A	19	5.439	8.651	8.650
ATOM	653	CA	LEU	A	19	6.255	7.661	9.347
ATOM	654	C	LEU	A	19	6.210	7.946	10.847
ATOM	655	O	LEU	A	19	6.685	8.992	11.288
ATOM	656	CB	LEU	A	19	7.701	7.763	8.871
ATOM	657	CG	LEU	A	19	7.901	7.850	7.359
ATOM	658	CD1	LEU	A	19	9.300	8.379	7.039
ATOM	659	CD2	LEU	A	19	7.669	6.482	6.748
ATOM	660	N	ASP	A	20	5.652	7.035	11.639
ATOM	661	CA	ASP	A	20	5.594	7.282	13.071
ATOM	662	C	ASP	A	20	7.001	7.289	13.662
ATOM	663	O	ASP	A	20	7.985	7.185	12.932
ATOM	664	CB	ASP	A	20	4.714	6.244	13.786
ATOM	665	CG	ASP	A	20	5.292	4.837	13.752
ATOM	666	OD1	ASP	A	20	6.533	4.678	13.775
ATOM	667	OD2	ASP	A	20	4.491	3.882	13.732
ATOM	668	N	GLU	A	21	7.089	7.413	14.981
ATOM	669	CA	GLU	A	21	8.375	7.451	15.669
ATOM	670	C	GLU	A	21	9.250	6.212	15.463
ATOM	671	O	GLU	A	21	10.459	6.246	15.738
ATOM	672	CB	GLU	A	21	8.164	7.699	17.171
ATOM	673	CG	GLU	A	21	7.220	6.731	17.868
ATOM	674	CD	GLU	A	21	5.828	6.726	17.257
ATOM	675	OE1	GLU	A	21	5.347	7.810	16.856
ATOM	676	OE2	GLU	A	21	5.210	5.640	17.185
ATOM	677	N	ASN	A	22	8.646	5.133	14.966
ATOM	678	CA	ASN	A	22	9.377	3.889	14.727
ATOM	679	C	ASN	A	22	9.682	3.647	13.249
ATOM	680	O	ASN	A	22	10.095	2.554	12.853
ATOM	681	CB	ASN	A	22	8.591	2.707	15.299
ATOM	682	CG	ASN	A	22	8.384	2.827	16.794
ATOM	683	OD1	ASN	A	22	9.349	2.930	17.560
ATOM	684	ND2	ASN	A	22	7.125	2.819	17.221
ATOM	685	N	GLU	A	23	9.485	4.672	12.435
ATOM	686	CA	GLU	A	23	9.749	4.558	11.015
ATOM	687	C	GLU	A	23	8.790	3.603	10.299
ATOM	688	O	GLU	A	23	9.145	2.996	9.292
ATOM	689	CB	GLU	A	23	11.203	4.129	10.784
ATOM	690	CG	GLU	A	23	12.232	5.210	11.082
ATOM	691	CD	GLU	A	23	12.072	6.410	10.166
ATOM	692	OE1	GLU	A	23	12.108	6.218	8.928
ATOM	693	OE2	GLU	A	23	11.907	7.541	10.677
ATOM	694	N	LYS	A	24	7.580	3.459	10.826
ATOM	695	CA	LYS	A	24	6.583	2.624	10.175
ATOM	696	C	LYS	A	24	5.815	3.540	9.228
ATOM	697	O	LYS	A	24	5.553	4.692	9.552
ATOM	698	CB	LYS	A	24	5.602	2.039	11.182
ATOM	699	CG	LYS	A	24	6.163	0.963	12.058
ATOM	700	CD	LYS	A	24	5.068	0.387	12.947
ATOM	701	CE	LYS	A	24	5.648	-0.511	14.031
ATOM	702	NZ	LYS	A	24	4.577	-1.091	14.886
ATOM	703	N	VAL	A	25	5.455	3.037	8.057
ATOM	704	CA	VAL	A	25	4.713	3.849	7.116
ATOM	705	C	VAL	A	25	3.237	3.737	7.444
ATOM	706	O	VAL	A	25	2.657	2.659	7.383
ATOM	707	CB	VAL	A	25	4.969	3.396	5.681
ATOM	708	CG1	VAL	A	25	4.250	4.317	4.708
ATOM	709	CG2	VAL	A	25	6.462	3.393	5.422
ATOM	710	N	VAL	A	25	2.637	4.864	7.800
ATOM	711	CA	VAL	A	25	1.231	4.916	8.170

ATOM	712	C	VAL	A	25	0.418	5.778	7.213
ATOM	713	O	VAL	A	25	0.871	6.841	6.774
ATOM	714	CB	VAL	A	25	1.062	5.531	9.577
ATOM	715	CG1	VAL	A	25	-0.341	5.253	10.115
ATOM	716	CG2	VAL	A	25	2.128	5.006	10.506
ATOM	717	N	LEU	A	26	-0.779	5.306	6.887
ATOM	718	CA	LEU	A	26	-1.706	6.048	6.040
ATOM	719	C	LEU	A	26	-2.862	6.358	6.992
ATOM	720	O	LEU	A	26	-3.679	5.497	7.297
ATOM	721	CB	LEU	A	26	-2.201	5.189	4.876
ATOM	722	CG	LEU	A	26	-3.204	5.898	3.952
ATOM	723	CD1	LEU	A	26	-2.519	7.077	3.262
ATOM	724	CD2	LEU	A	26	-3.755	4.925	2.929
ATOM	725	N	LYS	A	27	-2.910	7.584	7.489
ATOM	726	CA	LYS	A	27	-3.952	7.965	8.430
ATOM	727	C	LYS	A	27	-4.831	9.082	7.881
ATOM	728	O	LYS	A	27	-4.374	9.924	7.103
ATOM	729	CB	LYS	A	27	-3.305	8.409	9.738
ATOM	730	CG	LYS	A	27	-4.265	8.720	10.859
ATOM	731	CD	LYS	A	27	-3.509	9.382	11.994
ATOM	732	CE	LYS	A	27	-4.397	9.654	13.186
ATOM	733	NZ	LYS	A	27	-4.839	8.377	13.816
ATOM	734	N	ASN	A	28	-6.098	9.078	8.279
ATOM	735	CA	ASN	A	28	-7.045	10.095	7.843
ATOM	736	C	ASN	A	28	-7.147	11.103	8.979
ATOM	737	O	ASN	A	28	-7.815	10.842	9.969
ATOM	738	CB	ASN	A	28	-8.408	9.455	7.560
ATOM	739	CG	ASN	A	28	-9.518	10.485	7.364
ATOM	740	OD1	ASN	A	28	-9.360	11.444	6.597
ATOM	741	ND2	ASN	A	28	-10.653	10.288	8.050
ATOM	742	N	TYR	A	29	-6.473	12.241	8.837
ATOM	743	CA	TYR	A	29	-6.470	13.278	9.869
ATOM	744	C	TYR	A	29	-7.680	14.204	9.836
ATOM	745	O	TYR	A	29	-7.928	14.870	8.835
ATOM	746	CB	TYR	A	29	-5.197	14.130	9.768
ATOM	747	CG	TYR	A	29	-3.913	13.420	10.155
ATOM	748	CD1	TYR	A	29	-3.378	12.394	9.363
ATOM	749	CD2	TYR	A	29	-3.220	13.792	11.306
ATOM	750	CE1	TYR	A	29	-2.181	11.765	9.713
ATOM	751	CE2	TYR	A	29	-2.032	13.171	11.665
ATOM	752	CZ	TYR	A	29	-1.516	12.167	10.869
ATOM	753	OH	TYR	A	29	-0.319	11.603	11.231
ATOM	754	N	GLN	A	30	-8.408	14.254	10.950
ATOM	755	CA	GLN	A	30	-9.606	15.088	11.089
ATOM	756	C	GLN	A	30	-9.287	16.541	11.431
ATOM	757	O	GLN	A	30	-8.213	16.847	11.925
ATOM	758	CB	GLN	A	30	-10.500	14.541	12.202
ATOM	759	CG	GLN	A	30	-10.807	13.074	12.104
ATOM	760	CD	GLN	A	30	-11.744	12.749	10.969
ATOM	761	OE1	GLN	A	30	-11.900	11.582	10.602
ATOM	762	NE2	GLN	A	30	-12.385	13.773	10.405
ATOM	763	N	ASP	A	31	-10.238	17.430	11.173
ATOM	764	CA	ASP	A	31	-10.085	18.851	11.495
ATOM	765	C	ASP	A	31	-8.867	19.494	10.842
ATOM	766	O	ASP	A	31	-8.195	20.335	11.442
ATOM	767	CB	ASP	A	31	-10.000	19.025	13.019
ATOM	768	CG	ASP	A	31	-11.247	18.520	13.742
ATOM	769	OD1	ASP	A	31	-12.349	18.587	13.155
ATOM	770	OD2	ASP	A	31	-11.130	18.069	14.908
ATOM	771	N	MET	A	32	-8.582	19.113	9.606

ATOM	772	CA	MET	A	32	-7.426	19.662	8.918
ATOM	773	C	MET	A	32	-7.780	20.808	7.987
ATOM	774	O	MET	A	32	-7.021	21.768	7.855
ATOM	775	CB	MET	A	32	-6.741	18.559	8.125
ATOM	776	CG	MET	A	32	-6.037	17.540	8.980
ATOM	777	SD	MET	A	32	-4.559	18.231	9.714
ATOM	778	CE	MET	A	32	-3.406	18.041	8.318
ATOM	779	N	VAL	A	33	-8.942	20.707	7.351
ATOM	780	CA	VAL	A	33	-9.381	21.719	6.401
ATOM	781	C	VAL	A	33	-10.579	22.536	6.858
ATOM	782	O	VAL	A	33	-11.586	21.988	7.292
ATOM	783	CB	VAL	A	33	-9.701	21.056	5.027
ATOM	784	CG1	VAL	A	33	-10.388	22.040	4.087
ATOM	785	CG2	VAL	A	33	-8.423	20.561	4.412
ATOM	786	N	VAL	A	34	-10.465	23.855	6.739
ATOM	787	CA	VAL	A	34	-11.553	24.745	7.113
ATOM	788	C	VAL	A	34	-12.610	24.835	6.016
ATOM	789	O	VAL	A	34	-12.373	25.403	4.950
ATOM	790	CB	VAL	A	34	-11.057	26.176	7.407
ATOM	791	CG1	VAL	A	34	-12.240	27.097	7.601
ATOM	792	CG2	VAL	A	34	-10.222	26.186	8.655
ATOM	793	N	GLU	A	35	-13.779	24.266	6.282
ATOM	794	CA	GLU	A	35	-14.870	24.311	5.321
ATOM	795	C	GLU	A	35	-15.702	25.565	5.572
ATOM	796	O	GLU	A	35	-16.011	26.303	4.645
ATOM	797	CB	GLU	A	35	-15.733	23.054	5.447
ATOM	798	CG	GLU	A	35	-14.969	21.782	5.128
ATOM	799	CD	GLU	A	35	-14.515	21.732	3.676
ATOM	800	OE1	GLU	A	35	-15.036	22.519	2.858
ATOM	801	OE2	GLU	A	35	-13.643	20.902	3.344
ATOM	802	N	GLY	A	36	-16.053	25.811	6.829
ATOM	803	CA	GLY	A	36	-16.834	26.990	7.152
ATOM	804	C	GLY	A	36	-16.322	27.785	8.341
ATOM	805	O	GLY	A	36	-15.671	27.249	9.237
ATOM	806	N	CYS	A	37	-16.616	29.077	8.360
ATOM	807	CA	CYS	A	37	-16.177	29.917	9.466
ATOM	808	C	CYS	A	37	-17.347	30.502	10.249
ATOM	809	O	CYS	A	37	-18.467	30.628	9.741
ATOM	810	CB	CYS	A	37	-15.301	31.058	8.967
ATOM	811	SG	CYS	A	37	-13.785	30.558	8.098
ATOM	812	N	GLY	A	38	-17.079	30.867	11.494
ATOM	813	CA	GLY	A	38	-18.129	31.430	12.309
ATOM	814	C	GLY	A	38	-17.622	32.176	13.518
ATOM	815	O	GLY	A	38	-16.425	32.235	13.791
ATOM	816	N	CYS	A	39	-18.564	32.753	14.245
ATOM	817	CA	CYS	A	39	-18.253	33.505	15.439
ATOM	818	C	CYS	A	39	-18.543	32.670	16.665
ATOM	819	O	CYS	A	39	-19.620	32.084	16.794
ATOM	820	CB	CYS	A	39	-19.068	34.779	15.442
ATOM	821	SG	CYS	A	39	-18.539	35.799	14.053

102. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 97, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, wherein said peptidomimetic has a molecular weight comprised between 2,000 and 8,000 Daltons.

103. A pharmaceutical association for a use according to any one of claims 1, 2 and 4 to 97, wherein

said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, wherein said peptidomimetic has a molecular weight comprised between 2,000 and 6,000 Da.

104. A pharmaceutical association for a use according to claim 102 or 103, wherein the RMSD value of the atomic structure coordinates of said peptidomimetic with respect to PEPREF is 2.45Å (Angstroms) or less.

105. A pharmaceutical association for a use according to any one of claims 102 to 104, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, comprising between 20 and 50 amino acids.

106. A pharmaceutical association for a use according to any one of claims 102 to 104, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, comprising between 20 and 45 amino acids.

107. A pharmaceutical association for a use according to any one of claims 102 to 104, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, comprising between 23 and 60 amino acids.

108. A pharmaceutical association for a use according to any one of claims 102 to 104, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, comprising between 23 and 50 amino acids.

109. A pharmaceutical association for a use according to any one of claims 102 to 104, wherein said growth factor receptor-binding compound is a peptidomimetic having growth factor receptor-binding capability, comprising between 23 and 45 amino acids.

110. A pharmaceutical association for a use according to any one of claims 102 to 109, wherein said growth factor receptor-binding compound is a peptidomimetic comprising at least one peptide fragment with between 5-20 amino acids.

111. A pharmaceutical association for a use according to any one of claims 102 to 109, wherein said growth factor receptor-binding compound is a peptidomimetic comprising at least two peptide fragments, each of which with between 5-20 amino acids.

112. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, with between 15 and 60 amino acids, having a growth factor receptor-binding capability.

113. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, with

between 15 and 55 amino acids.

114. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, with between 19 and 60 amino acids.

115. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, with between 19 and 55 amino acids.

116. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising between 15 and 60 amino acids, having a growth factor receptor-binding capability.

117. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising between 15 and 55 amino acids.

118. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising between 19 and 60 amino acids.

119. A pharmaceutical association for a use according to any one of claims 1 and 3 to 97, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising between 19 and 55 amino acids.

120. A pharmaceutical association for a use according to any one of claims 116 to 119, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising at least one peptide fragment with between 5-20 amino acids.

121. A pharmaceutical association for a use according to any one of claims 116 to 119, wherein said growth factor receptor-binding compound is a cyclic peptidomimetic comprising at least two peptide fragments, each of which with between 5-20 amino acids.

122. A pharmaceutical association for a use according to any one of claims 1, 3 to 97 and 112 to 121, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, or a cyclic peptidomimetic, having a molecular weight of less than 6,000 Da.

123. A pharmaceutical association for a use according to any one of claims 1, 3 to 97 and 112 to 121, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, or a cyclic peptidomimetic, having a molecular weight comprised between 1,500 and 7,000 Da.

124. A pharmaceutical association for a use according to any one of claims 1, 3 to 97 and 112 to 121, wherein said growth factor receptor-binding compound is a cyclic peptide, or a variant or analog thereof, or a cyclic peptidomimetic, having a molecular weight comprised between 1,500 and 6,000 Da.

125. A pharmaceutical association for a use according to any one of claims 1 to 124, wherein said growth factor receptor-binding compound is selected from the group consisting of any one of peptides of SEQ ID NO: 1 to 100330.

126. A pharmaceutical association for a use according to any one of claims 1 to 125, wherein said association is administered locally.

127. A medical composition comprising at least one pharmaceutical association according to any one of claims 1 to 126 and at least one medically acceptable excipient, carrier or vehicle for use in the treatment, prevention and/or diagnostic of a neoplastic disease.

128. A medical composition according to claim 127, further comprising at least one other anti-cancer agent.

129. A screening method for selecting a growth factor receptor-binding compound having the ability, after being associated with a bioactive carrier, to convert a neoplastic cell into a non-neoplastic cell.

130. A screening method according to claim 129, wherein said method comprises providing a molecular model of the 3D structure coordinates of PEPREF and identifying a candidate analog having a RMSD value of 2.45Å or less.

131. A method of producing a growth factor receptor-binding compound having the ability, after being associated with a bioactive carrier, to convert a neoplastic cell into a non-neoplastic cell, the method comprising (a) providing a molecular model of the 3D structure coordinates of PEPREF; (b) identifying a candidate analog having a RMSD of 2.45Å or less; and (c) producing said candidate analog identified in step (b).

132. A method of producing a growth factor receptor-binding compound according to claim 131, wherein said method further comprising determining whether the compound produced in step (c) has a neoplastic cell recoding activity.

133. A method of producing a growth factor receptor-binding compound according to claim 131 or 132, wherein steps (a) and (b) are performed by means of an electronic processor.

134. A method of producing a growth factor receptor-binding compound according to any one of claims 131 to 133, wherein step (a) comprises storing a representation of the atomic coordinates of

PEPREF in a computer memory.

135. A process for manufacturing a neoplastic disease medicament, said process comprising providing a bioactive carrier and a growth factor receptor-binding compound both as defined in any one of claims 1 to 125, wherein providing said bioactive carrier and said growth factor receptor-binding compound manufactures said neoplastic disease medicament.

136. A process for manufacturing a neoplastic disease medicament precursor, said process comprising providing a growth factor receptor-binding compound or a bioactive carrier both as defined in any one of claims 1 to 125, wherein providing said bioactive carrier or said growth factor receptor-binding compound manufactures said neoplastic disease medicament precursor.

137. A method for converting a neoplastic cell into a non-neoplastic cell, in-vitro or ex-vivo, said method comprising administering to a neoplastic cell an effective amount of a pharmaceutical association or composition as defined in any one of claims 1 to 128.

138. Kit-of-parts comprising at least one bioactive carrier and at least one growth factor receptor-binding compound both as defined in any one of claims 1 to 125 for use in the treatment, prevention and/or diagnostic of a neoplastic disease.

139. Use of a pharmaceutical association as defined in any one of claims 1 to 126 for the preparation of a medical composition for the treatment or prevention of a neoplastic disease, in particular, cancer.

FIGURE 1

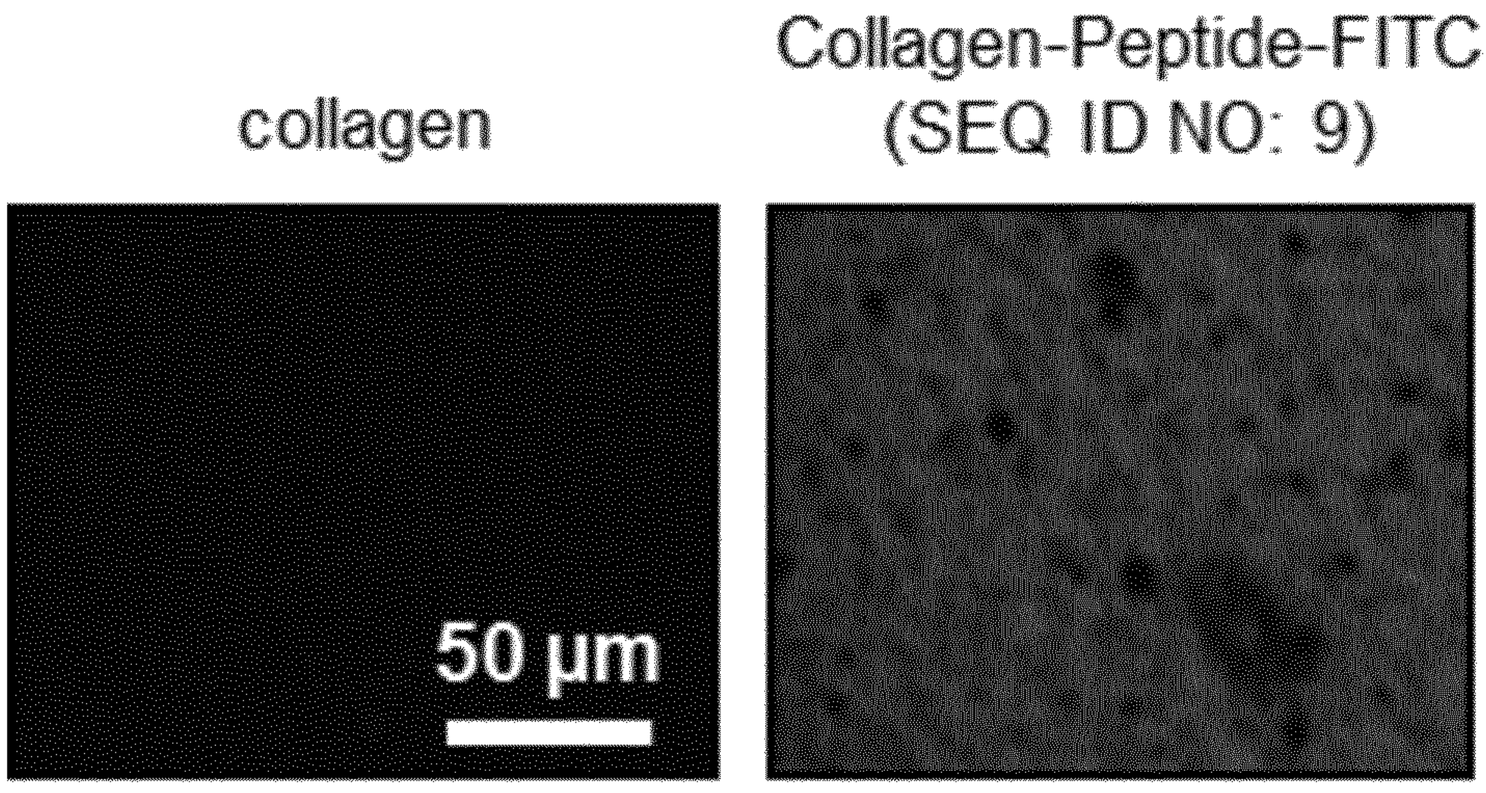

collagen
Collagen-Peptide-FITC
(SEQ ID NO: 9)
50 µm
apatite
apatite-Peptide-FITC
(SEQ ID NO: 10)
50 µm

FIGURE 2

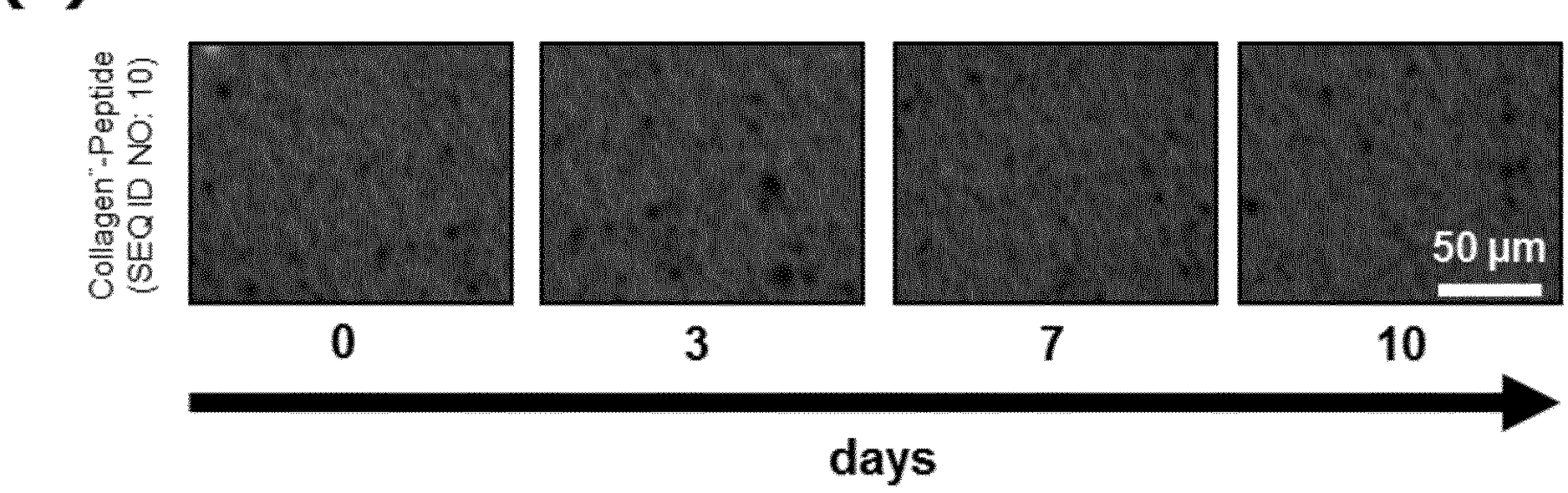

(a)
Collagen"-Peptide (SEQ ID NO: 10)
50 µm
0
3
7
10
days
(b)
Peptide-FITC apatite fluoresence intensity (a.u.)
40
35
30
25
20
15
10
5
0
1
3
7
10
Days

FIGURE 3

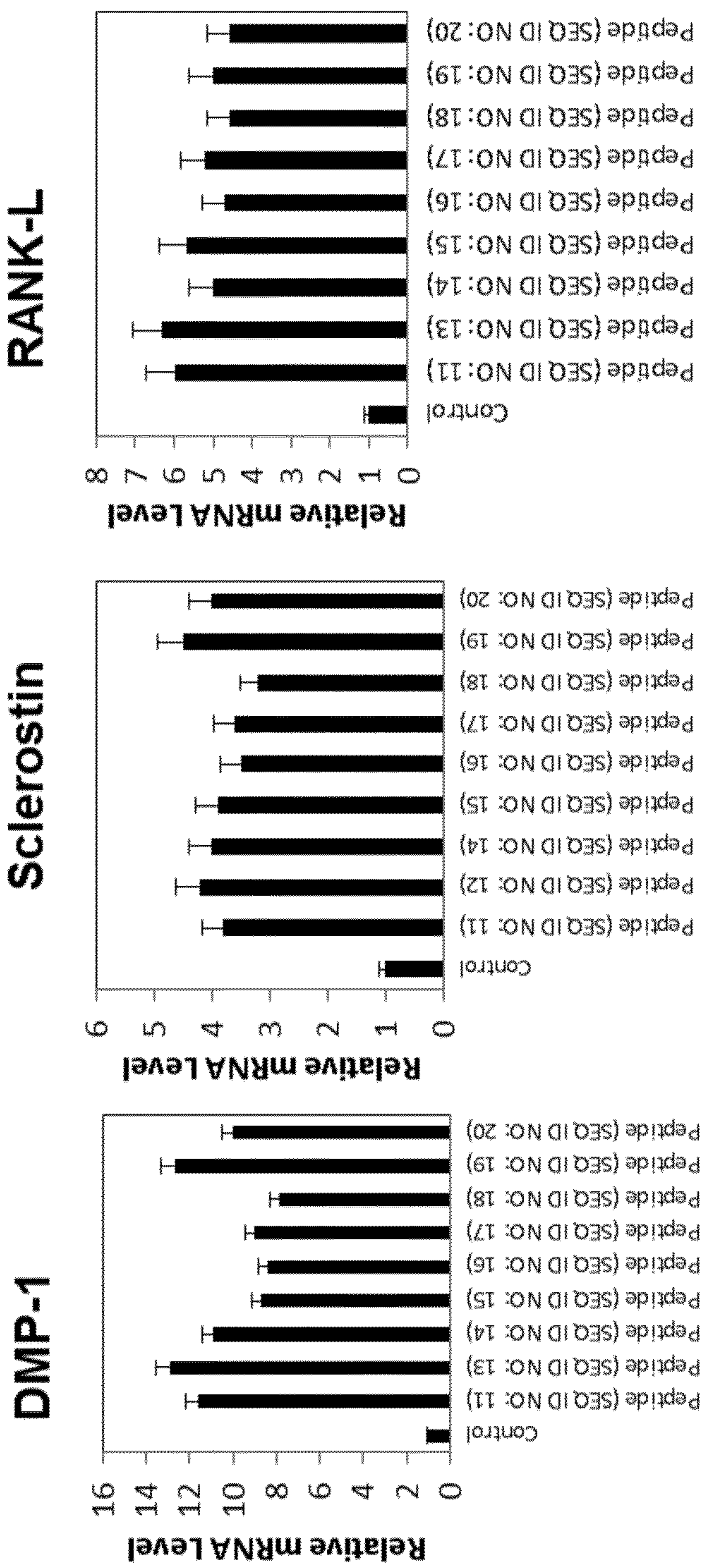

RANK-L
Relative mRNA Level
0
1
2
3
4
5
6
7
8
Control
Peptide (SEQ ID NO: 11)
Peptide (SEQ ID NO: 13)
Peptide (SEQ ID NO: 14)
Peptide (SEQ ID NO: 15)
Peptide (SEQ ID NO: 16)
Peptide (SEQ ID NO: 17)
Peptide (SEQ ID NO: 18)
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 20)
Sclerostin
Relative mRNA Level
0
1
2
3
4
5
6
Control
Peptide (SEQ ID NO: 11)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 14)
Peptide (SEQ ID NO: 15)
Peptide (SEQ ID NO: 16)
Peptide (SEQ ID NO: 17)
Peptide (SEQ ID NO: 18)
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 20)
DMP-1
Relative mRNA Level
0
2
4
6
8
10
12
14
16
Control
Peptide (SEQ ID NO: 11)
Peptide (SEQ ID NO: 13)
Peptide (SEQ ID NO: 14)
Peptide (SEQ ID NO: 15)
Peptide (SEQ ID NO: 16)
Peptide (SEQ ID NO: 17)
Peptide (SEQ ID NO: 18)
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 20)

FIGURE 4

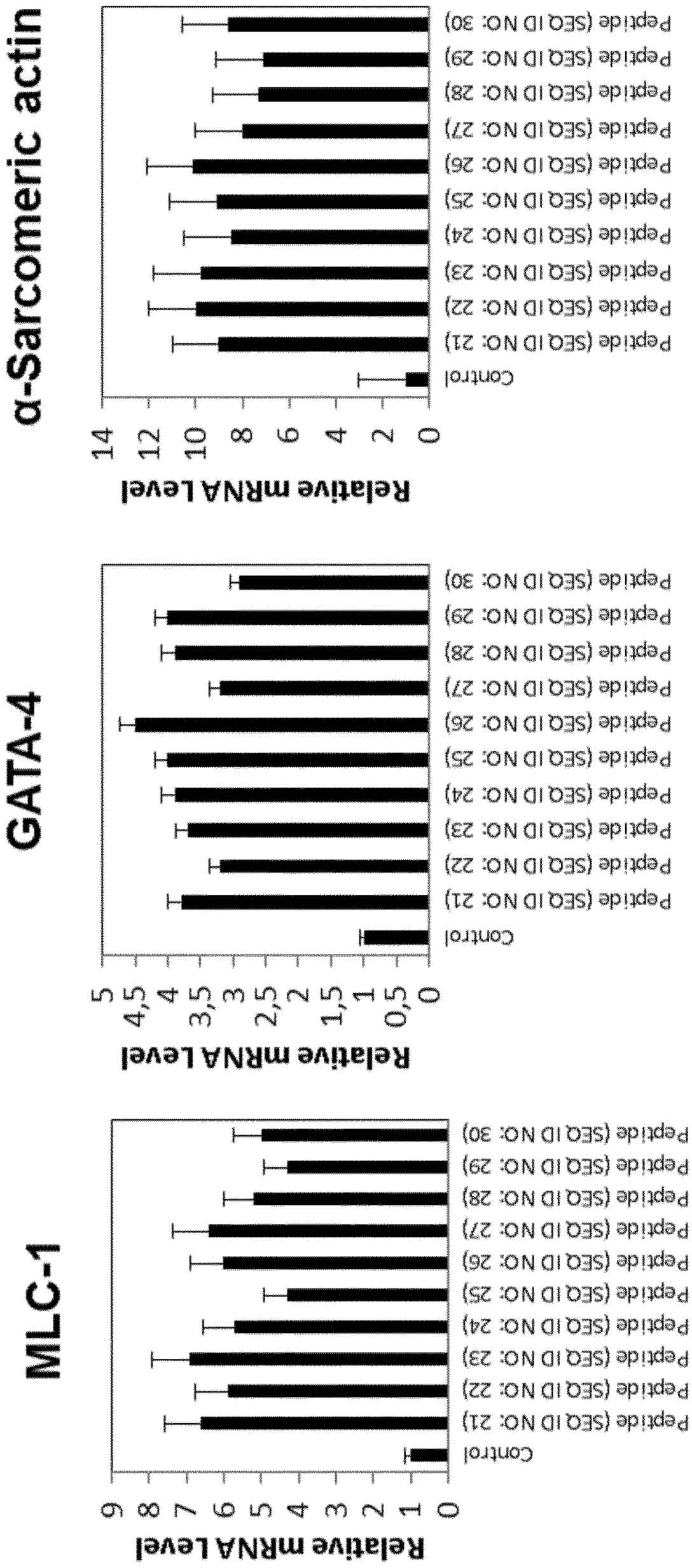

α-Sarcomeric actin
Relative mRNA Level
0
2
4
6
8
10
12
14
Control
Peptide (SEQ ID NO: 21)
Peptide (SEQ ID NO: 22)
Peptide (SEQ ID NO: 23)
Peptide (SEQ ID NO: 24)
Peptide (SEQ ID NO: 25)
Peptide (SEQ ID NO: 26)
Peptide (SEQ ID NO: 27)
Peptide (SEQ ID NO: 28)
Peptide (SEQ ID NO: 29)
Peptide (SEQ ID NO: 30)
GATA-4
Relative mRNA Level
0
0,5
1
1,5
2
2,5
3
3,5
4
4,5
5
Control
Peptide (SEQ ID NO: 21)
Peptide (SEQ ID NO: 22)
Peptide (SEQ ID NO: 23)
Peptide (SEQ ID NO: 24)
Peptide (SEQ ID NO: 25)
Peptide (SEQ ID NO: 26)
Peptide (SEQ ID NO: 27)
Peptide (SEQ ID NO: 28)
Peptide (SEQ ID NO: 29)
Peptide (SEQ ID NO: 30)
MLC-1
Relative mRNA Level
0
1
2
3
4
5
6
7
8
9

FIGURE 5

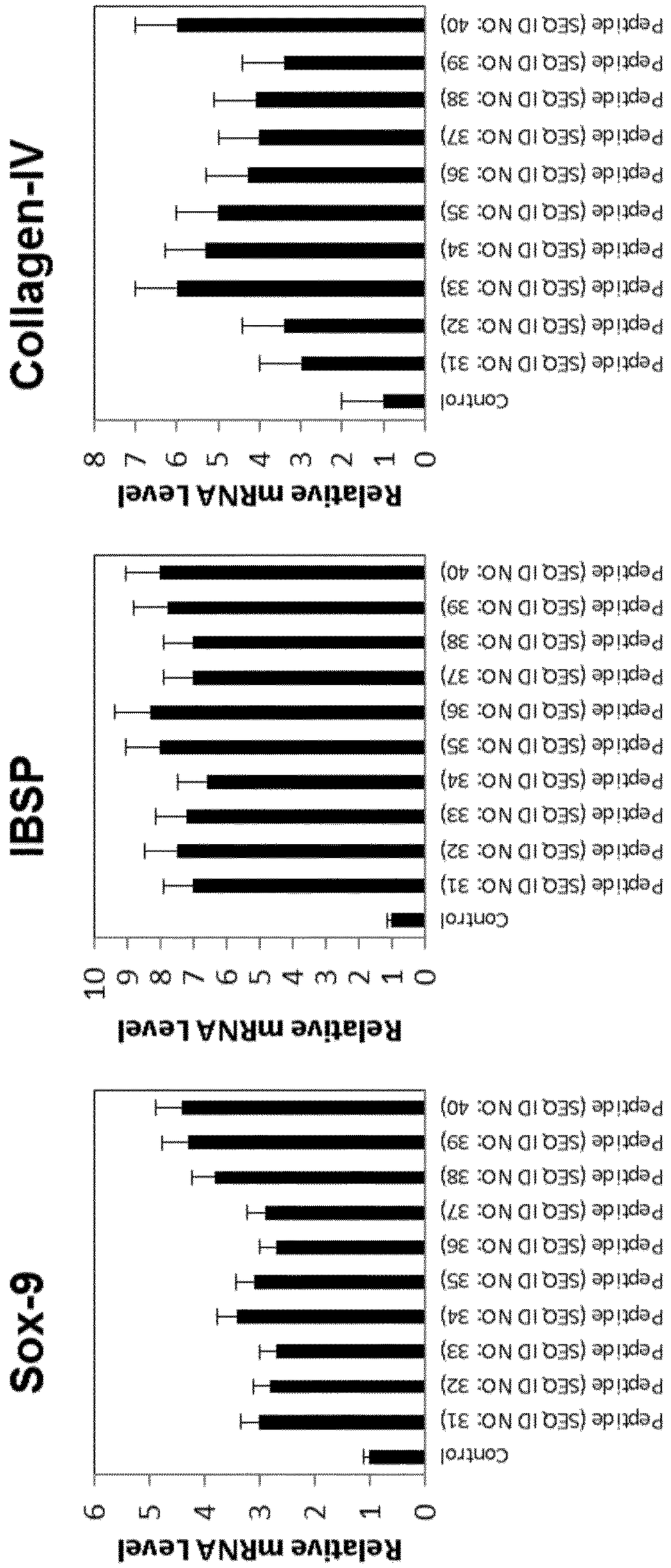

Collagen-IV
Relative mRNA Level
0 1 2 3 4 5 6 7 8
Control
Peptide (SEQ ID NO: 31)
Peptide (SEQ ID NO: 32)
Peptide (SEQ ID NO: 33)
Peptide (SEQ ID NO: 34)
Peptide (SEQ ID NO: 35)
Peptide (SEQ ID NO: 36)
Peptide (SEQ ID NO: 37)
Peptide (SEQ ID NO: 38)
Peptide (SEQ ID NO: 39)
Peptide (SEQ ID NO: 40)
IBSP
Relative mRNA Level
0 1 2 3 4 5 6 7 8 9 10
Control
Peptide (SEQ ID NO: 31)
Peptide (SEQ ID NO: 32)
Peptide (SEQ ID NO: 33)
Peptide (SEQ ID NO: 34)
Peptide (SEQ ID NO: 35)
Peptide (SEQ ID NO: 36)
Peptide (SEQ ID NO: 37)
Peptide (SEQ ID NO: 38)
Peptide (SEQ ID NO: 39)
Peptide (SEQ ID NO: 40)
Sox-9
Relative mRNA Level
0 1 2 3 4 5 6
Control
Peptide (SEQ ID NO: 31)
Peptide (SEQ ID NO: 32)
Peptide (SEQ ID NO: 33)
Peptide (SEQ ID NO: 34)
Peptide (SEQ ID NO: 35)
Peptide (SEQ ID NO: 36)
Peptide (SEQ ID NO: 37)
Peptide (SEQ ID NO: 38)
Peptide (SEQ ID NO: 39)
Peptide (SEQ ID NO: 40)

FIGURE 6

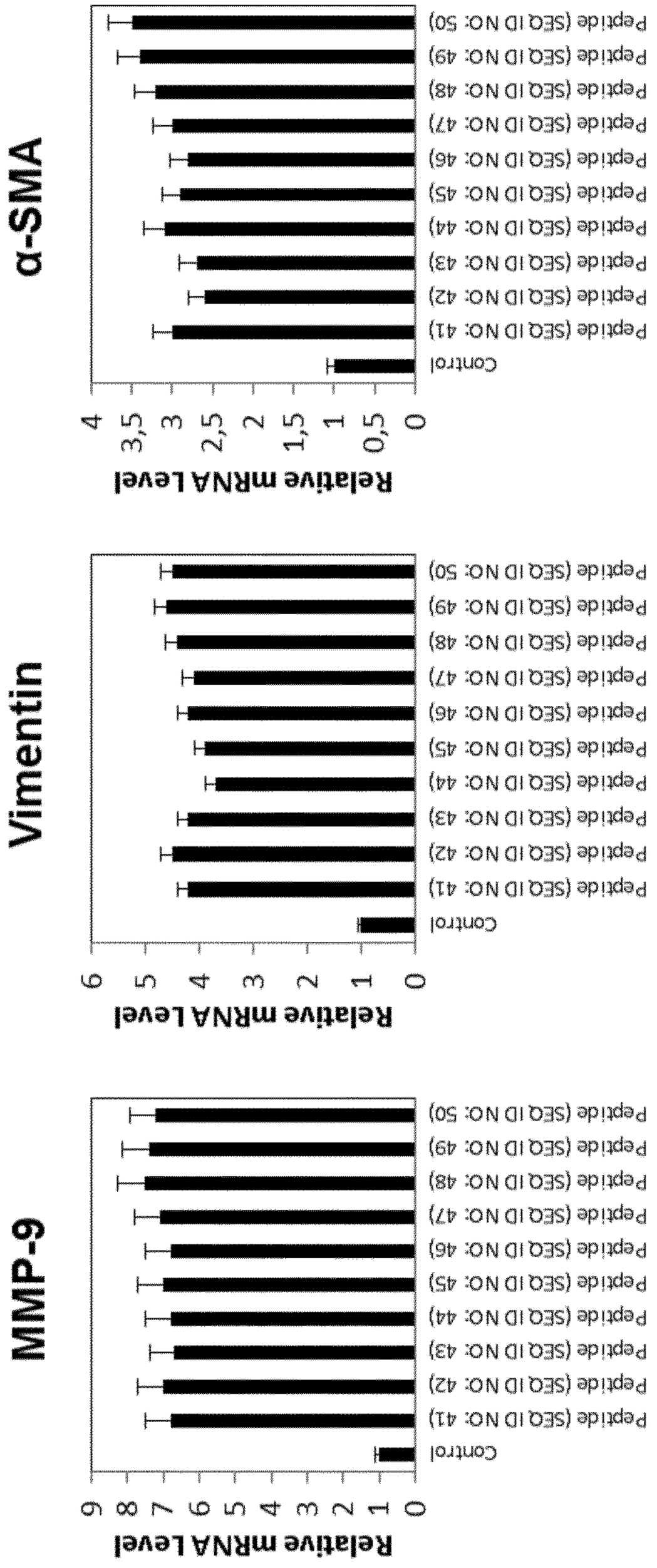

α-SMA
Relative mRNA Level
0
0,5
1
1,5
2
2,5
3
3,5
4
Control
Peptide (SEQ ID NO: 41)
Peptide (SEQ ID NO: 42)
Peptide (SEQ ID NO: 43)
Peptide (SEQ ID NO: 44)
Peptide (SEQ ID NO: 45)
Peptide (SEQ ID NO: 46)
Peptide (SEQ ID NO: 47)
Peptide (SEQ ID NO: 48)
Peptide (SEQ ID NO: 49)
Peptide (SEQ ID NO: 50)
Vimentin
Relative mRNA Level
0
1
2
3
4
5
6
Control
Peptide (SEQ ID NO: 41)
Peptide (SEQ ID NO: 42)
Peptide (SEQ ID NO: 43)
Peptide (SEQ ID NO: 44)
Peptide (SEQ ID NO: 45)
Peptide (SEQ ID NO: 46)
Peptide (SEQ ID NO: 47)
Peptide (SEQ ID NO: 48)
Peptide (SEQ ID NO: 49)
Peptide (SEQ ID NO: 50)
MMP-9
Relative mRNA Level
0
1
2
3
4
5
6
7
8
9
Control
Peptide (SEQ ID NO: 41)
Peptide (SEQ ID NO: 42)
Peptide (SEQ ID NO: 43)
Peptide (SEQ ID NO: 44)
Peptide (SEQ ID NO: 45)
Peptide (SEQ ID NO: 46)
Peptide (SEQ ID NO: 47)
Peptide (SEQ ID NO: 48)
Peptide (SEQ ID NO: 49)
Peptide (SEQ ID NO: 50)

FIGURE 7

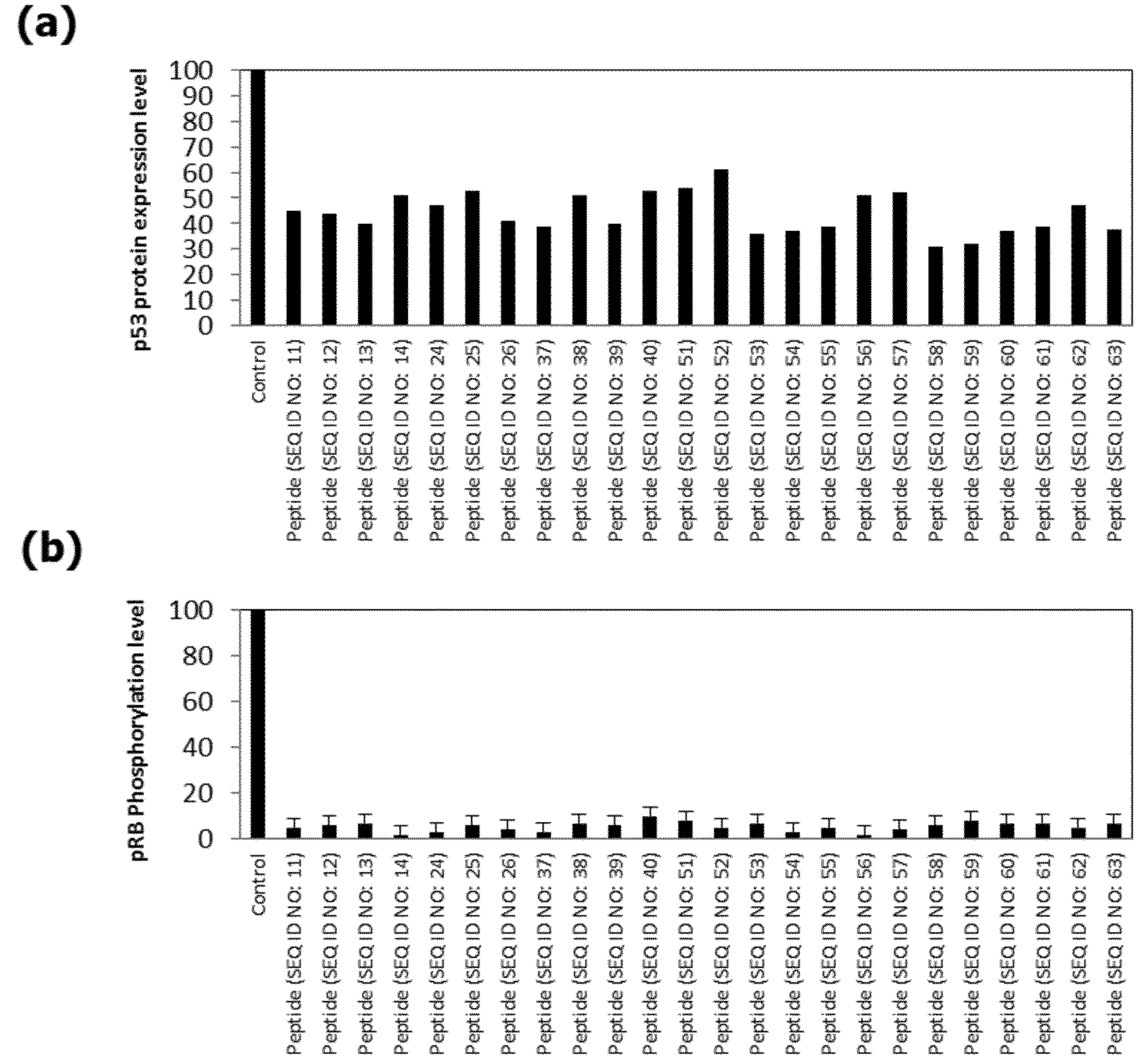

(a)
p53 protein expression level
100
90
80
70
60
50
40
30
20
10
0
Control
Peptide (SEQ ID NO: 11)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 13)
Peptide (SEQ ID NO: 14)
Peptide (SEQ ID NO: 24)
Peptide (SEQ ID NO: 25)
Peptide (SEQ ID NO: 26)
Peptide (SEQ ID NO: 37)
Peptide (SEQ ID NO: 38)
Peptide (SEQ ID NO: 39)
Peptide (SEQ ID NO: 40)
Peptide (SEQ ID NO: 51)
Peptide (SEQ ID NO: 52)
Peptide (SEQ ID NO: 53)
Peptide (SEQ ID NO: 54)
Peptide (SEQ ID NO: 55)
Peptide (SEQ ID NO: 56)
Peptide (SEQ ID NO: 57)
Peptide (SEQ ID NO: 58)
Peptide (SEQ ID NO: 59)
Peptide (SEQ ID NO: 60)
Peptide (SEQ ID NO: 61)
Peptide (SEQ ID NO: 62)
Peptide (SEQ ID NO: 63)
(b)
pRB Phosphorylation level
100
80
60
40
20
0
Control
Peptide (SEQ ID NO: 11)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 13)
Peptide (SEQ ID NO: 14)
Peptide (SEQ ID NO: 24)
Peptide (SEQ ID NO: 25)
Peptide (SEQ ID NO: 26)
Peptide (SEQ ID NO: 37)
Peptide (SEQ ID NO: 38)
Peptide (SEQ ID NO: 39)
Peptide (SEQ ID NO: 40)
Peptide (SEQ ID NO: 51)
Peptide (SEQ ID NO: 52)
Peptide (SEQ ID NO: 53)
Peptide (SEQ ID NO: 54)
Peptide (SEQ ID NO: 55)
Peptide (SEQ ID NO: 56)
Peptide (SEQ ID NO: 57)
Peptide (SEQ ID NO: 58)
Peptide (SEQ ID NO: 59)
Peptide (SEQ ID NO: 60)
Peptide (SEQ ID NO: 61)
Peptide (SEQ ID NO: 62)
Peptide (SEQ ID NO: 63)

FIGURE 8

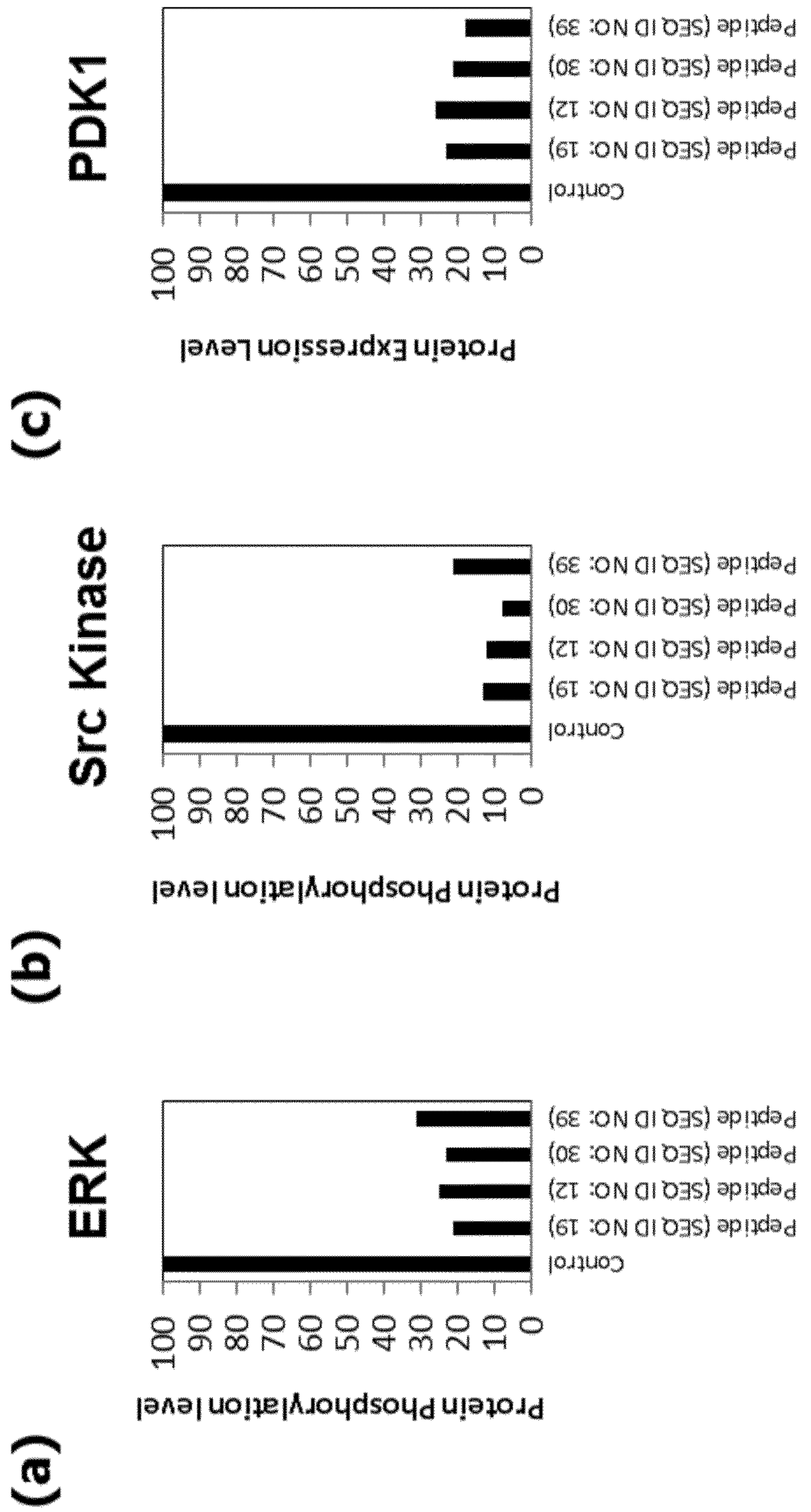
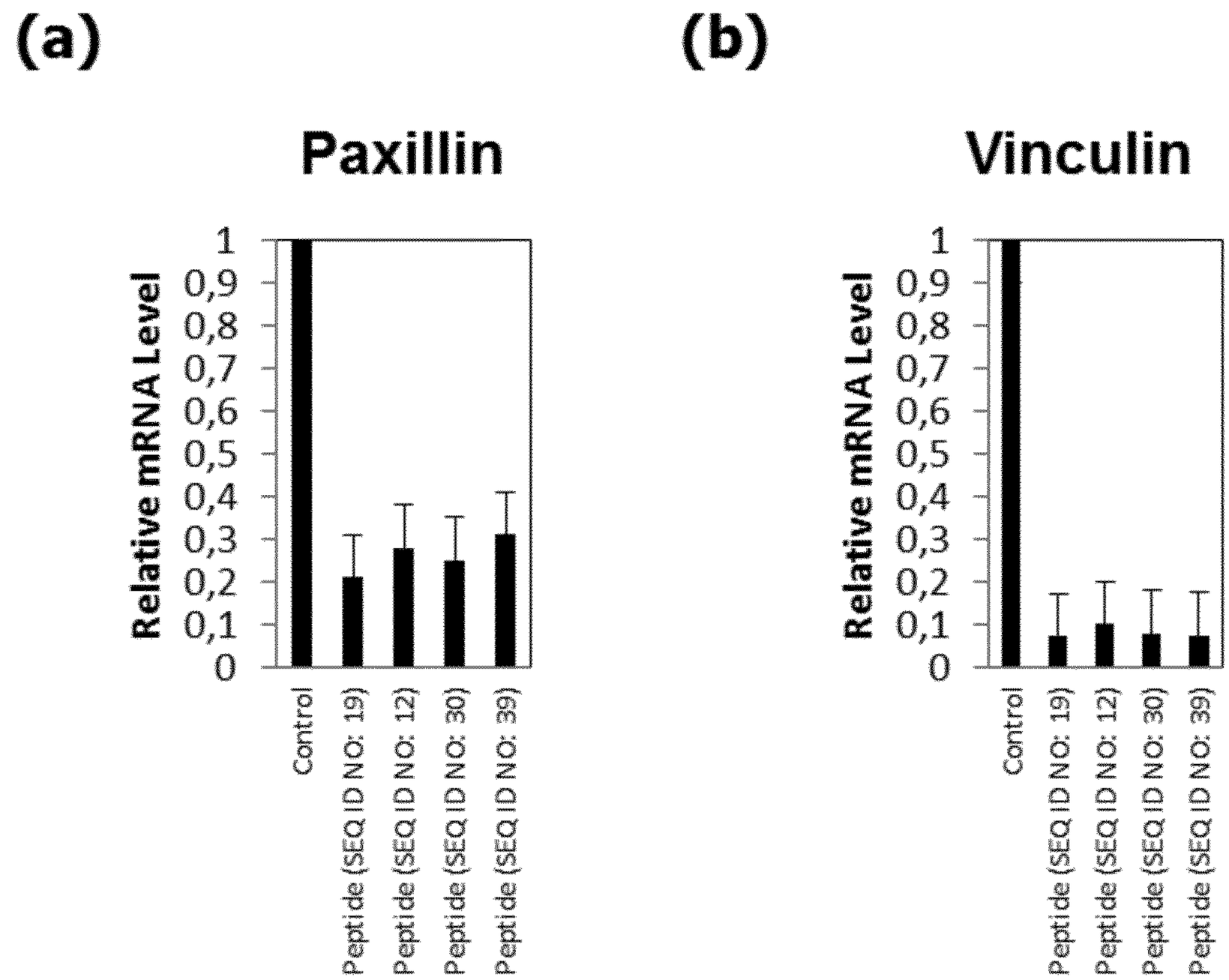

(a)
Protein Phosphorylation level
ERK
100
90
80
70
60
50
40
30
20
10
0
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)
(b)
Protein Phosphorylation level
Src Kinase
100
90
80
70
60
50
40
30
20
10
0
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)
(c)
Protein Expression Level
PDK1
100
90
80
70
60
50
40
30
20
10
0
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)

FIGURE 9


(a)
Paxillin
Relative mRNA Level
1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)
(b)
Vinculin
Relative mRNA Level
1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)

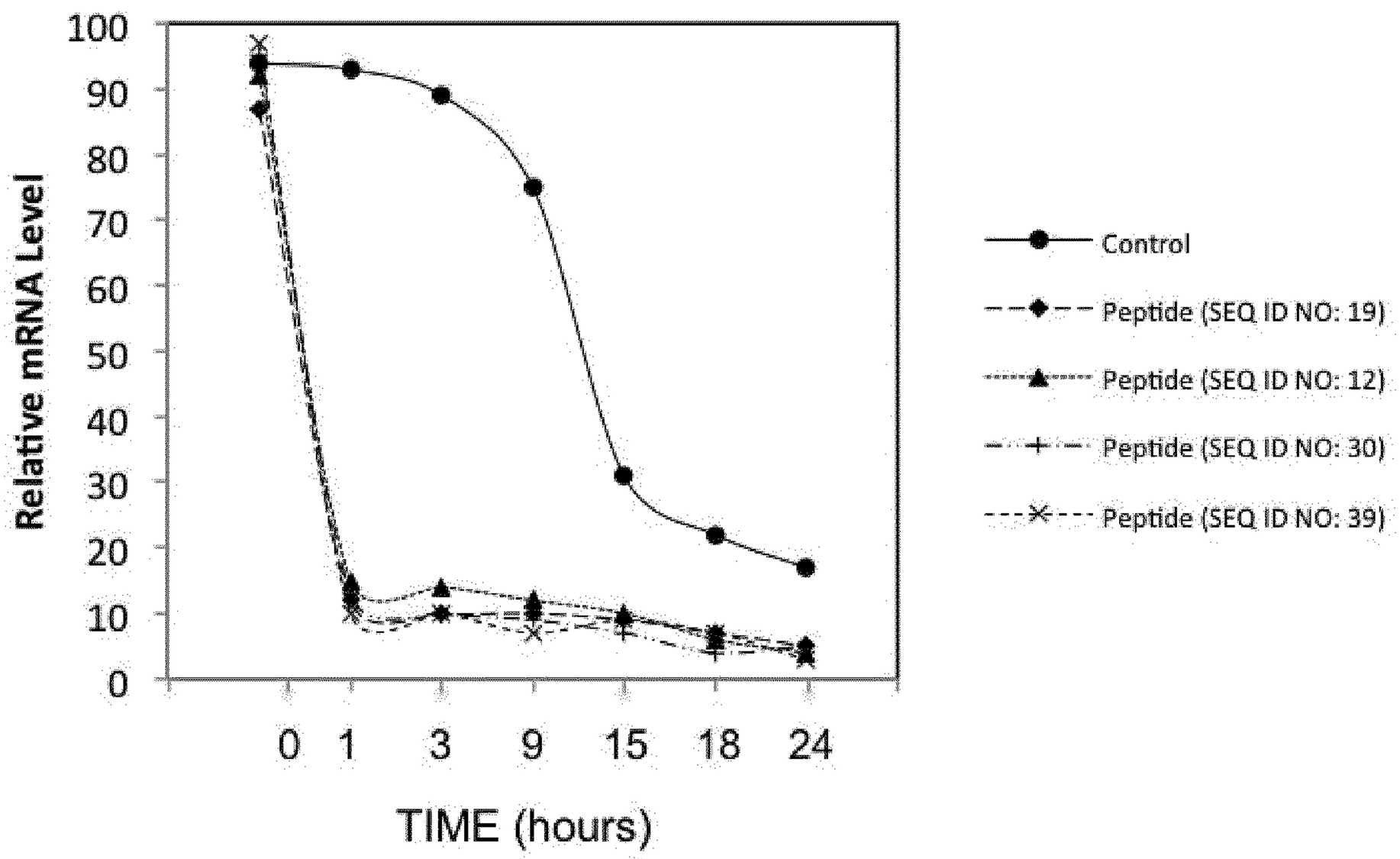
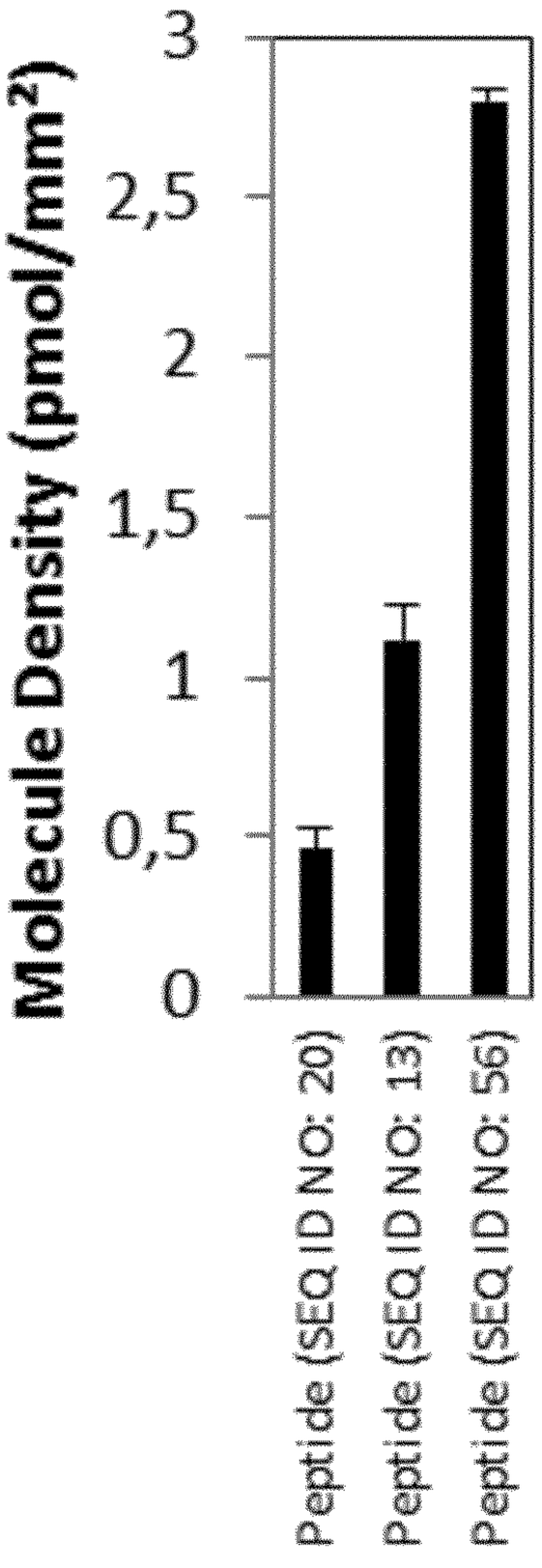

100
90
80
70
60
50
40
30
20
10
0
Relative mRNA Level
0
1
3
9
15
18
24
TIME (hours)
Control
Peptide (SEQ ID NO: 19)
Peptide (SEQ ID NO: 12)
Peptide (SEQ ID NO: 30)
Peptide (SEQ ID NO: 39)

FIG.10

FIGURE 11


Molecule Density (pmol/mm²)
3
2,5
2
1,5
1
0,5
0
Peptide (SEQ ID NO: 20)
Peptide (SEQ ID NO: 13)
Peptide (SEQ ID NO: 56)

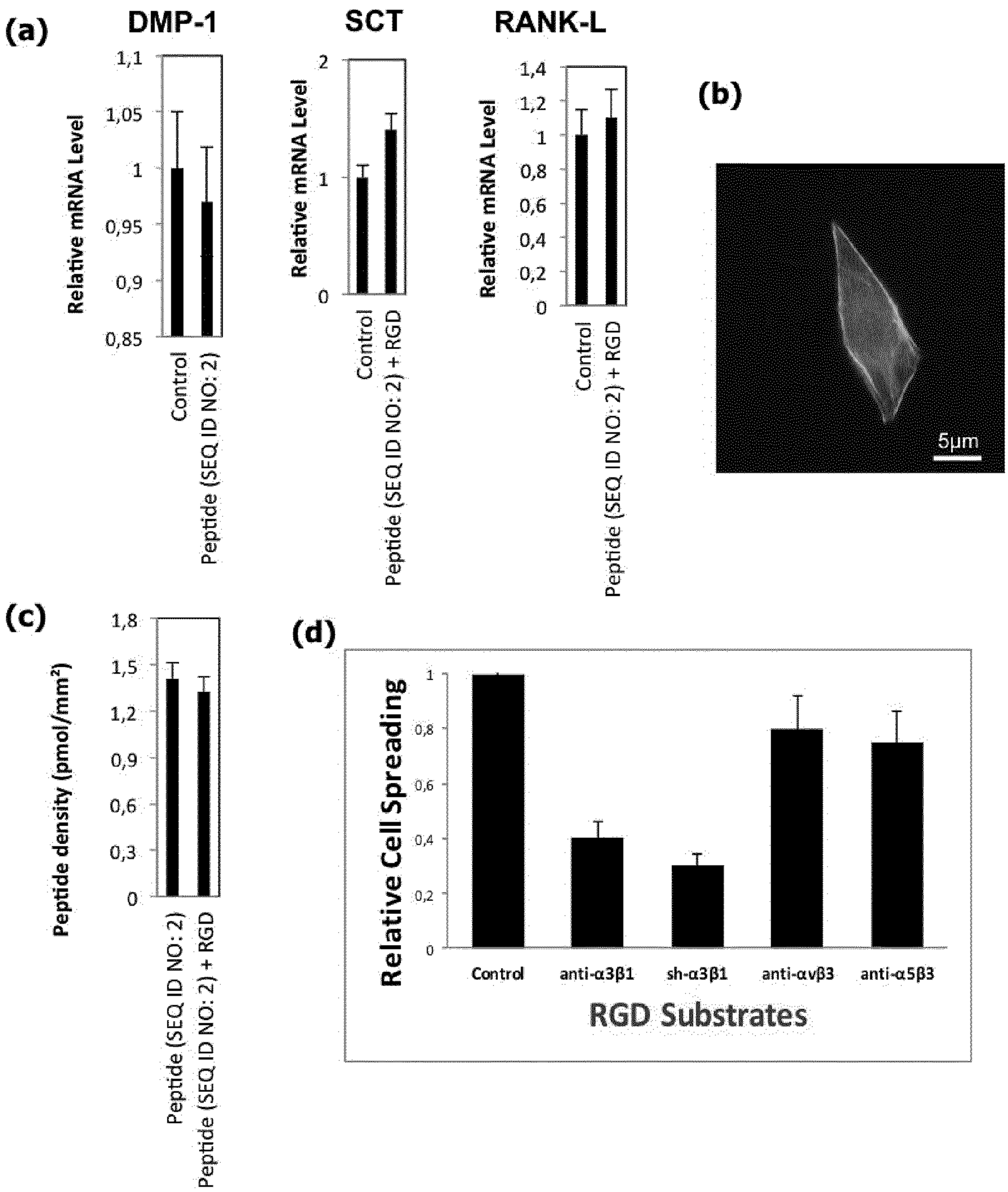
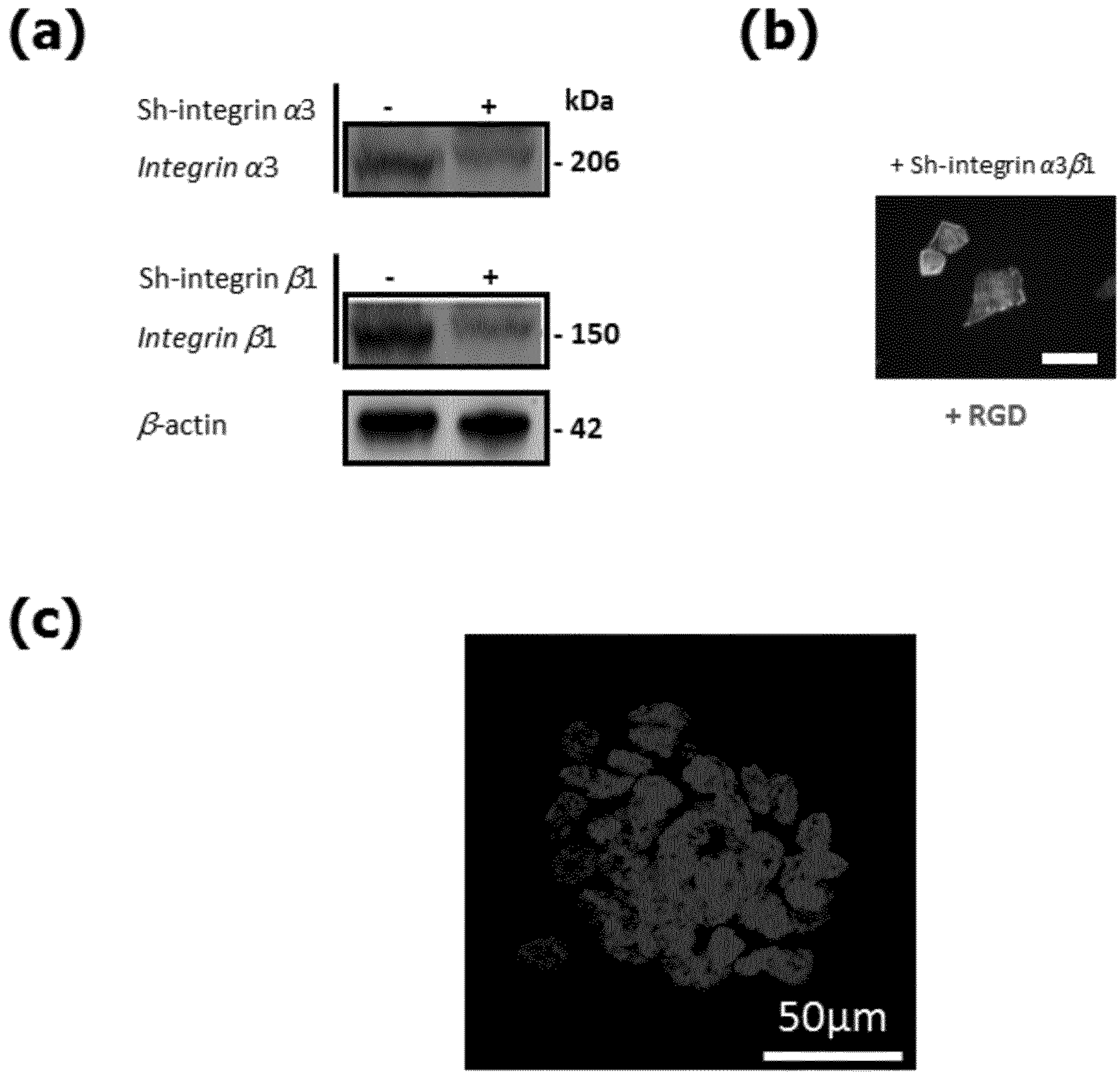

(a)
DMP-1
SCT
RANK-L
Relative mRNA Level
1,1
1,05
1
0,95
0,9
0,85
2
1
0
1,4
1,2
1
0,8
0,6
0,4
0,2
0
Control
Peptide (SEQ ID NO: 2)
Peptide (SEQ ID NO: 2) + RGD
(b)
5µm
(c)
Peptide density (pmol/mm²)
1,8
1,5
1,2
0,9
0,6
0,3
0
(d)
Relative Cell Spreading
1
0,8
0,6
0,4
0,2
0
Control
anti-α3β1
sh-α3β1
anti-αvβ3
anti-α5β3
RGD Substrates

FIG.12

FIGURE 13


(a)
Sh-integrin α3
Integrin α3
-
+
kDa
- 206
Sh-integrin β1
Integrin β1
- 150
β-actin
- 42
(b)
+ Sh-integrin α3β1
+ RGD
(c)
50µm

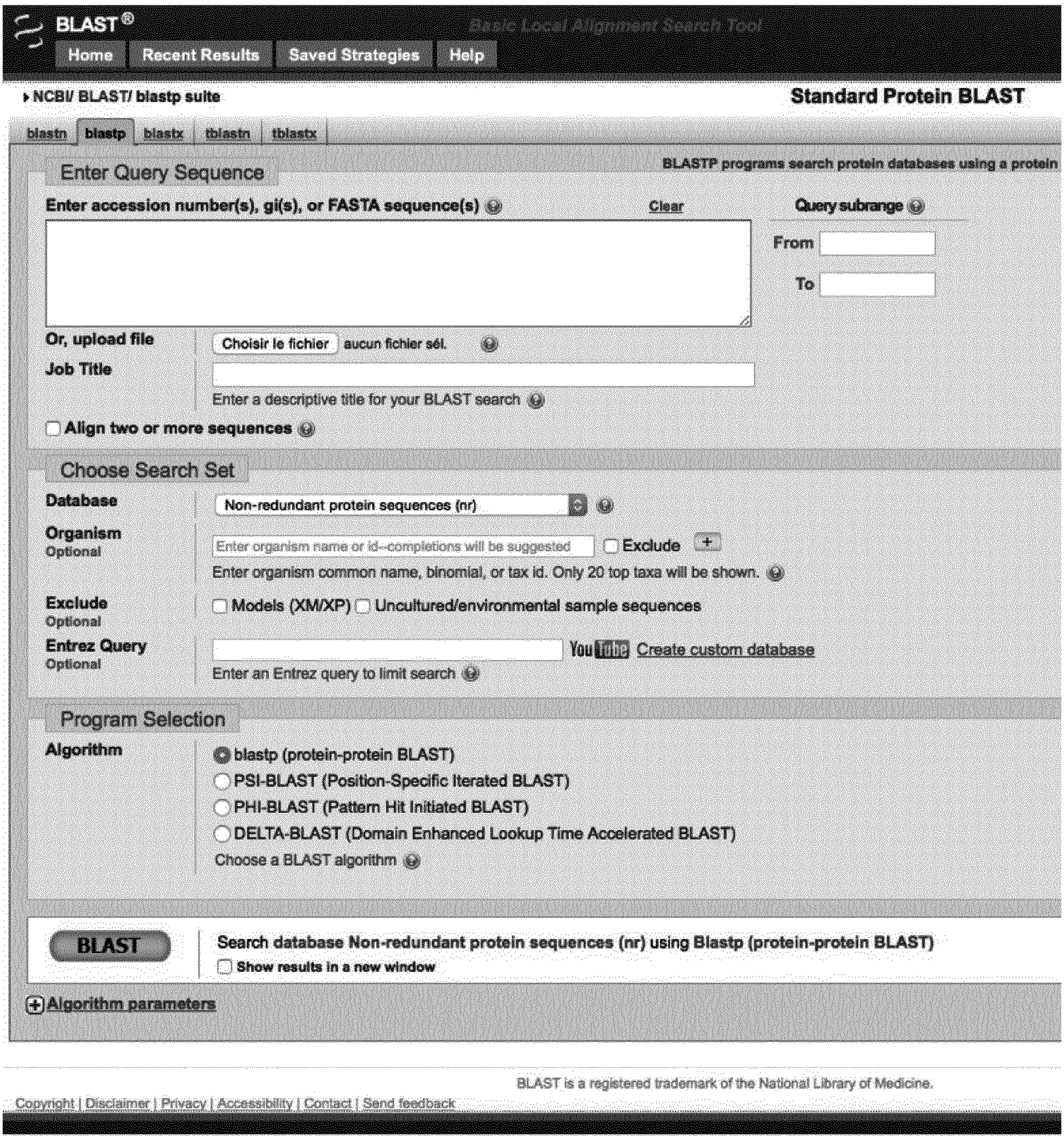
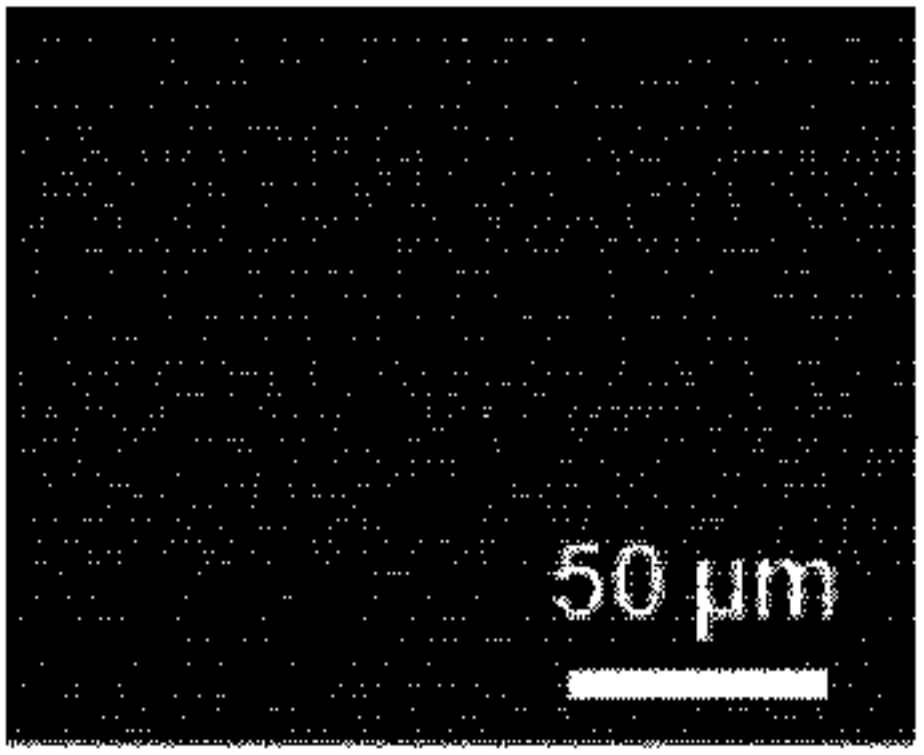

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Query subrange
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Or, upload file
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aucun fichier sél.
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Align two or more sequences
Choose Search Set
Database
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Exclude
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Uncultured/environmental sample sequences
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Optional
Create custom database
Enter an Entrez query to limit search
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Algorithm
blastp (protein-protein BLAST)
PSI-BLAST (Position-Specific Iterated BLAST)
PHI-BLAST (Pattern Hit Initiated BLAST)
DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
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BLAST
Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)
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FIG.14

FIGURE 1

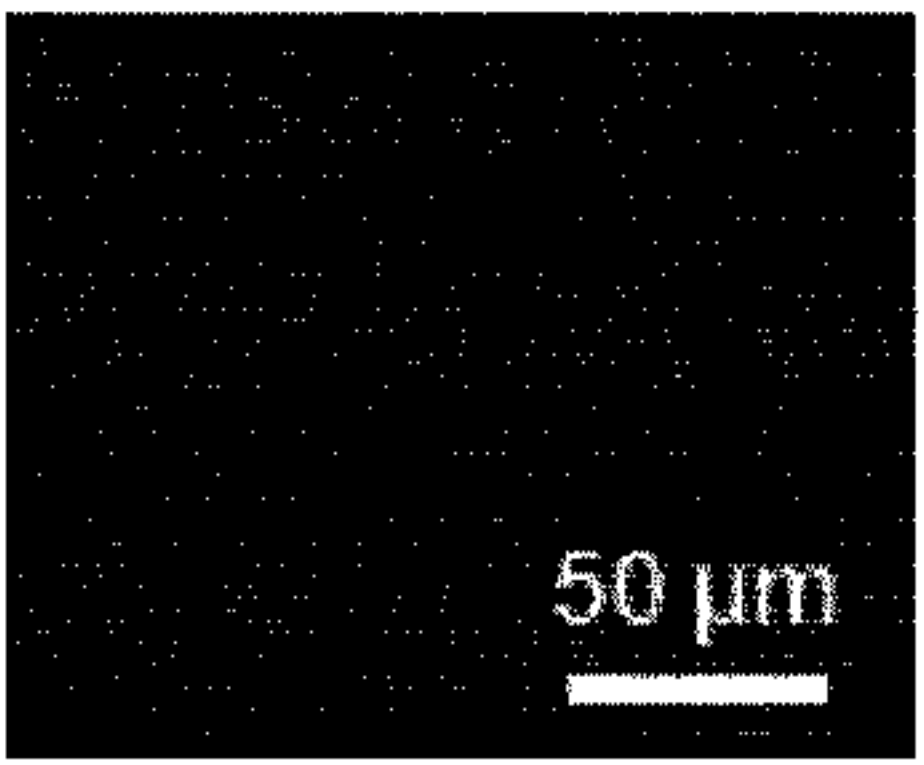
collagen



Collagen-Peptide-FITC
(SEQ ID NO: 9)



apatite



apatite-Peptide-FITC
(SEQ ID NO: 10)

