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WO 2009/013484 A1
Li, J. et al., "Antibodies targeting Clec9A promote strong humoral immunity without adjuvant in mice and nonhuman primates" European journal of immunology, 2015, 45(3), pp.854-864.
Macri, C. et al., Antibody-mediated targeting of antigen to C-type lectin-like receptors Clec9A and Clec12A elicits different vaccination outcomes. Molecular Immunology, 2017, 81, pp.143-150.
Tullett, K.M. et al., "Targeting CLEC9A delivers antigen to human CD141+ DC for CD4+ and CD8+ T cell recognition," JCI insight, 2016, 1(7).
US 2015/0265721 A1



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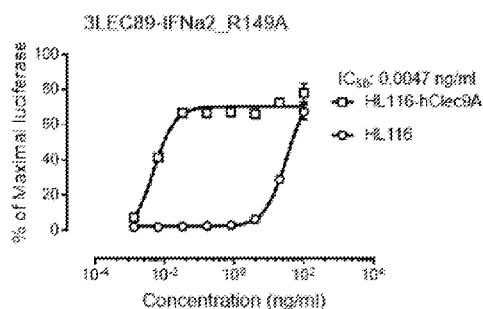
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(54) Title: CLEC9A BINDING AGENTS AND USE THEREOF

Figure 7B



(57) Abstract: The present invention relates, in part, to agents that bind Clec9A and their use as diagnostic and therapeutic agents. The present invention further relates to pharmaceutical compositions comprising the Clec9A binding agents and their use in the treatment of various diseases.



SUMMARY

In a first aspect there is provided a Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising an amino acid sequence having at least 98% identity with one of SEQ ID NOs: 332-336 and wherein the Clec9A binding agent comprises three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:

- (a) CDR1 comprises an amino acid sequence selected from any one of SEQ ID NO: 56;
- (b) CDR2 comprises an amino acid sequence selected from any one of SEQ ID NO: 191; and
- (c) CDR3 comprises an amino acid sequence selected from any one of SEQ ID NO: 202.

In a second aspect there is provided a Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:

- (a) CDR1 comprises an amino acid sequence of SEQ ID NO: 53;
- (b) CDR2 comprises an amino acid sequence of SEQ ID NO: 138; and
- (c) CDR3 comprises an amino acid sequence of SEQ ID NO: 256.

In a third aspect there is provided a Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:

- (a) CDR1 comprises an amino acid sequence of SEQ ID NO: 53;
- (b) CDR2 comprises an amino acid sequence of SEQ ID NO: 137; and
- (c) CDR3 comprises an amino acid sequence of SEQ ID NO: 256, and

wherein the Clec9A binding agent comprises an amino acid sequence having at least 98% identity with SEQ ID NO: 328 or SEQ ID NO: 329.

In a fourth aspect there is provided a recombinant nucleic acid composition encoding the Clec9A binding agent of any one of the first to third aspects.

In a fifth aspect there is provided a host cell comprising a nucleic acid of the fourth aspect.

In a sixth aspect there is provided a chimeric protein comprising:

- (a) a Clec9A binding agent of any one of the first to third aspects; and
- (b) a modified human IFN- β , said modified human IFN- β having one or more mutations that confer improved safety as compared to a wild type IFN- β ; and

wherein the targeting moiety and the modified signaling agent are optionally connected with one or more linkers, optionally wherein the modified human IFN- β comprises one or more mutations at positions W22, R27, L32, R35, V148, L151, R152, and Y155, optionally wherein the modified human IFN- β comprises one or more mutations selected from W22G, R27G, L32A, L32G, R35A, R35G, V148G, L151G, R152A, R152G.

In an seventh aspect there is provided use of a chimeric protein comprising a Clec9A binding agent of any one of the first to third aspects and a signaling agent that is a human interferon alpha 2, in the manufacture of a medicament for treating or preventing cancer that is a tumor.

It is to be noted that, throughout the description and claims of this specification, the word 'comprise' and variations of the word, such as 'comprising' and 'comprises', is not intended to exclude other variants or additional components, integers or steps. Modifications and improvements to the invention will be readily apparent to those skilled in the art. Such modifications and improvements are intended to be within the scope of this invention.

Any reference to or discussion of any document, act or item of knowledge in this specification is included solely for the purpose of providing a context for the present invention. It is not suggested or represented that any of these matters or any combination thereof formed at the priority date forms part of the common general knowledge, or was known to be relevant to an attempt to solve any problem with which this specification is concerned.

In various aspects, the present invention relates to Clec9A binding agents having at least one targeting moiety that specifically binds to Clec9A. In various embodiments, these Clec9A binding agents bind to, but do not functionally modulate (e.g. partially or fully neutralize) Clec9A. Therefore, in various embodiments, the present Clec9A binding agents have use in, for instance, directly or indirectly recruiting a Clec9A-expressing cell to a site of interest while still allowing the Clec9A-expressing cell to signal via Clec9A (i.e. the binding of the Clec9A binding agent does not reduce or eliminate Clec9A signaling at the site of interest). In an embodiment, the targeting moiety is a single domain antibody (VHH). In various embodiments, the Clec9A binding agent further comprises a signaling agent

e.g., without limitation, an interferon, an interleukin, and a tumor necrosis factor, that may be modified to attenuate activity. In various embodiments, the Clec9A binding agent comprises additional targeting moieties that bind to other targets (e.g. antigens, receptor) of interest. In an embodiment, the other targets (e.g. antigens, receptor) of interest are present on tumor cells. In another embodiment, the other targets (e.g. antigens, receptor) of interest are present on immune cells. In some embodiments, the present Clec9A binding agent may directly or indirectly recruit an immune cell (e.g. a dendritic cell) to a site of action (such as, by way of non-limiting example, the tumor microenvironment). In some embodiments, the present Clec9A binding agent facilitates the presentation of antigens (e.g., tumor antigens) by dendritic cells.

In various embodiments, the present Clec9A binding agents find use in the treatment of various diseases or disorders such as cancer, infections, immune disorders, and other diseases and disorders, and the present invention encompasses various methods of treatment.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1 depicts the nucleotide sequence of 66 different VHHs specific for human Clec9A. Gaps were introduced in order to align sequences. The sequences of Figure 1 are assigned sequence identifiers as shown in Example 1.

Figure 2 shows the amino acid sequences of 66 different VHHs specific for human Clec9A. Complementarity determining regions (CDR1, CDR2 and CDR3) as indicated are defined according to Kabat. Gaps were introduced in order to align sequences. The above 66 different VHHs belong to 25 different CDR3 groups (see Figure 3). VHHs belonging to the same group are very similar and their amino acid sequences suggest that they are from clonally-related B-cells resulting from somatic hypermutation or from the same B-cell but diversified due to RT and/or PCR error during library construction. VHHs belonging to the same group recognize the same epitope but their other characteristics (e.g. affinity, potency, stability, expression yield, etc.) can be different. The sequences of Figure 2 are assigned sequence identifiers as shown in Example 1.

Figure 3 provides a table depicting that the 66 different VHHs belonged to 25 different CDR3 groups.

Figure 4 shows the binding of various VHHs to Hek293 T cells transfected with human Clec9A.

Figure 5 shows a human dendritic cell pSTAT1 signaling assay. Chimeras studied were various anti-human Clec9A VHH/human IFN α R149A. Two doses of the agents were studied: 100 ng/ml and 500 ng/ml. PBS was the control and the data are expressed as a fold change of the percentage of pSTAT1⁺ dendritic cells (data is an average of a triplicate data set).

Figure 6 shows the purification and production of Clec9A targeting moieties R1CHCL50, 3LEC89, and variants thereof.

Figures 7A-B are graphs showing the biological activity of chimeric proteins having Clec9A targeting moieties (R1CHCL50 and 3LEC89) and mutated human IFN α 2 (R149A) signaling moieties against HL116 and HL116-hClec9A cells.

Figure 8 is a graph showing *in vivo* anti-tumoral activity of CLEC9A based-AFN (e.g., 2LEC16-hIFNa2_R149A, 3LEC22-hIFNa2_R149A, 1LEC28-hIFNa2_R149A, 3LEC30-hIFNa2_R149A, and 3LEC89-hIFNa2_R149A) in mice with a humanized immune system having an RL tumor.

DETAILED DESCRIPTION

The present invention is based, in part, on the discovery of agents (e.g. antibodies such as, by way of non-limiting example, VHHs) that recognize and bind to Clec9A. In some embodiments, the present Clec9A binding agents are part of a chimeric or fusion protein with one or more targeting moieties and/or one or more signaling agents. In some embodiments, these Clec9A binding agents bind to, but do not functionally modulate Clec9A.

In some embodiments, these Clec9A binding agents may bind and directly or indirectly recruit immune cells to sites in need of therapeutic action (e.g. a tumor or tumor microenvironment). In some embodiments, the Clec9A binding agents enhance tumor antigen presentation for elicitation of effective antitumor immune response.

In some embodiments, the Clec9A binding agents modulate antigen presentation. In some embodiments, the Clec9A binding agents temper the immune response to avoid or reduce autoimmunity. In some embodiments, the Clec9A binding agents provide immunosuppression. In some embodiments, the Clec9A binding agents cause an increase a ratio of Tregs to CD8+ T cells and/or CD4+ T cells in a patient. In some embodiments, the present methods relate to reduction of auto-reactive T cells in a patient.

The present invention provides pharmaceutical compositions comprising the Clec9A binding agents and their use in the treatment of various diseases, including cancer, autoimmune, and/or neurodegenerative diseases.

Clec9A Binding Agents

In various embodiments, the present Clec9A binding agent is a protein-based agent capable of specific binding to Clec9A. In various embodiments, the present Clec9A binding agent is a protein-based agent capable of specific binding to Clec9A without functional modulation (e.g., partial or full neutralization) of Clec9A. Clec9A is a group V C-type lectin-like receptor (CTLR) expressed on the surface of a subset of dendritic cells (*i.e.*, BDCA₃⁺ dendritic cells) specialized for the uptake and processing of materials from dead cells. Clec9A recognizes a conserved component within nucleated and non-nucleated cells, exposed when cell membranes are damaged. Clec9A is expressed at the cell surface as a glycosylated dimer and can mediate endocytosis, but not phagocytosis. Clec9A possesses a cytoplasmic immunoreceptor tyrosine-based activation-like motif that can recruit Syk kinase and induce pro-inflammatory cytokine production (see Huysamen *et al.* (2008), JBC, 283:16693-701).

In various embodiments, the Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that recognizes an epitope present on Clec9A. In an embodiment, the antigen-recognition domain recognizes one or more linear epitopes present on Clec9A. As used herein, a linear epitope refers to any continuous sequence of amino acids present on Clec9A. In another embodiment, the antigen-recognition domain recognizes one or more conformational epitopes present on Clec9A. As used herein, a conformation epitope refers

to one or more sections of amino acids (which may be discontinuous) which form a three-dimensional surface with features and/or shapes and/or tertiary structures capable of being recognized by an antigen recognition domain.

In various embodiments, the Clec9A binding agent of the present invention may bind to the full-length and/or mature forms and/or isoforms and/or splice variants and/or fragments and/or any other naturally occurring or synthetic analogs, variants, or mutants of human Clec9A. In various embodiments, the Clec9A binding agent of the invention may bind to any forms of the human Clec9A, including monomeric, dimeric, heterodimeric, multimeric and associated forms. In an embodiment, the Clec9A binding agent binds to the monomeric form of Clec9A. In another embodiment, the Clec9A binding agent binds to a dimeric form of Clec9A. In a further embodiment, the Clec9A binding agent binds to glycosylated form of Clec9A, which may be either monomeric or dimeric.

In an embodiment, the present Clec9A binding agent comprises a targeting moiety with an antigen recognition domain that recognizes one or more epitopes present on human Clec9A. In an embodiment, the human Clec9A comprises the amino acid sequence of:

MHEEEIYTSLQWDSPAPDTYQKCLSSNKCSGACCLVMVISCVFCMGLLTA
SIFLGVKLLQVSTIAMQQQEKLQKERALLNFTWKRSCALQMKYCQAFMQ
NSLSSAHNSSPCPNWQINRESCYYVSEIWSIWHTSQENCLKEGSTLLQIE
SKEEMDFITGSLRKIKGSYDYWVGLSQDGHSGRWLWQDGSSPSPGLLPA
ERSQSANQVCGYVKSNSLLSSNCSTWKYFICEKYALRSSV (SEQ ID NO:
1).

In various embodiments, the present Clec9A binding agent comprises a targeting moiety capable of specific binding. In various embodiments, the Clec9A binding agent comprises a targeting moiety having an antigen recognition domain such as an antibody or derivatives thereof. In an embodiment, the Clec9A binding agent comprises a targeting moiety which is an antibody. In various embodiments, the antibody is a full-length multimeric protein that includes two heavy chains and two light chains. Each heavy chain includes one variable region (e.g., V_H) and at least three constant regions (e.g., CH₁, CH₂ and CH₃), and each light chain includes one variable region (V_L) and one constant region (C_L). The variable regions determine the specificity of the antibody. Each variable region comprises three hypervariable regions also known as complementarity determining regions (CDRs) flanked by four relatively conserved framework regions (FRs). The three CDRs, referred to as CDR1, CDR2, and CDR3, contribute to the antibody binding specificity. In some embodiments, the antibody is a chimeric antibody. In some embodiments, the antibody is a humanized antibody.

In some embodiments, the Clec9A binding agent comprises a targeting moiety which is an antibody derivative or format. In some embodiments, the present Clec9A binding agent comprises a targeting moiety which is a single-domain antibody, a recombinant heavy-chain-only antibody (VHH), a single-chain antibody (scFv), a shark heavy-chain-only antibody (VNAR), a microprotein (cysteine knot protein, knottin), a DARPin; a Tetranectin; an Affibody; a Transbody; an Anticalin; an AdNectin; an Affilin; an Affimer, a Microbody; an aptamer; an alterase; a plastic antibody; a phylomer; a stradobody; a maxibody; an evibody; a fynomer, an armadillo repeat protein, a Kunitz

domain, an avimer, an atrimer, a probody, an immunobody, a triomab, a troybody; a pepbody; a vaccibody, a UniBody; a DuoBody, a Fv, a Fab, a Fab', a F(ab')₂, a peptide mimetic molecule, or a synthetic molecule, as described in US Patent Nos. or Patent Publication Nos. US 7,417,130, US 2004/132094, US 5,831,012, US 2004/023334, US 7,250,297, US 6,818,418, US 2004/209243, US 7,838,629, US 7,186,524, US 6,004,746, US 5,475,096, US 2004/146938, US 2004/157209, US 6,994,982, US 6,794,144, US 2010/239633, US 7,803,907, US 2010/119446, and/or US 7,166,697, the contents of which are hereby incorporated by reference in their entireties. See also, Storz MABs. 2011 May-Jun; 3(3): 310–317.

In some embodiments, the Clec9A binding agent comprises a targeting moiety which is a single-domain antibody, such as a VHH. The VHH may be derived from, for example, an organism that produces VHH antibody such as a camelid, a shark, or the VHH may be a designed VHH. VHHs are antibody-derived therapeutic proteins that contain the unique structural and functional properties of naturally-occurring heavy-chain antibodies. VHH technology is based on fully functional antibodies from camelids that lack light chains. These heavy-chain antibodies contain a single variable domain (V_HH) and two constant domains (CH2 and CH3).

In an embodiment, the Clec9A binding agent comprises a VHH. In some embodiments, the VHH is a humanized VHH or camelized VHH.

In some embodiments, the VHH comprises a fully human V_H domain, e.g. a HUMABODY (Crescendo Biologics, Cambridge, UK). In some embodiments, fully human V_H domain, e.g. a HUMABODY is monovalent, bivalent, or trivalent. In some embodiments, the fully human V_H domain, e.g. a HUMABODY is mono- or multi-specific such as monospecific, bispecific, or trispecific. Illustrative fully human V_H domains, e.g. a HUMABODIES are described in, for example, WO2016/113555 and WO2016/113557, the entire disclosure of which is incorporated by reference.

In some embodiments, the Clec9A binding agent comprises a targeting moiety which is a VHH comprising a single amino acid chain having four “framework regions” or FRs and three “complementary determining regions” or CDRs. As used herein, “framework region” or “FR” refers to a region in the variable domain which is located between the CDRs. As used herein, “complementary determining region” or “CDR” refers to variable regions in VHHs that contains the amino acid sequences capable of specifically binding to antigenic targets.

In various embodiments, the Clec9A binding agent comprises a VHH having a variable domain comprising at least one CDR1, CDR2, and/or CDR3 sequences. In various embodiments, the Clec9A binding agent comprises a VHH having a variable region comprising at least one FR1, FR2, FR3, and FR4 sequences.

In some embodiments, the CDR1 sequence is selected from:

GRISSNSMG (SEQ ID NO: 2); GSITSINAMG (SEQ ID NO: 3); GRFFRVNAMG (SEQ ID NO: 4); GSSDSINAMG (SEQ ID NO: 5); GSVFSINAWG (SEQ ID NO: 6); GSILSINSMG (SEQ ID NO: 7); VSISSINSMG (SEQ ID NO: 8); GRVFSINAMG (SEQ ID NO: 9); VNIDTLNSMA (SEQ ID NO: 10); GGISSNSMG (SEQ ID NO: 11); GSMHSVNSMA (SEQ ID NO: 12); GDISSINAMG (SEQ ID NO: 13); GSIFSIDAMG (SEQ ID NO: 14); GSIFSINAMG (SEQ ID NO: 15); GSIFSIAAMG (SEQ ID NO: 16); GNIASITAMG (SEQ ID NO: 17); GFTFDDYAIG

(SEQ ID NO: 18); GSISSINAMG (SEQ ID NO: 19); VSIFRSYFMG (SEQ ID NO: 20); GSIVSINAIG (SEQ ID NO: 21); RSFSSFNAMG (SEQ ID NO: 22); GSFSSINAMG (SEQ ID NO: 23); GTSFSINGMA (SEQ ID NO: 24); GRTFSTYAMG (SEQ ID NO: 25); GRIFDINAMG (SEQ ID NO: 26); GTLFSINGMA (SEQ ID NO: 27); GSIDSINAMG (SEQ ID NO: 28); GRAFSTNSMG (SEQ ID NO: 29); GSIISINSMG (SEQ ID NO: 30); RNFFSINAMG (SEQ ID NO: 31); GSIVSINSMG (SEQ ID NO: 32); GSIIGINSMG (SEQ ID NO: 33); GRTFPGYVMA (SEQ ID NO: 34); GRTFSINAMG (SEQ ID NO: 35); GRTLSSYTIG (SEQ ID NO: 36); GSFFSINAMG (SEQ ID NO: 37); GSIFSINSMG (SEQ ID NO: 38); GSIFSFNAMG (SEQ ID NO: 39); GRTFSTYAMA (SEQ ID NO: 40); VNIGSLNSMV (SEQ ID NO: 41); GRTLSNYAVG (SEQ ID NO: 42); GSVFSINAMG (SEQ ID NO: 43); GSIFEINSIG (SEQ ID NO: 44); GSIFNINSMG (SEQ ID NO: 45); VNIGTLNSMA (SEQ ID NO: 46); GRIGSINSMG (SEQ ID NO: 47); GRTLSNYAVA (SEQ ID NO: 48); RSFFSFNAMG (SEQ ID NO: 49); GIIFSINAMG (SEQ ID NO: 50); GRIFSVNAMG (SEQ ID NO: 51); GRTFSSYAMA (SEQ ID NO: 52); GSFSSINVMG (SEQ ID NO: 53); INSMG (SEQ ID NO: 54); INAMG (SEQ ID NO: 55); VNAME (SEQ ID NO: 56); INAWG (SEQ ID NO: 57); LNSMA (SEQ ID NO: 58); VNSMA (SEQ ID NO: 59); IDAMG (SEQ ID NO: 60); IAAMG (SEQ ID NO: 61); SITAMG (SEQ ID NO: 62); DYAI (SEQ ID NO: 63); SYFMG (SEQ ID NO: 64); INAIG (SEQ ID NO: 65); FNAMG (SEQ ID NO: 66); INGMA (SEQ ID NO: 67); TYAMG (SEQ ID NO: 68); TNSMG (SEQ ID NO: 69); GYVMA (SEQ ID NO: 70); SYTIG (SEQ ID NO: 71); TYAMA (SEQ ID NO: 72); LNSMV (SEQ ID NO: 73); NYAVG (SEQ ID NO: 74); INSIG (SEQ ID NO: 75); NYAVA (SEQ ID NO: 76); SYAMA (SEQ ID NO: 77); and INVMG (SEQ ID NO: 78).

In some embodiments, the CDR2 sequence is selected from:

AITNGGAKTYADSVKG (SEQ ID NO: 79); AITSGGRLSYADSVKG (SEQ ID NO: 80); AITNGGQTAYADSVKG (SEQ ID NO: 81); AITSGGRSTYIDSAKG (SEQ ID NO: 82); AITNQGRIAYAPSVNG (SEQ ID NO: 83); AITNDGRTTYVDSVK (SEQ ID NO: 84); AVTVGGRYAYADSAKN (SEQ ID NO: 85); AITNQGATTYADSVKG (SEQ ID NO: 86); GITSGQITYANSVRG (SEQ ID NO: 87); AITNGGRTVYGDSVK (SEQ ID NO: 88); AITSGGRLAYAPSVNG (SEQ ID NO: 89); AITNGGRTTYVDSVK (SEQ ID NO: 90); AITTGRTTYVDSVK (SEQ ID NO: 91); AITNQGRLTYADSVKG (SEQ ID NO: 92); AITSGGRRAYADSVKG (SEQ ID NO: 93); AITSASASRTTYADSVKG (SEQ ID NO: 94); CISRSDGSTYYDDSVKG (SEQ ID NO: 95); AITNQGRVTYADSVKG (SEQ ID NO: 96); AITDGGRLAYADSAKG (SEQ ID NO: 97); SITNQGIRNYSTSVMG (SEQ ID NO: 98); AITNQGRTTYADSVKG (SEQ ID NO: 99); AITNGGRIAYGIAVNG (SEQ ID NO: 100); AITNGGRIAYSDSAKG (SEQ ID NO: 101); GITSDGSTGYADSVKG (SEQ ID NO: 102); AISWSGGSTYADSVKG (SEQ ID NO: 103); AITDQGRLAYADSAKG (SEQ ID NO: 104); AITNGGQTTYADSVKG (SEQ ID NO: 105); AITTGRTAYVDSVK (SEQ ID NO: 106); AITSQGRITLADSVKG (SEQ ID NO: 107); AITVDGRLAYADSAKH (SEQ ID NO: 108); AITNGGRIAYGTSVMG (SEQ ID NO: 109); AITNGGQIAYADSVKG (SEQ ID NO: 110); AITDQGRTTYADSVKG (SEQ ID NO: 111); GITTQGRITYGNSVRG (SEQ ID NO: 112); AITSGGRTTYVDSVK (SEQ ID NO: 113); AINWRGGDTYYADSVKG (SEQ ID NO: 114); AITDGGAKTYADSVKG (SEQ ID NO: 115); AITNQGRLSYVDSVK (SEQ ID NO: 116); AITNQGRRTYADSVKG (SEQ ID NO: 117); AITNGGRIAYTDSVK (SEQ ID NO: 118); AITNGGRTTYADSVKG (SEQ ID NO: 119); AITDGGRLTYADSAKG (SEQ ID NO: 120); AISWSGGSTEYHDSVK (SEQ ID NO: 121); AITNQGRIAYADSVKG (SEQ ID NO: 122);

AINWSSGGISYSNSAKG (SEQ ID NO: 123); AITGQGRTTYADSVKG (SEQ ID NO: 124); AITNGGQIVYADSVKG (SEQ ID NO: 125); AITTQGRTTYEDSVKG (SEQ ID NO: 126); AITSGGITNYANSVQG (SEQ ID NO: 127); AITVGGRLAYADSAKG (SEQ ID NO: 128); GITGGGQITYANSVRG (SEQ ID NO: 129); AITSQGRSTYADSAKG (SEQ ID NO: 130); AITNGGATVYADSVKG (SEQ ID NO: 131); AITDGGRLTYADSAKN (SEQ ID NO: 132); AINWSSGGISYSNAAKG (SEQ ID NO: 133); AITNXGRTTYADSVKG (SEQ ID NO: 134); AIWWASGGISYANSAGK (SEQ ID NO: 135); AITNQGAPTYADSVKG (SEQ ID NO: 136); RITNLGLPNYADSVTG (SEQ ID NO: 137); RITNLGLPNYADSVKG (SEQ ID NO: 138); AITNGGAKT (SEQ ID NO: 139); AITSGGRLS (SEQ ID NO: 140); AITNGGQTA (SEQ ID NO: 141); AITSGGRST (SEQ ID NO: 142); ITNQGRIA (SEQ ID NO: 143); ITNQGRIAYAPSVNG (SEQ ID NO: 144); AITNDGRTT (SEQ ID NO: 145); AVTVGGRYA (SEQ ID NO: 146); AITNQGATT (SEQ ID NO: 147); GITGSGQIT (SEQ ID NO: 148); AITNGGRTV (SEQ ID NO: 149); AITSGGRLA (SEQ ID NO: 150); AITNGGRTT (SEQ ID NO: 151); AITTGGRTT (SEQ ID NO: 152); AITNQGRLT (SEQ ID NO: 153); AITSGGRRRA (SEQ ID NO: 154); AITSASASRTT (SEQ ID NO: 155); CISRSDGSTY (SEQ ID NO: 156); AITNQGRVT (SEQ ID NO: 157); AITDGGRLA (SEQ ID NO: 158); SITNQGIRN (SEQ ID NO: 159); AITNQGRTT (SEQ ID NO: 160); AITNGGRIA (SEQ ID NO: 161); GITSDGSTG (SEQ ID NO: 162); AISWSSGGSTY (SEQ ID NO: 163); AITDQGRLA (SEQ ID NO: 164); AITNGGQTT (SEQ ID NO: 165); AITTGGRTA (SEQ ID NO: 166); AITSQGRIT (SEQ ID NO: 167); AITVDGRLA (SEQ ID NO: 168); AITNGGQIA (SEQ ID NO: 169); AITDQGRTT (SEQ ID NO: 170); GITTQGRIT (SEQ ID NO: 171); AITSGGRTT (SEQ ID NO: 172); AINWRGGDTY (SEQ ID NO: 173); AITDGGAKT (SEQ ID NO: 174); AITNQGRLS (SEQ ID NO: 175); AITNQGRRT (SEQ ID NO: 176); AITDGGRLT (SEQ ID NO: 177); AISWSSGGSTE (SEQ ID NO: 178); AITNQGRIA (SEQ ID NO: 179); AINWSSGGIS (SEQ ID NO: 180); AITGQGRTT (SEQ ID NO: 181); AITNGGQIV (SEQ ID NO: 182); AITTQGRTT (SEQ ID NO: 183); AITSGGITN (SEQ ID NO: 184); AITVGGRLA (SEQ ID NO: 185); GITGGGQIT (SEQ ID NO: 186); AITSQGRST (SEQ ID NO: 187); AITNGGATV (SEQ ID NO: 188); AITNXGRTT (SEQ ID NO: 189); AIWWASGGIS (SEQ ID NO: 190); AITNQGAPT (SEQ ID NO: 191); and RITNLGLPN (SEQ ID NO: 192).

In some embodiments, the CDR3 sequence is selected from:

FTRRDDY (SEQ ID NO: 193); FQSSGID (SEQ ID NO: 194); WAADYQQY (SEQ ID NO: 195); WNRDRQQY (SEQ ID NO: 196); KPTPVYGSTVG DY (SEQ ID NO: 197); FTRDKDY (SEQ ID NO: 198); WDRDRQQY (SEQ ID NO: 199); FTRTDDY (SEQ ID NO: 200); YDRSSTPY (SEQ ID NO: 201); FTRGDDY (SEQ ID NO: 202); LNSATTY (SEQ ID NO: 203); YTRDEDY (SEQ ID NO: 204); FTRDEDY (SEQ ID NO: 205); KWYDPLVIEYYDN (SEQ ID NO: 206); KADHNDY (SEQ ID NO: 207); FRSGADDY (SEQ ID NO: 208); EVPSTYSCSGFREDY (SEQ ID NO: 209); FAASGMEY (SEQ ID NO: 210); WTTDRQQY (SEQ ID NO: 211); FAGWGKEDY (SEQ ID NO: 212); FSPTGDY (SEQ ID NO: 213); KPTPVYGSTVG DY (SEQ ID NO: 214); KASPVYGSTVEDY (SEQ ID NO: 215); STPRGDSY (SEQ ID NO: 216); EAEGSGREGNFYERS (SEQ ID NO: 217); WDRDRQQY (SEQ ID NO: 218); FTRSDDY (SEQ ID NO: 219); STPRGDSY (SEQ ID NO: 220); FTRDTDY (SEQ ID NO: 221); WTTLGTF (SEQ ID NO: 222); WVRDGQQY (SEQ ID NO: 223); KAIPVYGSTVEDY (SEQ ID NO: 224); KAAATHLSTVADY (SEQ ID NO: 225); FGRFDDY (SEQ ID NO: 226); WGVKTGPESGSGTL (SEQ ID NO: 227); FTRDEDY (SEQ ID NO: 228); RLTTYDYAY (SEQ ID NO: 229); FTRGNDY (SEQ ID NO: 230); FQSSGID (SEQ ID NO: 231); FSPTDDF (SEQ

ID NO: 232); KAIPYGSTAEDY (SEQ ID NO: 233); FSLTDDY (SEQ ID NO: 234); WTRDRQQY (SEQ ID NO: 235); FTRDEDF (SEQ ID NO: 236); EVEGSGREGNFYGA (SEQ ID NO: 237); PGWDY (SEQ ID NO: 238); YDRSATAY (SEQ ID NO: 239); ASSVLSGTVDY (SEQ ID NO: 240); FAADGMEY (SEQ ID NO: 241); KAAASYVSTVADY (SEQ ID NO: 242); TAKDDY (SEQ ID NO: 243); FTGWGKEDY (SEQ ID NO: 244); WAADYQQY (SEQ ID NO: 245); YDRSATPY (SEQ ID NO: 246); WARDRQQY (SEQ ID NO: 247); WTKDRQQY (SEQ ID NO: 248); FTRTYDY (SEQ ID NO: 249); ASSILSGTVDY (SEQ ID NO: 250); WAADYQQY (SEQ ID NO: 251); KPAPVYGSTVGDY (SEQ ID NO: 252); FAADGMEY (SEQ ID NO: 253); FGSGGG (SEQ ID NO: 254); ASSVLSGTADY (SEQ ID NO: 255); VALKAEY (SEQ ID NO: 256); and EAEGSGREGNFYERS (SEQ ID NO: 257).

In various exemplary embodiments, the Clec9A binding agent comprises an amino acid sequence selected from the following sequences:

1LEC 7 (SEQ ID NO: 258)

QVQLQESGGGLVQPGGSLRLSCAASGRISINSIMGWYRQAPGNQRELVAITNGGAKTYADSVKGRFTISTDNA
GNTVYLQMDSLRPEDTAVYYCKAFTRRDDYWGQGTQITVSSAAAPYDVPDYGSHHHHHH;

1LEC 9 (SEQ ID NO: 259)

QVQLQESGGGLVQAGGSLRLSCAASGSITSINAMGWYRQAPGKQRELVAITSGGRLSYADSVKGRFTISRDN
ESTVALQMNSLKPEDTAVYSCAAFQSSGIDWGQGTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 26 (SEQ ID NO: 260)

QVQLQESGGGLVQPGGSLRLSCAASGRFFRVNAMGWYRQAPGKQRELVAITNGGQTAYADSVKGRFTISKES
ARNTVHLQMSSLKPEDTAVYYCTIWAADYQQYWGQGTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 27 (SEQ ID NO: 261)

QVQLQESGGGLVQAGESLRLSCAASGSSDSINAMGWYRQAPGKQRELVAITSGGRSTYIDSAKGRATISRDN
RNTAYLQMSSLKAEDTAVYYCTIWNDRDQQYWGQGTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 28 (SEQ ID NO: 262)

QVQLQESGGGLVQSGGSLRLSCAASGSVFSINAWGWYRQAPGKQRELVAITNQGRIAYAPSVNGRFTISRDS
AKNTVYLQMNSLKPEDTAVYYCNAKPTPVYGSTVGDYWGQGTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 30 (SEQ ID NO: 263)

QVQLQESGGGLVQAGGSLRLSCAASGSILSINSIMGWYRPALGNQRELVAITNDGRTTYVDSVKGRFTISRDN
KNTVYLQMNSLKPEDTAVYWCKAFTRDKDYWGQGTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 38 (SEQ ID NO: 264)

QVQLQESGGGLVQTGGSLRLSCAASVSISINSIMGWYRQAPGKERELVAAVTVGGRYAYADSAKNRFTISRDD
AQNTVHLQMSSLRAEDTAVYYCTIWDNRDQQYWGXTQVTVSSAAAPYDVPDYGSHHHHHH;

1LEC 42 (SEQ ID NO: 265)

QVQLQESGGGLVQPGGSLRLSCAASGRVFSINAMGWYRQAPGKQRELVAAITNQGATTYADSVKGRFTISRDT
AGNTVYLQMNSLRPEDTAVHYCKAFTRTDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 51 (SEQ ID NO: 266)

QVQLQESGGGLVQAGGSLRLSCAASVNIDTLNSMAWYRQAPGKQRELVAGITGSGQITYANSVRGRFTVSRDN
AKSTVYLQMNTLQPEDTAVYYCAAYDRSSTPYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 61 (SEQ ID NO: 267)

QVQLQESGGGLVQPGGSLRLSCAASGGISSINSMGWYRQAPGNQRELVAAITNGGRTVYGDSVKGRFTISRDS
AGNTVHLQMDSLRLPEDTGVIYCKAFTRGDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 62 (SEQ ID NO: 268)

QVQLQESGGGLVQPGGFLSLSCAASGSMHSVNSMAWYRQVPGKQRELVAAITSGGRLAYAPSVNGRFTISRDI
AKNTIHLQMNSLEPEDTAVYYCAALNSATTYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 63 (SEQ ID NO: 269)

QVQLQESGGGLVQAGGSLRLSCAATGDISSINAMGWHRPARGNERELVAAITNGGRTTYVDSVKGRFTISRDN
KNTVYLQMNSLKPEDTAVYFCKAYTRDEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 64 (SEQ ID NO: 270)

QVQLQESGGGLVRAGGSLRLSCAASGSIFSIDAMGWYRPAHGEQRELVAAITTGGRRTTYVDSVKGRFTISRDN
KNTVYLQMNSLKPEDTAVYFCKAFTRDEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 70 (SEQ ID NO: 271)

QVQLQESGGGLVQPGGSLRLSCAASGSIFSINAMGWYRQAPGKQRELVAAITNQGRITYADSVKGRFTISRDN
KNTVFLQMDSLKPEDTAVYYCNAKWYDPLVIEYDNWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 84 (SEQ ID NO: 272)

QVQLQESGGGLVQPGGSLRLSCAASGSIFSIAAMGWYRQAPGKQRELVAAITSGGRRAYADSVKGRFTISRDN
ENTVALQMNSLKPEDTDVYYCNAKADHNDYWGQGTQITVSSAAAYPYDVPDYGSHHHHHH;

1LEC 88 (SEQ ID NO: 273)

QVQLQESGGGLVQPGGSLRLSCAAGNIASITAMGWYRQAPGKQRELVAAITSSASRTTYADSVKGRFTISRDN
AKNTVYLQMNSLQPEDTAVYYCKGFRSGADDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 91 (SEQ ID NO: 274)

QVQLQESGGGLVQPGGSLRLSCAASGFTFDDYAIQWFRQAPGKEHEGVSCISRSDGSTYYDDSVKGRFTISSD
NAKNTVYLQMNSLKPEDTAVYYCAAEPSTYSCSGFREDYKKGKTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 92 (SEQ ID NO: 275)

QVQLQESGGGLVQPGGSLRLSCAASGSISSINAMGWYRQAPGNQRELVAITNQGRVTYADSVKGRFTISR
AKNTVYLQMNSLKPEDTAVYYCKVFAASGMEYWGKGTQVTVSSAAAYPYDVPDYGSHHHHHH;

1LEC 94 (SEQ ID NO: 276)

QVQLQESGGGLVQAGESLRLSCAASVSIFRSYFMGWYRQAPGKQRELVAITDGGRLAYADSAKGRFTISRED
RNTVHLQMSSLKAEDTAVYYCTIWTTDRQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 6 (SEQ ID NO: 277)

QVQLQESGGGWVQPGGSLRLSCAATGSIVSINAIGWYRQAPGKQRELVASITNQGIRNYSTSVMGRFTISRDD
KNTVSLQMNSLKPEDSAVYYCKGFAGWGKEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 13 (SEQ ID NO: 278)

QVQLQESGGGLVQAGASLRLSCAASGSIFSINAMGWYRQAPGKQRELVAITNQGRTTYADSVKGRFTISRDN
KNTVYLQMDSLEPEDTAIYYCKGFSPTGDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 16 (SEQ ID NO: 279)

QVQLQESGGGLVQPGGSLRLSCLASRSFSSFNAMGWYRQAPGKERELVAITNGGRIAYGIAVNGRFTISRDN
KNTVYLQMNSLKPEDTAVYYCNAKPTPVYGSTVGDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 20 (SEQ ID NO: 280)

QVQLQESGGGLVQAGGSLTLSCAASGSFSSINAMGYRQAPGKQRELVAITNGGRIAYSDSA KGRFTISRDSA
KNTMYLQMNSLKPEDTDVYYCNAKASPVYGSTVEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 23 (SEQ ID NO: 281)

QVQLQESGGGLVQPGGSLRLSCAASGTSFSINGMAWYRQAPGGQRELVGGITSDGSTGYADSVKGRFTVSRD
NAKNTVYLQMNRLKPEDTAVYYCGTSTPRGDSYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 24 (SEQ ID NO: 282)

QVQLQESGGGLVQAGGSLRLSCAASGRFTFSTYAMGWFRQAPGKERGLVA AISWGGSTYYADSVKGRFTIFRD
NAENTVYLQMNSLKPEDTAVYYCAA EAEGSGREGNFYERSWYQGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 26 (SEQ ID NO: 283)

QVQLQESGGGLVETGGSLRLSCAASGSIFSINAMGWYRQAPGKQRELVAITDQGRLAYADSAKGRFTISRENA
RNTLHLQMSSLKAEDTAVYYCTIWDRDRQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 38 (SEQ ID NO: 284)

QVQLQESGGGLVQPGGSLRLSCAASGRIFDINAMGWYRQAPGKQRELVAITNGGQTTYADSVKGRFTISRDN
AGNTVYLQMNSLRPEDTAVYYCKAFTRSDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 48 (SEQ ID NO: 285)

QVQLQESGGGLVQAGGSLRLSCAASGTLFSINGMAWYRQAPGKRRELVGGITSDGSTGYADSVKGRFTISRDN
AKNTAYLQMNSLKPEDTAVYYCGTSTPRGDSYWGGGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 53 (SEQ ID NO: 286)

QVQLQESGGGLVQAGGSLRLSCAASGSIDSINAMGWYRPALGEQRELVAAITTGGRITAYVDSVKGRFTISRDA
KNTVYLQMNSLKPEDTAVYSCKAFTRDIDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 54 (SEQ ID NO: 287)

QVQLQESGGGLAQPGGSLRLSCAASGRAFTNSMGWYRQASGKQRELVAAITSQGRITLADSVKGRFTISSDN
TKNTVFLQMNSLKPEDTAVYYCNAWTLGTFTGGGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 55 (SEQ ID NO: 288)

QVQLQESGGGLVQTGESLSLSCAVASGSIISINSMGWYRQAPKQRELVAAITVDGRLAYADSAKHRFTISKESA
RNTVHLHMSSLKPEDTAVYYCTIWRDGGQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 59 (SEQ ID NO: 289)

QVQLQESGGGLVQPGGSLRLSCAVSRNFFSINAMGWYRQAPGKQRELVAAITNGGRIAYGTSVMGRFTISRDD
AKNTVDLQMNSLRPEDTAVYYCNAKAIPVYGSTVEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 60 (SEQ ID NO: 290)

QVQLQESGGGLVQPGGSLRLSCAASGRFFRVNAMGWYRQVPGKQRELVAAITNGGQIAYADSVKGRFTISRDS
AKNTVYLQMNSLKSEDTDVYYCNAKAAATHLSTVADYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 61 (SEQ ID NO: 291)

QVQLQESGGGLVQPGGSLRLSCAASGSIVSINSMGWYRQAPGKQRELVAAITDQGRTTYADSVKGRFTISRDDA
KNKNTVYLQMNSLKAEDTAVYACKAFGRFDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 62 (SEQ ID NO: 292)

QVQLQESGGGLVQPGGSLRLSCAAYGSIFSINAMGWYRQAPGKERELVAGITTQGRITYGNSVRGRFTISGDNA
KNTVYLQMKSLKPEDTAVYYCSAWGVKTGPESGSGTLEGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 63 (SEQ ID NO: 293)

QVQLQESGGGLVQAGGSLRLSCAASGSIIIGINSMGYRTAPGKQRELVAAITSGGRTTYVDSVKGRFTISRDN
KNTVYLQMNSLKPEDTAVYFCKAFTRDEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 67 (SEQ ID NO: 294)

QVQLQESGGGLVQAGGSLRLSCAASGRFTPGYVMAWFRQSPGQEREFAAAINWRGGDTYYADSVKGRFTISR
DNVKNVFLQMNSLKPEDTAVYFCAARLTTEYDAYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 68 (SEQ ID NO: 295)

QVQLQESGGGLVQPGESLRLSCAASGSIFSINAMGWYRQAPGKQRELVAAITDGGAKTYADSVKGRFTISTDNA
GNTVYLQMDSLRLPEDTAVYYCKAFTRGNDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 76 (SEQ ID NO: 296)

QVQLQESGGGLVQAGESLRLSCVWSGRTFSINAMGWYRQAPGKQRELVAAITNQGRLSYVDSVKGRFTISRDN
AANTVYLQMNSLKPEDTAVYYCAAFQSSGIDWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 83 (SEQ ID NO: 297)

QVQLQESGGGLVQAGGSLRLSCAASGRTLSSYTIGWYRQAPGKQRELVAAITNQGRRTYADSVKGRFTISRDN
AKNTVYLQMDSLKSEDTAVYYCKGFSPTDDFWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 88 (SEQ ID NO: 298)

QVQLQESGGGLVQPGGSLRLSCTASGSFFSINAMGWYRQAPGNQRELVAAITNGGRIAYTDSVKGRFTISNDNA
KNTVYLQMNSLKPEDTDVYYCNAKAIPYIGSTAEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 89 (SEQ ID NO: 299)

QVQLQESGGGLVQAGGSLRLSCAASGSIFSINSMGWYRQAPGKQRELVAAITNGGRTTYADSVKGRFTISRDN
KNTVYLQMDSLKPEDTAVYYCKGFSLTDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 90 (SEQ ID NO: 300)

QVQLQESGGGLVQTGGSLRLSCAASGSIFSINAMGWYRQAPGKQRELVAAITDGGRLTYADSAKGRFTISRENT
RNTVHLQMSSLKAEDTADYYCTIWTRDRQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 93 (SEQ ID NO: 301)

QVQLQESGGGLVQAGGSLRLSCAASGSIFSINAMGWYRQALGEQRELVAAITTGGRRTTYVDSVKGRFISRDN
KNTVYLQMNSLKPEDTAVYFCKAFTRDEDFWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

2LEC 95 (SEQ ID NO: 302)

QVQLQESGGGLVQAGGSLRLSCEASGRTFSTYAMAWFRQAPGKERDLVAAISWGGSTEYHDSVKGRFTISRDN
NTKNTVYLQMNSLKAEDTAVYYCAAEEVSGREGNFYGASWYPGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 4 (SEQ ID NO: 303)

QVQLQESGGGLVQPGGSLRLSCAASGSFFSINAMGWYRQAPGKQRELVAAITNQGRIAYADSVKGRFTISRDN
KNTVYLQMNSLKPEDTAVYYCGRPGWDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 6 (SEQ ID NO: 304)

QVQLQESGGGLVQAGGSLRLSCVASVNISSLNSMVWYRQSPGKQRELVAGITGSGQITYANSVRGRFTVSRDIA
KSTAYLQMNTLKPEDTAVYYCAAAYDRSATAYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 9 (SEQ ID NO: 305)

QVQLQESGGGLVQAGGSLRVSCAASGRTLSTNYAVGWWRQAPGKQREFVAAINWSSGGISYSNSAKGRFALSR
DNAKNTVYLQMDSLKPEDTAVYYCAAASSVLSGTVDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 11 (SEQ ID NO: 306)

QVQLQESGGGLVQPGGSLRLSCAASGSISSINAMGWYRQAPGKQRELVAAITGQGRTTYADSVKGRFTISRDLG
AKNTVYLQMNSLKPEDTAVYYCKVFAADGMEYWGKGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 13 (SEQ ID NO: 307)

QVQLQESGGGLVQPGGSLRLSCAASGRFFRVNAMGWYRQAPGKQRELVAAITNGGQIVYADSVKGRFTISRDS
AKNTVYLQMNSLKSSEDVAVYYCNAKAAASYVSTVADYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 15 (SEQ ID NO: 308)

QVQLQESGGGLVQAGGSLRLSCAASGSVFSINAMGWYRQAPGKQRELVAAITTQGRTTYEDSVKGRFTISRDLG
AQNTVYLQMDSLKPEDTAVYYCKAWTAKDDYWGKGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 22 (SEQ ID NO: 309)

QVQLQESGGGRVQPGGSLRLSCAAGSIFEINSIGWYRQAPGKQRELVAAITSGGITNYANSVQGRSTISRDNVN
NTVYLQMNSLKPEDSAVYYCKGFTGWGKEDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 23 (SEQ ID NO: 310)

QVQLQESGGGLVQTGGSLRLSCAASGSIFNINSMGWYRQAPGKQRELVAAITVGGRLAYADSAKGRFTISKESA
RNTVHLQMSSLKPEDTAVYYCTIWAADYQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 27 (SEQ ID NO: 311)

QVQLQESGGGLVQAGGSLRLSCAASVNIGTLNSMAWYREAPGKQRELVAGITGGGQITYANSVRGRFTVSRDIA
KSTAYLQMNTLKPEDTAVYYCAAYDRSATPYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 30 (SEQ ID NO: 312)

QVQLQESGGGLVQTGGSLRLSCAASGSIFSINSMGWYRQAPGKQRELVAAITSQGRSTYADSAKGRFTISLGNA
RNTVNLQMSSLKTEDTAVYYCTIWARDRQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 36 (SEQ ID NO: 313)

QVQLQESGGGLVQPGGSLRLSCAASGRIGSINSMGWYRQAPGKQREMVAAITNGGATVYADSVKGRFTISRDN
AGNTVDLHMNSLRPEDSAVYYCKAFTRGDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 55 (SEQ ID NO: 314)

QVQLQESGGGLVQPGGSLRLSCAASGSIFSINAMGWYRQAPGKQRELVAAITDGGRLTYADSAKNRFTISRENT
RNTVHLQMSSLKAEDTAVYYCTIWKDRQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 57 (SEQ ID NO: 315)

QVQLQESGGGLVQPGGSLRLSCAASGRISNSMGWYRQAPGKQRELVAAITNGGAKTYADSVKGRFTISR
AGNTVYLQMDNLRPEDTAVYYCKAFTRTYDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 61 (SEQ ID NO: 316)

QVQLQESGGGLVQAGGSLRVSCAASGRITLSNYAVAWFRQAPGKQREFVAAINWSSGGISYSNAAKGRFALS
DNAKNTVYLQMDSLKPEDTAVYYCAAASSILSGTVDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 62 (SEQ ID NO: 317)

QVQLQESGGGLVQPGGSLRLSCAASGRIGSINSMGWYRQAPGKQREMVAAITNGGATVYADSVKGRFTISR
AGNTVDLHMNSLRPEDSAVYYCTIWAADYQQYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 66 (SEQ ID NO: 318)

QVQLQESGGGLVQPGGSLRLSCAASRSFFSFNAMGWYRQAPGKQRELVAAITNGGRIAYGTSVMGRFTISR
AKNTVYLQMDSLKPEDTAVYYCNAKPAPVYGSTVGDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 69 (SEQ ID NO: 319)

QVQLQESGGGLVQPGGSPRLSCAASGRFFRVNAMGWYRQAPGKQRELVAAITNGGQTAYADSVKGRFTISR
SAKNTVYLQMNSLKSEDTAVYYCKVFAADGMEYWGKGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 76 (SEQ ID NO: 320)

QVQLQESGGGLVQPGESLRLSCAASGIIFSINAMGWYRQAPGKQRELVAAITNXGRTTYADSVKGRFTISR
NTVTLMNSLKPEDTAVYYCNAFGSGGGVGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 82 (SEQ ID NO: 321)

QVQLQESGGGLVQAGGSLRLSCAASGRITLSNYAVAWFRQAPGKQRELVAAIWWASGGISYANSAGRFVLS
DNAKNTVYLQMDSLKPEDTAVYYCAAASSVLSGTADYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH;

3LEC 89 (SEQ ID NO: 322)

QVQLQESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAAITNQGAPTYADSVKGRFTISR
AGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSSAAAYPYDVPDYGSHHHHHH; or

3LEC 94 (SEQ ID NO: 323)

QVQLQESGGGSVQAGGSLRLSCAASGRITFSSYAMAWFRQAPGMERELVAAISWSGGSTYYADSVKGRFTIS
DNAENTVYLQMNSLKPEDTAVYYCAAEEGSGREGNFYERSWYQGQGTQVTVSSAAAYPYDVPDYGSHHHHH
H.

In various exemplary embodiments, the Clec9A binding agent comprises an amino acid sequence selected from any one of the sequences provided above without the terminal histidine tag sequence (*i.e.*, HHHHHH; SEQ ID NO: 324).

In some embodiments, the Clec9A targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 258-323 (provided above) without the HA tag (*i.e.*, YPYDVPDYGS; SEQ ID NO: 325).

In some embodiments, the Clec9A targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 258-323 (provided above) without the AAA linker (*i.e.*, AAA).

In some embodiments, the Clec9A targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 258-323 (provided above) without the AAA linker, HA tag, and terminal histidine tag sequence (*i.e.*, AAAPYDVPDYGSHHHHHH; SEQ ID NO: 326).

In various exemplary embodiments, the Clec9A binding agent comprises an amino acid sequence selected from the following sequences:

R1CHCL50:

QVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 327);

R1CHCL50_opt1 (E1D-A74S-K83R-Q108L):

DVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 328);

R1CHCL50_opt2 (E1D-A74S-K83R-Q108L-H13Q):

DVQLVESGGGLVQPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 329);

R1CHCL50_opt3 (E1D-A74S-K83R-Q108L-T64K):

DVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVKGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 330);

R1CHCL50_opt4 (E1D-A74S-K83R-Q108L-H13Q-T64K):

DVQLVESGGGLVQPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVKGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 331);

3LEC_89 (wild type):

QVQLQESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
AGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 332);

3LEC_89_opt1 (E1D-Q5V-Q108L):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
AGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 333);

3LEC_89_opt2 (E1D-Q5V-Q108L-A74S):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAAITNQGAPTYADSVKGRFTISRDN
SGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTLVTVSS (SEQ ID NO: 334);

3LEC_89_opt3 (E1D-Q5V-Q108L-G75K):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAAITNQGAPTYADSVKGRFTISRDN
AKNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTLVTVSS (SEQ ID NO: 335); and

3LEC_89_opt4 (E1D-Q5V-Q108L-A74S-G75K):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAAITNQGAPTYADSVKGRFTISRDN
SKNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTLVTVSS (SEQ ID NO: 336).

In an embodiment, the targeting moiety comprises the anti-Clec9A antibody as disclosed in Tullett et al., JCI Insight. 2016;1(7):e87102, the entire disclosures of which are hereby incorporated by reference.

In various embodiments, the present invention contemplates the use of any natural or synthetic analogs, mutants, variants, alleles, homologs and orthologs (herein collectively referred to as "analog") of the Clec9A binding agent of the invention as described herein. In various embodiments, the amino acid sequence of the Clec9A binding agent further includes an amino acid analog, an amino acid derivative, or other non-classical amino acids.

In various embodiments, the Clec9A binding agent comprises a targeting moiety comprising a sequence that is at least 60% identical to any one of the sequences disclosed herein. For example, the Clec9A binding agent may comprise a targeting moiety comprising a sequence that is at least about 60%, at least about 61%, at least about 62%, at least about 63%, at least about 64%, at least about 65%, at least about 66%, at least about 67%, at least about 68%, at least about 69%, at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to any of the sequences disclosed herein (e.g. about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, about 99% or about 100% sequence identity to any one of the sequences disclosed herein, e.g., SEQ ID NOs: 327-336).

In various embodiments, the Clec9A binding agent comprises a targeting moiety comprising an amino acid sequence having one or more amino acid mutations with respect to any one of the sequences disclosed herein. In various embodiments, the Clec9A binding agent comprises a targeting moiety comprising an amino acid sequence

having one, or two, or three, or four, or five, or six, or seven, or eight, or nine, or ten, or fifteen, or twenty amino acid mutations with respect to any one of the sequences disclosed herein. In some embodiments, the one or more amino acid mutations may be independently selected from substitutions, insertions, deletions, and truncations.

In some embodiments, the amino acid mutations are amino acid substitutions, and may include conservative and/or non-conservative substitutions.

"Conservative substitutions" may be made, for instance, on the basis of similarity in polarity, charge, size, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the amino acid residues involved. The 20 naturally occurring amino acids can be grouped into the following six standard amino acid groups: (1) hydrophobic: Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr; Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; and (6) aromatic: Trp, Tyr, Phe.

As used herein, "conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed within the same group of the six standard amino acid groups shown above. For example, the exchange of Asp by Glu retains one negative charge in the so modified polypeptide. In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices.

As used herein, "non-conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed in a different group of the six standard amino acid groups (1) to (6) shown above.

In various embodiments, the substitutions may also include non-classical amino acids. Exemplary non-classical amino acids include, but are not limited to, selenocysteine, pyrrolysine, *N*-formylmethionine β -alanine, GABA and δ -Aminolevulinic acid, 4-aminobenzoic acid (PABA), D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general.

In various embodiments, the amino acid mutation may be in the CDRs of the targeting moiety (e.g., the CDR1, CDR2 or CDR3 regions). In another embodiment, amino acid alteration may be in the framework regions (FRs) of the targeting moiety (e.g., the FR1, FR2, FR3, or FR4 regions).

Modification of the amino acid sequences may be achieved using any known technique in the art e.g., site-directed mutagenesis or PCR based mutagenesis. Such techniques are described, for example, in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., 1989 and Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y., 1989.

In various embodiments, the mutations do not substantially reduce the present Clec9A binding agent's capability to specifically bind to Clec9A. In various embodiments, the mutations do not substantially reduce the present

Clec9A binding agent's capability to specifically bind to Clec9A and without functionally modulating (e.g., partially or fully neutralizing) Clec9A.

In various embodiments, the binding affinity of the Clec9A binding agent of the invention for the full-length and/or mature forms and/or isoforms and/or splice variants and/or fragments and/or monomeric and/or dimeric forms and/or any other naturally occurring or synthetic analogs, variants, or mutants (including monomeric and/or dimeric forms) of human Clec9A may be described by the equilibrium dissociation constant (K_D). In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds to the full-length and/or mature forms and/or isoforms and/or splice variants and/or fragments and/or any other naturally occurring or synthetic analogs, variants, or mutants (including monomeric and/or dimeric forms) of human Clec9A with a K_D of less than about 1 μ M, about 900 nM, about 800 nM, about 700 nM, about 600 nM, about 500 nM, about 400 nM, about 300 nM, about 200 nM, about 100 nM, about 90 nM, about 80 nM, about 70 nM, about 60 nM, about 50 nM, about 40 nM, about 30 nM, about 20 nM, about 10 nM, or about 5 nM, or about 1 nM.

In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds but does not functionally modulate (e.g., partially or fully neutralize) the antigen of interest, *i.e.*, Clec9A. For instance, in various embodiments, the targeting moiety of the Clec9A binding agent simply targets the antigen but does not substantially functionally modulate (e.g. partially or fully inhibit, reduce or neutralize) a biological effect that the antigen has. In various embodiments, the targeting moiety of the Clec9A binding agent binds an epitope that is physically separate from an antigen site that is important for its biological activity (e.g. an antigen's active site).

Such binding without significant function modulation finds use in various embodiments of the present invention, including methods in which the present Clec9A binding agent is used to directly or indirectly recruit active immune cells to a site of need via an effector antigen. For example, in various embodiments, the present Clec9A binding agent may be used to directly or indirectly recruit dendritic cells via Clec9A to a tumor cell in a method of reducing or eliminating a tumor (e.g. the Clec9A binding agent may comprise a targeting moiety having an anti-Clec9A antigen recognition domain and a targeting moiety having a recognition domain (e.g. antigen recognition domain) directed against a tumor antigen or receptor). In such embodiments, it is desirable to directly or indirectly recruit dendritic cells but not to functionally modulate or neutralize the Clec9A activity. In these embodiments, Clec9A signaling is an important piece of the tumor reducing or eliminating effect.

In some embodiments, the Clec9A binding agent enhances antigen-presentation by dendritic cells. For example, in various embodiments, the present Clec9A binding agent directly or indirectly recruits dendritic cells via Clec9A to a tumor cell, where tumor antigens are subsequently endocytosed and presented on the dendritic cell for induction of potent humoral and cytotoxic T cell responses.

In other embodiments (for example, related to treating autoimmune or neurodegenerative disease), the Clec9A binding agent comprises a targeting moiety that binds and neutralizes the antigen of interest, *i.e.*, Clec9A. For instance, in various embodiments, the present methods may inhibit or reduce Clec9A signaling or expression, e.g. to cause a reduction in an immune response.

Therapeutic Agents Comprising the Present Clec9A Binding Agents

Chimeras and Fusions with Signaling Agents

In various embodiments, the Clec9A binding agent of the invention is part of a chimera or fusion with one or more signaling agents. Accordingly, the present invention provides for chimeric or fusion proteins that include, for example, a targeting moiety against Clec9A and one or more signaling agents.

In various embodiments, the signaling agent is modified to have reduced affinity or activity for one or more of its receptors, which allows for attenuation of activity (inclusive of agonism or antagonism) and/or prevents non-specific signaling or undesirable sequestration of the chimeric or fusion protein. In various embodiments, the signaling agent is antagonistic in its wild type form and bears one or more mutations that attenuate its antagonistic activity. In various embodiments, the signaling agent is antagonistic due to one or more mutations, e.g. an agonistic signaling agent is converted to an antagonistic signaling agent and, such a converted signaling agent, optionally, also bears one or more mutations that attenuate its antagonistic activity (e.g. as described in WO 2015/007520, the entire contents of which are hereby incorporated by reference).

Accordingly, in various embodiments, the signaling agent is a modified (e.g. mutant) form of the signaling agent having one or more modifications (e.g. mutations). In various embodiments, the mutations allow for the modified signaling agent to have one or more of attenuated activity such as one or more of reduced binding affinity, reduced endogenous activity, and reduced specific bioactivity relative to unmutated, *i.e.* the wild type form of the signaling agent (e.g. comparing the same signaling agent in a wild type form versus a modified (e.g. mutant) form). In some embodiments, the mutations which attenuate or reduce binding or affinity include those mutations which substantially reduce or ablate binding or activity. In some embodiments, the mutations which attenuate or reduce binding or affinity are different than those mutations which substantially reduce or ablate binding or activity. Consequentially, in various embodiments, the mutations allow for the signaling agent to have improved safety, e.g. reduced systemic toxicity, reduced side effects, and reduced off-target effects relative to unmutated, *i.e.* wild type, signaling agent (e.g. comparing the same signaling agent in a wild type form versus a modified (e.g. mutant) form).

As described herein, the agent may have improved safety due to one of more modifications, e.g. mutations. In various embodiments, improved safety means that the present chimeric protein provides lower toxicity (e.g. systemic toxicity and/or tissue/organ-associated toxicities); and/or lessened or substantially eliminated side effects; and/or increased tolerability, lessened or substantially eliminated adverse events; and/or reduced or substantially eliminated off-target effects; and/or an increased therapeutic window.

In various embodiments, the signaling agent is modified to have one or more mutations that reduce its binding affinity or activity for one or more of its receptors. In some embodiments, the signaling agent is modified to have one or more mutations that substantially reduce or ablate binding affinity or activity for the receptors. In some embodiments, the activity provided by the wild type signaling agent is agonism at the receptor (e.g. activation of a cellular effect at a site of therapy). For example, the wild type signaling agent may activate its receptor. In such embodiments, the mutations result in the modified signaling agent to have reduced or ablated activating activity at

the receptor. For example, the mutations may result in the modified signaling agent to deliver a reduced activating signal to a target cell or the activating signal could be ablated. In some embodiments, the activity provided by the wild type signaling agent is antagonism at the receptor (e.g. blocking or dampening of a cellular effect at a site of therapy). For example, the wild type signaling agent may antagonize or inhibit the receptor. In these embodiments, the mutations result in the modified signaling agent to have a reduced or ablated antagonizing activity at the receptor. For example, the mutations may result in the modified signaling agent to deliver a reduced inhibitory signal to a target cell or the inhibitory signal could be ablated. In various embodiments, the signaling agent is antagonistic due to one or more mutations, e.g. an agonistic signaling agent is converted to an antagonistic signaling agent (e.g. as described in WO 2015/007520, the entire contents of which are hereby incorporated by reference) and, such a converted signaling agent, optionally, also bears one or mutations that reduce its binding affinity or activity for one or more of its receptors or that substantially reduce or ablate binding affinity or activity for one or more of its receptors.

In some embodiments, the reduced affinity or activity at the receptor is restorable by attachment with one or more of the targeting moieties as described herein (e.g., targeting moiety against Clec9A). In other embodiments, the reduced affinity or activity at the receptor is not substantially restorable by the activity of one or more of the targeting moieties.

In various embodiments, the chimeric proteins of the present invention reduce off-target effects because their signaling agents have mutations that weaken or ablate binding affinity or activity at a receptor. In various embodiments, this reduction in side effects is observed relative with, for example, the wild type signaling agents. In various embodiments, the signaling agent is active on target cells because the targeting moiety(ies) compensates for the missing/insufficient binding (e.g., without limitation and/or avidity) required for substantial activation. In various embodiments, the modified signaling agent is substantially inactive *en route* to the site of therapeutic activity and has its effect substantially on specifically targeted cell types which greatly reduces undesired side effects.

In some embodiments, the signaling agent may include one or more mutations that attenuate or reduce binding or affinity for one receptor (*i.e.*, a therapeutic receptor) and one or more mutations that substantially reduce or ablate binding or activity at a second receptor. In such embodiments, these mutations may be at the same or at different positions (*i.e.*, the same mutation or multiple mutations). In some embodiments, the mutation(s) that reduce binding and/or activity at one receptor is different than the mutation(s) that substantially reduce or ablate at another receptor. In some embodiments, the mutation(s) that reduce binding and/or activity at one receptor is the same as the mutation(s) that substantially reduce or ablate at another receptor. In some embodiments, the present chimeric proteins have a modified signaling agent that has both mutations that attenuate binding and/or activity at a therapeutic receptor and therefore allow for a more controlled, on-target therapeutic effect (e.g. relative wild type signaling agent) and mutations that substantially reduce or ablate binding and/or activity at another receptor and therefore reduce side effects (e.g. relative to wild type signaling agent).

In some embodiments, the substantial reduction or ablation of binding or activity is not substantially restorable with a targeting moiety (e.g., a targeting moiety against Clec9A or any other targeting moiety described herein). In some embodiments, the substantial reduction or ablation of binding or activity is restorable with a targeting moiety. In various embodiments, substantially reducing or ablating binding or activity at a second receptor also may prevent deleterious effects that are mediated by the other receptor. Alternatively, or in addition, substantially reducing or ablating binding or activity at the other receptor causes the therapeutic effect to improve as there is a reduced or eliminated sequestration of the therapeutic chimeric proteins away from the site of therapeutic action. For instance, in some embodiments, this obviates the need of high doses of the present chimeric proteins that compensate for loss at the other receptor. Such ability to reduce dose further provides a lower likelihood of side effects.

In various embodiments, the modified signaling agent comprises one or more mutations that cause the signaling agent to have reduced, substantially reduced, or ablated affinity, e.g. binding (e.g. K_D) and/or activation (for instance, when the modified signaling agent is an agonist of its receptor, measurable as, for example, K_A and/or EC_{50}) and/or inhibition (for instance, when the modified signaling agent is an antagonist of its receptor, measurable as, for example, K_I and/or IC_{50}), for one or more of its receptors. In various embodiments, the reduced affinity at the immunomodulating agent's receptor allows for attenuation of activity (inclusive of agonism or antagonism). In such embodiments, the modified signaling agent has about 1%, or about 3%, about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or about 10%-20%, about 20%-40%, about 50%, about 40%-60%, about 60%-80%, about 80%-100% of the affinity for the receptor relative to the wild type signaling agent. In some embodiments, the binding affinity is at least about 2-fold lower, about 3-fold lower, about 4-fold lower, about 5-fold lower, about 6-fold lower, about 7-fold lower, about 8-fold lower, about 9-fold lower, at least about 10-fold lower, at least about 15-fold lower, at least about 20-fold lower, at least about 25-fold lower, at least about 30-fold lower, at least about 35-fold lower, at least about 40-fold lower, at least about 45-fold lower, at least about 50-fold lower, at least about 100-fold lower, at least about 150-fold lower, or about 10-50-fold lower, about 50-100-fold lower, about 100-150-fold lower, about 150-200-fold lower, or more than 200-fold lower relative to the wild type signaling agent.

In embodiments wherein the modified signaling agent has mutations that reduce binding at one receptor and substantially reduce or ablate binding at a second receptor, the attenuation or reduction in binding affinity of a modified signaling agent for one receptor is less than the substantial reduction or ablation in affinity for the other receptor. In some embodiments, the attenuation or reduction in binding affinity of a modified signaling agent for one receptor is less than the substantial reduction or ablation in affinity for the other receptor by about 1%, or about 3%, about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In various embodiments, substantial reduction or ablation refers to a greater reduction in binding affinity and/or activity than attenuation or reduction.

In various embodiments, the modified signaling agent comprises one or more mutations that reduce the endogenous activity of the signaling agent to about 75%, or about 70%, or about 60%, or about 50%, or about 40%, or about 30%, or about 25%, or about 20%, or about 10%, or about 5%, or about 3%, or about 1%, e.g., relative to the wild type signaling agent.

In some embodiments, the modified signaling agent comprises one or more mutations that cause the signaling agent to have reduced affinity for its receptor that is lower than the binding affinity of the targeting moiety(ies) for its(their) receptor(s). In some embodiments, this binding affinity differential is between signaling agent/receptor and targeting moiety/receptor on the same cell. In some embodiments, this binding affinity differential allows for the signaling agent, e.g. mutated signaling agent, to have localized, on-target effects and to minimize off-target effects that underlie side effects that are observed with wild type signaling agent. In some embodiments, this binding affinity is at least about 2-fold, or at least about 5-fold, or at least about 10-fold, or at least about 15-fold lower, or at least about 25-fold, or at least about 50-fold lower, or at least about 100-fold, or at least about 150-fold.

Receptor binding activity may be measured using methods known in the art. For example, affinity and/or binding activity may be assessed by Scatchard plot analysis and computer-fitting of binding data (e.g. Scatchard, 1949) or by reflectometric interference spectroscopy under flow through conditions, as described by Brecht *et al.* (1993), the entire contents of all of which are hereby incorporated by reference.

In various embodiments, the signaling agent is an immune-modulating agent, e.g. one or more of an interleukin, interferon, and tumor necrosis factor.

In some embodiments, the signaling agent is an interleukin or a modified interleukin, including for example IL-1; IL-2; IL-3; IL-4; IL-5; IL-6; IL-7; IL-8; IL-9; IL-10; IL-11; IL-12; IL-13; IL-14; IL-15; IL-16; IL-17; IL-18; IL-19; IL-20; IL-21; IL-22; IL-23; IL-24; IL-25; IL-26; IL-27; IL-28; IL-29; IL-30; IL-31; IL-32; IL-33; IL-35; IL-36 or a fragment, variant, analogue, or family-member thereof. Interleukins are a group of multi- functional cytokines synthesized by lymphocytes, monocytes, and macrophages. Known functions include stimulating proliferation of immune cells (e.g., T helper cells, B cells, eosinophils, and lymphocytes), chemotaxis of neutrophils and T lymphocytes, and/or inhibition of interferons. Interleukin activity can be determined using assays known in the art: Matthews *et al.*, in *Lymphokines and Interferens: A Practical Approach*, Clemens *et al.*, eds, IRL Press, Washington, D.C. 1987, pp. 221-225; and Orencole & Dinarello (1989) Cytokine 1, 14-20.

In some embodiments, the signaling agent is an interferon or a modified version of an interferon such as interferon types I, II, and III. Illustrative interferons, including for example, interferon- α -1, 2, 4, 5, 6, 7, 8, 10, 13, 14, 16, 17, and 21, interferon- β and interferon- γ , interferon κ , interferon ϵ , interferon τ , and interferon ω .

In some embodiments, the signaling agent is a tumor necrosis factor (TNF) or a modified version of a tumor necrosis factor (TNF) or a protein in the TNF family, including but not limited to, TNF- α , TNF- β , LT- β , CD40L, CD27L, CD30L, FASL, 4-1BBL, OX40L, and TRAIL.

The amino acid sequences of the wild type signaling agents described herein are well known in the art. Accordingly, in various embodiments the modified signaling agent comprises an amino acid sequence that has at least about 60%, or at least about 61%, or at least about 62%, or at least about 63%, or at least about 64%, or at least about 65%, or at least about 66%, or at least about 67%, or at least about 68%, or at least about 69%, or at least about 70%, or at least about 71%, or at least about 72%, or at least about 73%, or at least about 74%, or at least about 75%, or at least about 76%, or at least about 77%, or at least about 78%, or at least about 79%, or at least about 80%, or at least about 81%, or at least about 82%, or at least about 83%, or at least about 84%, or at least about 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 89%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the known wild type amino acid sequences of the signaling agents described herein (e.g. about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity).

In various embodiments the modified signaling agent comprises an amino acid sequence that has at least about 60%, or at least about 61%, or at least about 62%, or at least about 63%, or at least about 64%, or at least about 65%, or at least about 66%, or at least about 67%, or at least about 68%, or at least about 69%, or at least about 70%, or at least about 71%, or at least about 72%, or at least about 73%, or at least about 74%, or at least about 75%, or at least about 76%, or at least about 77%, or at least about 78%, or at least about 79%, or at least about 80%, or at least about 81%, or at least about 82%, or at least about 83%, or at least about 84%, or at least about 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 89%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with any amino acid sequences of the signaling agents described herein (e.g. about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity).

In various embodiments, the modified signaling agent comprises an amino acid sequence having one or more amino acid mutations. In some embodiments, the one or more amino acid mutations may be independently selected from substitutions, insertions, deletions, and truncations. In some embodiments, the amino acid mutations

are amino acid substitutions, and may include conservative and/or non-conservative substitutions, as described elsewhere herein. In various embodiments, the substitutions may also include non-classical amino acids as described elsewhere herein.

As described herein, the modified signaling agents bear mutations that affect affinity and/or activity at one or more receptors. In various embodiments, there is reduced affinity and/or activity at a therapeutic receptor, *e.g.* a receptor through which a desired therapeutic effect is mediated (*e.g.* agonism or antagonism). In various embodiments, the modified signaling agents bear mutations that substantially reduce or ablate affinity and/or activity at a receptor, *e.g.* a receptor through which a desired therapeutic effect is not mediated (*e.g.* as the result of promiscuity of binding). The receptors of any modified signaling agents, *e.g.* one of the cytokines, growth factors, and hormones as described herein, are known in the art.

Illustrative mutations which provide reduced affinity and/or activity (*e.g.* agonistic) at a receptor are found in WO 2013/107791 and PCT/EP2017/061544 (*e.g.* with regard to interferons), WO 2015/007542 (*e.g.* with regard to interleukins), and WO 2015/007903 (*e.g.* with regard to TNF), the entire contents of each of which are hereby incorporated by reference. Illustrative mutations which provide reduced affinity and/or activity (*e.g.* antagonistic) at a therapeutic receptor are found in WO 2015/007520, the entire contents of which are hereby incorporated by reference.

In some embodiments, the modified signaling agent comprises one or more mutations that cause the signaling agent to have reduced affinity and/or activity for a type I cytokine receptor, a type II cytokine receptor, a chemokine receptor, a receptor in the Tumor Necrosis Factor Receptor (TNFR) superfamily, TGF-beta Receptors, a receptor in the immunoglobulin (Ig) superfamily, and/or a receptor in the tyrosine kinase superfamily.

In various embodiments, the receptor for the signaling agent is a Type I cytokine receptor. Type I cytokine receptors are known in the art and include, but are not limited to receptors for IL2 (beta-subunit), IL3, IL4, IL5, IL6, IL7, IL9, IL11, IL12, GM-CSF, G-CSF, LIF, CNTF, and also the receptors for Thrombopoietin (TPO), Prolactin, and Growth hormone. Illustrative type I cytokine receptors include, but are not limited to, GM-CSF receptor, G-CSF receptor, LIF receptor, CNTF receptor, TPO receptor, and type I IL receptors.

In various embodiments, the receptor for the signaling agent is a Type II cytokine receptor. Type II cytokine receptors are multimeric receptors composed of heterologous subunits, and are receptors mainly for interferons. This family of receptors includes, but is not limited to, receptors for interferon- α , interferon- β and interferon- γ , IL10, IL22, and tissue factor. Illustrative type II cytokine receptors include, but are not limited to, IFN- α receptor (*e.g.* IFNAR1 and IFNAR2), IFN- β receptor, IFN- γ receptor (*e.g.* IFNGR1 and IFNGR2), and type II IL receptors.

In various embodiments, the receptor for the signaling agent is a G protein-coupled receptor. Chemokine receptors are G protein-coupled receptors with seven transmembrane structure and coupled to G-protein for signal transduction. Chemokine receptors include, but are not limited to, CC chemokine receptors, CXC chemokine receptors, CX3C chemokine receptors, and XC chemokine receptor (XCR1). Exemplary chemokine receptors

include, but are not limited to, CCR1, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CCR10, CXCR1, CXCR2, CXCR3, CXCR3B, CXCR4, CXCR5, CSCR6, CXCR7, XCR1, and CX3CR1.

In various embodiments, the receptor for the signaling agent is a TNFR family member. Tumor necrosis factor receptor (TNFR) family members share a cysteine-rich domain (CRD) formed of three disulfide bonds surrounding a core motif of CXXCXXC creating an elongated molecule. Exemplary tumor necrosis factor receptor family members include: CDI 20a (TNFRSF1A), CD 120b (TNFRSF1B), Lymphotoxin beta receptor (LTBR, TNFRSF3), CD 134 (TNFRSF4), CD40 (CD40, TNFRSF5), FAS (FAS, TNFRSF6), TNFRSF6B (TNFRSF6B), CD27 (CD27, TNFRSF7), CD30 (TNFRSF8), CD137 (TNFRSF9), TNFRSF10A (TNFRSF10A), TNFRSF10B, (TNFRSF10B), TNFRSF10C (TNFRSF10C), TNFRSF10D (TNFRSF10D), RANK (TNFRSF1A), Osteoprotegerin (TNFRSF1B), TNFRSF12A (TNFRSF12A), TNFRSF13B (TNFRSF13B), TNFRSF13C (TNFRSF13C), TNFRSF14 (TNFRSF14), Nerve growth factor receptor (NGFR, TNFRSF16), TNFRSF17 (TNFRSF17), TNFRSF18 (TNFRSF18), TNFRSF19 (TNFRSF19), TNFRSF21 (TNFRSF21), and TNFRSF25 (TNFRSF25). In an embodiment, the TNFR family member is CD120a (TNFRSF1A) or TNF-R1. In another embodiment, the TNFR family member is CD 120b (TNFRSF1B) or TNF-R2.

In various embodiments, the receptor for the signaling agent is a TGF-beta receptor. TGF-beta receptors are single pass serine/threonine kinase receptors. TGF-beta receptors include, but are not limited to, TGFBR1, TGFBR2, and TGFBR3.

In various embodiments, the receptor for the signaling agent is an Ig superfamily receptor. Receptors in the immunoglobulin (Ig) superfamily share structural homology with immunoglobulins. Receptors in the Ig superfamily include, but are not limited to, interleukin-1 receptors, CSF-1R, PDGFR (e.g. PDGFRA and PDGFRB), and SCFR.

In various embodiments, the receptor for the signaling agent is a tyrosine kinase superfamily receptor. Receptors in the tyrosine kinase superfamily are well known in the art. There are about 58 known receptor tyrosine kinases (RTKs), grouped into 20 subfamilies. Receptors in the tyrosine kinase superfamily include, but are not limited to, FGF receptors and their various isoforms such as FGFR1, FGFR2, FGFR3, FGFR4, and FGFR5.

In an embodiment, the modified signaling agent is interferon α . In such embodiments, the modified IFN- α agent has reduced affinity and/or activity for the IFN- α/β receptor (IFNAR), *i.e.*, IFNAR1 and/or IFNAR2 chains. In some embodiments, the modified IFN- α agent has substantially reduced or ablated affinity and/or activity for the IFN- α/β receptor (IFNAR), *i.e.*, IFNAR1 and/or IFNAR2 chains.

Mutant forms of interferon α are known to the person skilled in the art. In an illustrative embodiment, the modified signaling agent is the allelic form IFN- α 2a having the amino acid sequence of SEQ ID NO: 337.

In an illustrative embodiment, the modified signaling agent is the allelic form IFN- α 2b having the amino acid sequence of (which differs from IFN- α 2a at amino acid position 23) SEQ ID NO: 338.

In some embodiments, said IFN- α 2 mutant (IFN- α 2a or IFN- α 2b) is mutated at one or more amino acids at positions 144-154, such as amino acid positions 148, 149 and/or 153. In some embodiments, the IFN- α 2 mutant comprises

one or more mutations selected from L153A, R149A, and M148A. Such mutants are described, for example, in WO2013/107791 and Piehler *et al.*, (2000) J. Biol. Chem, 275:40425-33, the entire contents of all of which are hereby incorporated by reference.

In some embodiments, the IFN- α 2 mutants have reduced affinity and/or activity for IFNAR1. In some embodiments, the IFN- α 2 mutant comprises one or more mutations selected from F64A, N65A, T69A, L80A, Y85A, and Y89A, as described in WO2010/030671, the entire contents of which is hereby incorporated by reference.

In some embodiments, the IFN- α 2 mutant comprises one or more mutations selected from K133A, R144A, R149A, and L153A as described in WO2008/124086, the entire contents of which is hereby incorporated by reference.

In some embodiments, the IFN- α 2 mutant comprises one or more mutations selected from R120E and R120E/K121E, as described in WO2015/007520 and WO2010/030671, the entire contents of which are hereby incorporated by reference. In such embodiments, said IFN- α 2 mutant antagonizes wild type IFN- α 2 activity. In such embodiments, said mutant IFN- α 2 has reduced affinity and/or activity for IFNAR1 while affinity and/or activity of IFNAR2 is retained.

In some embodiments, the human IFN- α 2 mutant comprises (1) one or more mutations selected from R120E and R120E/K121E, which, without wishing to be bound by theory, create an antagonistic effect and (2) one or more mutations selected from K133A, R144A, R149A, and L153A, which, without wishing to be bound by theory, allow for an attenuated effect at, for example, IFNAR2. In an embodiment, the human IFN- α 2 mutant comprises R120E and L153A.

In some embodiments, the human IFN- α 2 mutant comprises one or more mutations selected from, L15A, A19W, R22A, R23A, L26A, F27A, L30A, L30V, K31A, D32A, R33K, R33A, R33Q, H34A, D35A, Q40A, D114R, L117A, R120A, R125A, K134A, R144A, A145G, A145M, M148A, R149A, S152A, L153A, and N156A as disclosed in WO 2013/059885, the entire disclosures of which are hereby incorporated by reference. In some embodiments, the human IFN- α 2 mutant comprises the mutations H57Y, E58N, Q61S, and/or L30A as disclosed in WO 2013/059885. In some embodiments, the human IFN- α 2 mutant comprises the mutations H57Y, E58N, Q61S, and/or R33A as disclosed in WO 2013/059885. In some embodiments, the human IFN- α 2 mutant comprises the mutations H57Y, E58N, Q61S, and/or M148A as disclosed in WO 2013/059885. In some embodiments, the human IFN- α 2 mutant comprises the mutations H57Y, E58N, Q61S, and/or L153A as disclosed in WO 2013/059885. In some embodiments, the human IFN- α 2 mutant comprises the mutations N65A, L80A, Y85A, and/or Y89A as disclosed in WO 2013/059885. In some embodiments, the human IFN- α 2 mutant comprises the mutations N65A, L80A, Y85A, Y89A, and/or D114A as disclosed in WO 2013/059885.

In an embodiment, the modified signaling agent is interferon β . In such embodiments, the modified interferon β agent has reduced affinity and/or activity for the IFN- α/β receptor (IFNAR), *i.e.*, IFNAR1 and/or IFNAR2 chains. In some embodiments, the modified interferon β agent has substantially reduced or ablated affinity and/or activity for the IFN- α/β receptor (IFNAR), *i.e.*, IFNAR1 and/or IFNAR2 chains.

In an illustrative embodiment, the modified signaling agent is IFN- β . In various embodiments, the IFN- β encompasses functional derivatives, analogs, precursors, isoforms, splice variants, or fragments of IFN- β . In various embodiments, the IFN- β encompasses IFN- β derived from any species. In an embodiment, the chimeric protein comprises a modified version of mouse IFN- β . In another embodiment, the chimeric protein comprises a modified version of human IFN- β . Human IFN- β is a polypeptide with a molecular weight of about 22 kDa comprising 166 amino acid residues. The amino acid sequence of human IFN- β is SEQ ID NO: 339.

In some embodiments, the human IFN- β is IFN- β -1a which is a glycosylated form of human IFN- β . In some embodiments, the human IFN- β is IFN- β -1b which is a non-glycosylated form of human IFN- β that has a Met-1 deletion and a Cys-17 to Ser mutation.

In various embodiments, the modified IFN- β has one or more mutations that reduce its binding to or its affinity for the IFNAR1 subunit of IFNAR. In one embodiment, the modified IFN- β has reduced affinity and/or activity at IFNAR1. In various embodiments, the modified IFN- β is human IFN- β and has one or more mutations at positions F67, R71, L88, Y92, I95, N96, K123, and R124. In some embodiments, the one or more mutations are substitutions selected from F67G, F67S, R71A, L88G, L88S, Y92G, Y92S, I95A, N96G, K123G, and R124G. In an embodiment, the modified IFN- β comprises the F67G mutation. In an embodiment, the modified IFN- β comprises the K123G mutation. In an embodiment, the modified IFN- β comprises the F67G and R71A mutations. In an embodiment, the modified IFN- β comprises the L88G and Y92G mutations. In an embodiment, the modified IFN- β comprises the Y92G, I95A, and N96G mutations. In an embodiment, the modified IFN- β comprises the K123G and R124G mutations. In an embodiment, the modified IFN- β comprises the F67G, L88G, and Y92G mutations. In an embodiment, the modified IFN- β comprises the F67S, L88S, and Y92S mutations.

In some embodiments, the modified IFN- β has one or more mutations that reduce its binding to or its affinity for the IFNAR2 subunit of IFNAR. In one embodiment, the modified IFN- β has reduced affinity and/or activity at IFNAR2. In various embodiments, the modified IFN- β is human IFN- β and has one or more mutations at positions W22, R27, L32, R35, V148, L151, R152, and Y155. In some embodiments, the one or more mutations are substitutions selected from W22G, R27G, L32A, L32G, R35A, R35G, V148G, L151G, R152A, R152G, and Y155G. In an embodiment, the modified IFN- β comprises the W22G mutation. In an embodiment, the modified IFN- β comprises the L32A mutation. In an embodiment, the modified IFN- β comprises the L32G mutation. In an embodiment, the modified IFN- β comprises the R35A mutation. In an embodiment, the modified IFN- β comprises the R35G mutation. In an embodiment, the modified IFN- β comprises the V148G mutation. In an embodiment, the modified IFN- β comprises the R152A mutation. In an embodiment, the modified IFN- β comprises the R152G mutation. In an embodiment, the modified IFN- β comprises the Y155G mutation. In an embodiment, the modified IFN- β comprises the W22G and R27G mutations. In an embodiment, the modified IFN- β comprises the L32A and R35A mutation. In an embodiment, the modified IFN- β comprises the L151G and R152A mutations. In an embodiment, the modified IFN- β comprises the V148G and R152A mutations.

In some embodiments, the modified IFN- β has one or more of the following mutations: R35A, R35T, E42K, M62I, G78S, A141Y, A142T, E149K, and R152H. In some embodiments, the modified IFN- β has one or more of the following mutations: R35A, R35T, E42K, M62I, G78S, A141Y, A142T, E149K, and R152H in combination with C17S or C17A.

In some embodiments, the modified IFN- β has one or more of the following mutations: R35A, R35T, E42K, M62I, G78S, A141Y, A142T, E149K, and R152H in combination with any of the other IFN- β mutations described herein.

The crystal structure of human IFN- β is known and is described in Karpusas et al., (1998) PNAS, 94(22): 11813–11818. Specifically, the structure of human IFN- β has been shown to include five α -helices (*i.e.*, A, B, C, D, and E) and four loop regions that connect these helices (*i.e.*, AB, BC, CD, and DE loops). In various embodiments, the modified IFN- β has one or more mutations in the A, B, C, D, E helices and/or the AB, BC, CD, and DE loops which reduce its binding affinity or activity at a therapeutic receptor such as IFNAR. Exemplary mutations are described in WO2000/023114 and US20150011732, the entire contents of which are hereby incorporated by reference. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 15, 16, 18, 19, 22, and/or 23. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 28-30, 32, and 33. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 36, 37, 39, and 42. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 64 and 67 and a serine substitution at position 68. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 71-73. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 92, 96, 99, and 100. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 128, 130, 131, and 134. In an exemplary embodiment, the modified IFN- β is human IFN- β comprising alanine substitutions at amino acid positions 149, 153, 156, and 159. In some embodiments, the mutant IFN β comprises 339 and a mutation at W22, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at R27, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at W22, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at R27, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L32, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at R35, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L32, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V) and a mutation at R35, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at F67, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at R71, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at F67, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at R71, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L88, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at F67, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at L88, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V) and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L88, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V) and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at I95, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), methionine (M), and valine (V).

and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at N96, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at Y92, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at I95, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), methionine (M), and valine (V) and a mutation at N96, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at K123, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at R124, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at K123, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at R124, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L151, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at R152, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at L151, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), isoleucine (I), methionine (M), and valine (V) and a mutation at R152, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at V148, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), and methionine (M).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at V148, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V) and a mutation at R152, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the mutant IFN β comprises SEQ ID NO: 339 and a mutation at Y155, the mutation being an aliphatic hydrophobic residue selected from glycine (G), alanine (A), leucine (L), isoleucine (I), methionine (M), and valine (V).

In some embodiments, the present invention relates to a chimeric protein comprising: (a) a modified IFN- β , having the amino acid sequence of SEQ ID NO: 339 and a mutation at position W22, wherein the mutation is an aliphatic hydrophobic residue; and (b) one or more targeting moieties, said targeting moieties comprising recognition domains which specifically bind to antigens or receptors of interest (e.g., Clec9A), the modified IFN- β and the one or more targeting moieties are optionally connected with one or more linkers. In various embodiments the mutation at position W22 is aliphatic hydrophobic residue is selected from G, A, L, I, M, and V. In various embodiments the mutation at position W22 is G.

Additional exemplary IFN β mutants are provided in PCT/EP2017/061544, the entire disclosure of which is incorporated by reference herein.

In an embodiment, the modified signaling agent is interferon γ . In such embodiments, the modified interferon γ agent has reduced affinity and/or activity for the interferon-gamma receptor (IFNGR), *i.e.*, IFNGR1 and IFNGR2 chains. In some embodiments, the modified interferon γ agent has substantially reduced or ablated affinity and/or activity for the interferon-gamma receptor (IFNGR), *i.e.*, IFNGR1 and/or IFNGR2 chains.

IFN- γ is the only member of the type II class of interferons. IFN- γ is produced predominantly by natural killer (NK) and natural killer T (NKT) cells as part of the innate immune response. IFN- γ is also produced by CD4 Th1 and CD8 cytotoxic T lymphocyte (CTL) effector T cells, macrophages, dendritic cells, and B cells. Activated IFN- γ forms a dimer which acts through a heterodimeric receptor (*i.e.*, IFN- γ receptor or IFN- γ R) composed of IFN- γ receptor 1 and IFN- γ receptor 2 subunits. IFN- γ receptor 1 is the major ligand-binding subunit, while IFN- γ receptor 2 is necessary for signal transduction and also increases the affinity of IFN- γ receptor 1 for its ligand. Binding of the IFN- γ dimer to the receptor activates the JAK-STAT signaling pathway to elicit various biological effects.

In various embodiments, the the modified signaling agent comprises a modified version of IFN- γ as a signaling agent. In various embodiments, the IFN- γ encompasses functional derivatives, analogs, precursors, isoforms, splice variants, or fragments of IFN- γ . In various embodiments, the IFN- γ encompasses IFN- γ derived from any

species. In an embodiment, the modified signaling agent comprises a modified version of mouse IFN- γ . In another embodiment, the modified signaling agent comprises a modified version of human IFN- γ .

Human IFN- γ is a polypeptide comprising 166 amino acid residues. In an embodiment, the human IFN- γ has the amino acid sequence of SEQ ID NO: 340, in which the signal peptide comprises the first 23 amino acids.

As used herein, human IFN- γ may also refer to mature human IFN- γ without the N-terminal signal peptide. In this embodiment, the mature human IFN- γ comprises 143 amino acids and has the amino acid sequence of SEQ ID NO: 341.

In some embodiments, the human IFN- γ is a glycosylated form of human IFN- γ . In some embodiments, the human IFN- γ is a non-glycosylated form of human IFN- γ .

The sequences of IFN- γ are known in the art. In various embodiments the modified IFN- γ comprises an amino acid sequence that has at least about 60%, or at least about 61%, or at least about 62%, or at least about 63%, or at least about 64%, or at least about 65%, or at least about 66%, or at least about 67%, or at least about 68%, or at least about 69%, or at least about 70%, or at least about 71%, or at least about 72%, or at least about 73%, or at least about 74%, or at least about 75%, or at least about 76%, or at least about 77%, or at least about 78%, or at least about 79%, or at least about 80%, or at least about 81%, or at least about 82%, or at least about 83%, or at least about 84%, or at least about 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 89%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the known wild type amino acid sequences of IFN- γ (e.g., about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity).

In some embodiments the modified IFN- γ comprises an amino acid sequence that has at least about 60%, or at least about 61%, or at least about 62%, or at least about 63%, or at least about 64%, or at least about 65%, or at least about 66%, or at least about 67%, or at least about 68%, or at least about 69%, or at least about 70%, or at least about 71%, or at least about 72%, or at least about 73%, or at least about 74%, or at least about 75%, or at least about 76%, or at least about 77%, or at least about 78%, or at least about 79%, or at least about 80%, or at least about 81%, or at least about 82%, or at least about 83%, or at least about 84%, or at least about 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 89%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with human IFN- γ having an amino acid sequence of SEQ ID NO: 340 (e.g., about 60%, or about 61%, or about 62%, or about

63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity).

In some embodiments the modified IFN- γ comprises an amino acid sequence that has at least about 60%, or at least about 61%, or at least about 62%, or at least about 63%, or at least about 64%, or at least about 65%, or at least about 66%, or at least about 67%, or at least about 68%, or at least about 69%, or at least about 70%, or at least about 71%, or at least about 72%, or at least about 73%, or at least about 74%, or at least about 75%, or at least about 76%, or at least about 77%, or at least about 78%, or at least about 79%, or at least about 80%, or at least about 81%, or at least about 82%, or at least about 83%, or at least about 84%, or at least about 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 89%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with human IFN- γ having an amino acid sequence of SEQ ID NO: 341 (e.g., about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity).

In various embodiments, the modified IFN- γ comprises an amino acid sequence having one or more amino acid mutations. In some embodiments, the one or more amino acid mutations may be independently selected from substitutions, insertions, deletions, and truncations.

In some embodiments, the amino acid mutations are amino acid substitutions, and may include conservative and/or non-conservative substitutions.

"Conservative substitutions" may be made, for instance, on the basis of similarity in polarity, charge, size, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the amino acid residues involved. The 20 naturally occurring amino acids can be grouped into the following six standard amino acid groups: (1) hydrophobic: Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; and (6) aromatic: Trp, Tyr, Phe.

As used herein, "conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed within the same group of the six standard amino acid groups shown above. For example, the exchange of Asp by Glu retains one negative charge in the so modified polypeptide. In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices.

As used herein, "non-conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed in a different group of the six standard amino acid groups (1) to (6) shown above.

In various embodiments, the substitutions may also include non-classical amino acids (e.g., selenocysteine, pyrrolysine, N-formylmethionine β -alanine, GABA and δ -Aminolevulinic acid, 4-aminobenzoic acid (PABA), D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general).

In various embodiments, the IFN- γ is modified to have one or more mutations. In some embodiments, the mutations allow for the modified IFN- γ to have one or more of attenuated activity such as one or more of reduced binding affinity, reduced endogenous activity, and reduced specific bioactivity relative to unmutated, e.g., the wild type form of IFN- γ . For instance, the one or more of attenuated activity such as reduced binding affinity, reduced endogenous activity, and reduced specific bioactivity relative to unmutated, e.g., the wild type form of IFN- γ may be at a therapeutic receptor such as the IFN- γ receptor. Consequentially, in various embodiments, the mutations allow for the modified soluble agent to have reduced systemic toxicity, reduced side effects, and reduced off-target effects relative to unmutated, e.g., the wild type form of IFN- γ .

In various embodiments, the IFN- γ is modified to have a mutation that reduces its binding affinity and/or activity at a therapeutic receptor such as the IFN- γ receptor comprising the IFN- γ receptor 1 and IFN- γ receptor 2 subunits. In some embodiments, the activity provided by the wild type IFN- γ is agonism at the therapeutic receptor (e.g., activation of a cellular effect at a site of therapy). For example, the wild type IFN- γ may activate the therapeutic receptor. In such embodiments, the mutation results in the modified IFN- γ to have reduced activating activity at the therapeutic receptor.

In some embodiments, the reduced affinity and/or activity at the therapeutic receptor (e.g., IFN- γ receptor) is restorable by attachment with a targeting moiety. In other embodiments, the reduced affinity and/or activity at the therapeutic receptor is not substantially restorable by attachment with the targeting moiety. In various embodiments, the therapeutic chimeric proteins of the present invention reduce off-target effects because the IFN- γ has mutations that weaken binding affinity and/or activity at a therapeutic receptor. In various embodiments, this reduces side effects observed with, for example, the wild type IFN- γ . In various embodiments, the modified IFN- γ is substantially inactive en route to the site of therapeutic activity and has its effect substantially on specifically targeted cell types which greatly reduces undesired side effects.

In various embodiments, the modified IFN- γ has one or more mutations that cause the IFN- γ to have attenuated or reduced affinity and/or activity, e.g., binding (e.g., KD) and/or activation (measurable as, for example, KA and/or EC50) for one or more therapeutic receptors (e.g., IFN- γ receptor). In various embodiments, the reduced affinity

and/or activity at the therapeutic receptor allows for attenuation of activity and/or signaling from the therapeutic receptor.

In various embodiments, the modified IFN- γ has one or more mutations that reduce its binding to or its affinity for and/or biological activity for the IFN- γ receptor 1 subunit. In one embodiment, the modified IFN- γ has reduced affinity and/or activity at the IFN- γ receptor 1 subunit. In various embodiments, the modified IFN- γ is human IFN- γ that has one or more mutations at amino acid residues involved with binding to the IFN- γ receptor 1 subunit. In some embodiments, the modified IFN- γ is human IFN- γ that has one or more mutations at amino acids located at the interface with the IFN- γ receptor 1 subunit. In various embodiments, the one or more mutations are at amino acids selected from, but not limited to Q1, V5, E9, K12, H19, S20, V22, A23, D24, N25, G26, T27, L30, K108, H111, E112, I114, Q115, A118, E119, and K125 (each with respect SEQ ID NO: 341, which is a wild type human IFN- γ and which lacks its N-terminal signal sequence). In some embodiments, the one or more mutations are substitutions selected from V5E, S20E, V22A, A23G, A23F, D24G, G26Q, H111A, H111D, I114A, Q115A, and A118G (each with respect SEQ ID NO: 341). In embodiments, the one or more mutations are substitutions selected from V22A, A23G, D24G, H111A, H111D, I114A, Q115A, and A118G.

In an embodiment, the modified IFN- γ comprises the mutations A23G and D24G. In another embodiment, the modified IFN- γ comprises the mutations I114A and A118G. In a further embodiment, the modified IFN- γ comprises the mutations V5E, S20E, A23F, and G26Q.

In various embodiments, the modified IFN- γ has one or more of the following mutations: deletion of residue A23, deletion of residue D24, an S20I substitution, an A23V substitution, a D21K substitution and a D24A substitution.

In some embodiments, the modified IFN- γ has one or more mutations that reduce its binding to or its affinity and/or biological activity for the IFN- γ receptor 2 subunit.

In some embodiments, the modified IFN- γ has one or more mutations that reduce its binding to or its affinity and/or biological activity for both IFN- γ receptor 1 and IFN- γ receptor 2 subunits.

In some embodiments, the modified IFN- γ has one or more mutations that reduce its binding to or its affinity and/or biological activity for IFN- γ receptor 1 and one or more mutations that substantially reduce or ablate binding to or its affinity and/or biological activity for IFN- γ receptor 2. In some embodiments, chimeric proteins with such modified IFN- γ can provide target-selective IFN- γ receptor 1 activity (e.g., IFN- γ receptor 1 activity is restorable via targeting through the targeting moiety).

In some embodiments, the modified IFN- γ has one or more mutations that reduce its binding to or its affinity and/or biological activity for IFN- γ receptor 1 and one or more mutations that reduce its binding to or its affinity and/or biological activity for IFN- γ receptor 1. In some embodiments, chimeric proteins with such modified IFN- γ can provide target-selective IFN- γ receptor 1 and/or IFN- γ receptor 1 activity (e.g., IFN- γ receptor 1 and IFN- γ receptor 2 activities are restorable via targeting through the targeting moiety).

In various embodiments, the modified IFN- γ is truncated at the C-terminus. In some embodiments, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with deletions of the C-terminal terminus. In such embodiments, the mature IFN- γ may comprise a C-terminal truncation of at least about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, or about 25 amino acid residues. In an embodiment, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with C-terminal deletions of 5 amino acids. In an embodiment, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with C-terminal deletions of 7 amino acids. In an embodiment, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with C-terminal deletions of 14 amino acids. In an embodiment, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with C-terminal deletions of 15 amino acids. In an embodiment, the modified IFN- γ is mature IFN- γ comprising the amino acid sequence of SEQ ID NO: 341 with C-terminal deletions of 16 amino acids. Additional modified IFN- γ with C-terminal truncations that may be utilized in the present invention is described in Haelewyn et al., *Biochem. J.* (1997), 324:591-595 and Lundell et al., *Protein Eng.* (1991) 4:335-341, the entire contents are hereby incorporated by reference.

In various embodiments, the modified IFN- γ is a single chain IFN- γ as described, for example, in Randal et al. (2001) *Structure* 9:155-163 and Randal et al. (1998) *Protein Sci.* 7:1057-1060, the entire contents are hereby incorporated by reference. In some embodiments, the single chain IFN- γ comprises a first IFN- γ chain linked at its C-terminus to the N-terminus of a second IFN- γ chain. In various embodiments, the first and second IFN- γ chains are linked by a linker, as described elsewhere herein.

In some embodiments, the first IFN- γ chain comprises a C-terminal truncation of at least about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, or about 25 amino acid residues. In an embodiment, the first IFN- γ chain comprises a C-terminal truncation of about 24 amino acid residues. In some embodiments, the second IFN- γ chain comprises an N-terminal truncation of at least about 1, about 2, about 3, about 4, or about 5 amino acid residues. In an embodiment, the second IFN- γ chain comprises an N-terminal truncation of about 3 amino acid residues. In some embodiments, the second IFN- γ chain comprises a C-terminal truncation of at least about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, or about 25 amino acid residues. In various embodiments, the first and/or second IFN- γ chains comprise one or more amino acid mutations at Q1, V5, E9, K12, H19, S20, V22, A23, D24, N25, G26, T27, L30, K108, H111, E112, I114, Q115, A118, E119, and K125, as described elsewhere herein. In various embodiments, the first and/or second IFN- γ chains comprise one or more substitutions selected from V5E, S20E, V22A, A23G, A23F, D24G, G26Q, H111A, H111D, I114A, Q115A, and A118G. In various embodiments, the first and/or second IFN- γ chains comprise one or more substitutions selected from V22A, A23G, D24G, H111A, H111D, I114A, Q115A, and A118G. In various embodiments, the first and/or second IFN- γ chains comprise the

A23G and the D24G substitution. In various embodiments, the first and/or second IFN- γ chains comprise the I114A and the A118G substitution. In another embodiment, the mutations are V5E, S20E, A23F, and G26Q.

In various embodiments, a first and/or second IFN- γ chain comprises one or more substitutions as disclosed herein and the first and/or second IFN- γ chain comprises a C-terminal truncation as disclosed herein.

In various embodiments, a first and/or second IFN- γ chain comprises one or more substitutions as disclosed herein and a C-terminal truncation as disclosed herein.

The crystal structure of human IFN- γ is known and is described in, for example, Ealick et al., (1991) Science, 252: 698-702. Specifically, the structure of human IFN- γ has been shown to include a core of six α -helices and an extended unfolded sequence in the C-terminal region. In various embodiments, the modified IFN- γ has one or more mutations in the one or more helices which reduce its binding affinity and/or biological activity at a therapeutic receptor (e.g., IFN- γ receptor).

In various embodiments, the modified IFN- γ has about 1%, or about 3%, about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or about 10%-20%, about 20%-40%, about 50%, about 40%-60%, about 60%-80%, about 80%-100% of the affinity and/or biological activity for the therapeutic receptor (e.g., IFN- γ receptor or any one of its IFN- γ receptor 1 and IFN- γ receptor 2 subunits) relative to the wild type IFN- γ . In some embodiments, the binding affinity and/or biological activity is at least about 2-fold lower, about 3-fold lower, about 4-fold lower, about 5-fold lower, about 6-fold lower, about 7-fold lower, about 8-fold lower, about 9-fold lower, at least about 10-fold lower, at least about 15-fold lower, at least about 20-fold lower, at least about 25-fold lower, at least about 30-fold lower, at least about 35-fold lower, at least about 40-fold lower, at least about 45-fold lower, at least about 50-fold lower, at least about 100-fold lower, at least about 150-fold lower, or about 10-50-fold lower, about 50-100-fold lower, about 100-150-fold lower, about 150-200-fold lower, or more than 200-fold lower relative to the wild type IFN- γ .

In various embodiments, the modified IFN- γ comprises one or more mutations that reduce the endogenous activity of the IFN- γ to about 75%, or about 70%, or about 60%, or about 50%, or about 40%, or about 30%, or about 25%, or about 20%, or about 10%, or about 5%, or about 3%, or about 1%, e.g., relative to the wild type IFN- γ .

In some embodiments, the modified IFN- γ comprises one or more mutations that cause the modified IFN- γ to have reduced affinity and/or biological activity for a receptor. In some embodiments, the modified IFN- γ 's binding affinity and/or biological activity for a receptor is lower than the binding affinity and/or biological activity of the targeting moiety for its receptor. In some embodiments, this binding affinity and/or biological activity differential is between the modified IFN- γ /receptor and targeting moiety/receptor on the same cell. In some embodiments, this binding affinity and/or biological activity, differential allows for the modified IFN- γ to have localized, on-target effects and to minimize off-target effects that underlie side effects that are observed with wild type IFN- γ . In some embodiments, this binding affinity and/or biological activity is at least about 2-fold, or at least about 5-fold, or at

least about 10-fold, or at least about 15-fold lower, or at least about 25-fold, or at least about 50-fold lower, or at least about 100-fold, or at least about 150-fold less.

Receptor binding activity may be measured using methods known in the art. For example, affinity and/or binding activity may be assessed by Scatchard plot analysis and computer-fitting of binding data (e.g., Scatchard, 1949) or by reflectometric interference spectroscopy under flow through conditions, as described by Brecht et al. (1993), the entire contents of all of which are hereby incorporated by reference.

In some embodiments, the modified signaling agent is a consensus interferon. The consensus interferon is generated by scanning the sequences of several human non-allelic IFN- α subtypes and assigning the most frequently observed amino acid in each corresponding position. The consensus interferon differs from IFN- α 2b at 20 out of 166 amino acids (88% homology), and comparison with IFN- β shows identity at over 30% of the amino acid positions. In various embodiments, the consensus interferon comprises the following amino acid sequence SEQ ID NO: 342.

In some embodiments, the consensus interferon comprises the amino acid sequence of SEQ ID NO: 343, which differs from the amino acid sequence of SEQ ID NO: 342 by one amino acid, i.e., SEQ ID NO: 343 lacks the initial methionine residue of SEQ ID NO: 342.

In various embodiments, the consensus interferon comprises a modified version of the consensus interferon, i.e., a consensus interferon variant, as a signaling agent. In various embodiments, the consensus interferon variant encompasses functional derivatives, analogs, precursors, isoforms, splice variants, or fragments of the consensus interferon.

In an embodiment, the consensus interferon variants are selected from the consensus interferon variants disclosed in U.S. Patent Nos. 4,695,623, 4,897,471, 5,541,293, and 8,496,921, the entire contents of all of which are hereby incorporated by reference. For example, the consensus interferon variant may comprise the amino acid sequence of IFN-CON2 or IFN-CON3 as disclosed in U.S. Patent Nos. 4,695,623, 4,897,471, and 5,541,293. In an embodiment, the consensus interferon variant comprises the amino acid sequence of IFN-CON₂, SEQ ID NO: 344.

In an embodiment, the consensus interferon variant comprises the amino acid sequence of IFN-CON₃, SEQ ID NO: 345.

In an embodiment, the consensus interferon variant comprises the amino acid sequence of any one of the variants disclosed in U.S. Patent No. 8,496,921. For example, the consensus variant may comprise the amino acid sequence of SEQ ID NO: 346.

In another embodiment, the consensus interferon variant may comprise the amino acid sequence of SEQ ID NO: 347.

In some embodiments, the consensus interferon variant may be PEGylated, i.e., comprises a PEG moiety. In an embodiment, the consensus interferon variant may comprise a PEG moiety attached at the S156C position of SEQ ID NO: 347.

In some embodiments, the engineered interferon is a variant of human IFN- α 2a, with an insertion of Asp at approximately position 41 in the sequence SEQ ID NO: 348 to yield SEQ ID NO: 349 (which resulted in a renumbering of the sequence relative to IFN- α 2a sequence) and the following mutations of Arg23Lys, Leu26Pro, Glu53Gln, Thr54Ala, Pro56Ser, Asp86Glu, Ile104Thr, Gly106Glu, Thr110Glu, Lys117Asn, Arg125Lys, and Lys136Thr. All embodiments herein that describe consensus interferons apply equally to this engineered interferon.

In various embodiments, the consensus interferon variant comprises an amino acid sequence having one or more amino acid mutations. In some embodiments, the one or more amino acid mutations may be independently selected from substitutions, insertions, deletions, and truncations.

In some embodiments, the amino acid mutations are amino acid substitutions, and may include conservative and/or non-conservative substitutions.

In various embodiments, the substitutions may also include non-classical amino acids (e.g. selenocysteine, pyrrolysine, N-formylmethionine β -alanine, GABA and δ -Aminolevulinic acid, 4-aminobenzoic acid (PABA), D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteine, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general).

In various embodiments, the consensus interferon is modified to have one or more mutations. In some embodiments, the mutations allow for the consensus interferon variant to have one or more of attenuated activity such as one or more of reduced binding affinity, reduced endogenous activity, and reduced specific bioactivity relative to unmutated, e.g., the wild type form of the consensus interferon (e.g., the consensus interferon having an amino acid sequence of SEQ ID NO: 345 or 346). For instance, the one or more of attenuated activity such as reduced binding affinity, reduced endogenous activity, and reduced specific bioactivity relative to unmutated, e.g. the wild type form of the consensus interferon, may be at a therapeutic receptor such as IFNAR. Consequentially, in various embodiments, the mutations allow for the consensus interferon variant to have reduced systemic toxicity, reduced side effects, and reduced off-target effects relative to unmutated, e.g. the wild type form of the consensus interferon.

In various embodiments, the consensus interferon is modified to have a mutation that reduces its binding affinity or activity at a therapeutic receptor such as IFNAR. In some embodiments, the activity provided by the consensus interferon is agonism at the therapeutic receptor (e.g. activation of a cellular effect at a site of therapy). For example, the consensus interferon may activate the therapeutic receptor. In such embodiments, the mutation results in the consensus interferon variant to have reduced activating activity at the therapeutic receptor.

In some embodiments, the reduced affinity or activity at the therapeutic receptor is restorable by attachment with a targeting moiety. In other embodiments, the reduced affinity or activity at the therapeutic receptor is not substantially restorable by attachment with the targeting moiety. In various embodiments, the therapeutic Fc-based

chimeric proteins of the present invention reduce off-target effects because the consensus interferon variant has mutations that weaken binding affinity or activity at a therapeutic receptor. In various embodiments, this reduces side effects observed with, for example, the wild type consensus interferon. In various embodiments, the consensus interferon variant is substantially inactive en route to the site of therapeutic activity and has its effect substantially on specifically targeted cell types which greatly reduces undesired side effects.

In various embodiments, the consensus interferon variant has one or more mutations that cause the consensus interferon variant to have attenuated or reduced affinity, e.g. binding (e.g. KD) and/or activation (measurable as, for example, KA and/or EC50) for one or more therapeutic receptors. In various embodiments, the reduced affinity at the therapeutic receptor allows for attenuation of activity and/or signaling from the therapeutic receptor.

In various embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for the IFNAR1 subunit of IFNAR. In one embodiment, the consensus interferon variant has reduced affinity and/or activity at IFNAR1. In some embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for the IFNAR2 subunit of IFNAR. In some embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for both IFNAR1 and IFNAR2 subunits.

In some embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for IFNAR1 and one or more mutations that substantially reduce or ablate binding to or its affinity for IFNAR2. In some embodiments, Fc-based chimeric proteins with such consensus interferon variant can provide target-selective IFNAR1 activity (e.g. IFNAR1 activity is restorable via targeting through the targeting moiety, e.g., SIRPα).

In some embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for IFNAR2 and one or more mutations that substantially reduce or ablate binding to or its affinity for IFNAR1. In some embodiments, Fc-based chimeric proteins with such consensus interferon variant can provide target-selective IFNAR2 activity (e.g. IFNAR2 activity is restorable via targeting through the targeting moiety, e.g., SIRPα).

In some embodiments, the consensus interferon variant has one or more mutations that reduce its binding to or its affinity for IFNAR1 and one or more mutations that reduce its binding to or its affinity for IFNAR2. In some embodiments, Fc-based chimeric proteins with such consensus interferon variant can provide target-selective IFNAR1 and/or IFNAR2 activity (e.g. IFNAR1 and/or IFNAR2 activity is restorable via targeting through the targeting moiety, e.g., SIRPα).

In some embodiments, the consensus interferon is modified to have a mutation at one or more amino acids at positions 145-155, such as amino acid positions 149, 150 and/or 154, with reference to SEQ ID NO: 346. In some embodiments, the consensus interferon is modified to have a mutation at one or more amino acids at positions 145-155, such as amino acid positions 149, 150 and/or 154, with reference to SEQ ID NO: 346, the substitutions optionally being hydrophobic and selected from alanine, valine, leucine, and isoleucine. In some embodiments, the

consensus interferon mutant comprises one or more mutations selected from M149A, R150A, and L154A, and, with reference to SEQ ID NO: 342.

In an embodiment, the consensus interferon is modified to have a mutation at amino acid position 121 (i.e., K121), with reference to SEQ ID NO: 342. In an embodiment, the consensus interferon comprises a K121E mutation, with reference to SEQ ID NO: 342.

In some embodiments, the modified signaling agent is vascular endothelial growth factor (VEGF). VEGF is a potent growth factor that plays major roles in physiological but also pathological angiogenesis, regulates vascular permeability and can act as a growth factor on cells expressing VEGF receptors. Additional functions include, among others, stimulation of cell migration in macrophage lineage and endothelial cells. Several members of the VEGF family of growth factors exist, as well as at least three receptors (VEGFR-1, VEGFR -2, and VEGFR -3). Members of the VEGF family can bind and activate more than one VEGFR type. For example, VEGF-A binds VEGFR-1 and -2, while VEGF-C can bind VEGFR-2 and -3. VEGFR-1 and -2 activation regulates angiogenesis while VEGFR-3 activation is associated with lymphangiogenesis. The major pro-angiogenic signal is generated from activation of VEGFR-2. VEGFR-1 activation has been reported to be possibly associated with negative role in angiogenesis. It has also been reported that VEGFR-1 signaling is important for progression of tumors *in vivo* via bone marrow-derived VEGFR-1 positive cells (contributing to formation of premetastatic niche in the bone). Several therapies based on VEGF-A directed/neutralizing therapeutic antibodies have been developed, primarily for use in treatment of various human tumors relying on angiogenesis. These are not without side effects though. This may not be surprising considering that these operate as general, non-cell/tissue specific VEGF/VEGFR interaction inhibitors. Hence, it would be desirable to restrict VEGF (e.g. VEGF-A)/VEGFR-2 inhibition to specific target cells (e.g. tumor vasculature endothelial cells).

In some embodiments, the VEGF is VEGF-A, VEGF-B, VEGF-C, VEGF-D, or VEGF-E and isoforms thereof including the various isoforms of VEGF-A such as VEGF₁₂₁, VEGF_{121b}, VEGF₁₄₅, VEGF₁₆₅, VEGF_{165b}, VEGF₁₈₉, and VEGF₂₀₆. In some embodiments, the modified signaling agent has reduced affinity and/or activity for VEGFR-1 (Flt-1) and/or VEGFR-2 (KDR/Flk-1). In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for VEGFR-1 (Flt-1) and/or VEGFR-2 (KDR/Flk-1). In an embodiment, the modified signaling agent has reduced affinity and/or activity for VEGFR-2 (KDR/Flk-1) and/or substantially reduced or ablated affinity and/or activity for VEGFR-1 (Flt-1). Such an embodiment finds use, for example, in wound healing methods or treatment of ischemia-related diseases (without wishing to be bound by theory, mediated by VEGFR-2's effects on endothelial cell function and angiogenesis). In various embodiments, binding to VEGFR-1 (Flt-1), which is linked to cancers and pro-inflammatory activities, is avoided. In various embodiments, VEGFR-1 (Flt-1) acts a decoy receptor and therefore substantially reduces or ablates affinity at this receptor avoids sequestration of the therapeutic agent. In an embodiment, the modified signaling agent has substantially reduced or ablated affinity and/or activity for VEGFR-1 (Flt-1) and/or substantially reduced or ablated affinity and/or activity for VEGFR-2 (KDR/Flk-1). In some embodiments, the VEGF is VEGF-C or VEGF-D. In such embodiments, the

modified signaling agent has reduced affinity and/or activity for VEGFR-3. Alternatively, the modified signaling agent has substantially reduced or ablated affinity and/or activity for VEGFR-3.

Proangiogenic therapies are also important in various diseases (*e.g.* ischemic heart disease, bleeding *etc.*), and include VEGF-based therapeutics. Activation of VEGFR-2 is proangiogenic (acting on endothelial cells). Activation of VEGFR-1 can cause stimulation of migration of inflammatory cells (including, for example, macrophages) and lead to inflammation associated hypervascular permeability. Activation of VEGFR-1 can also promote bone marrow associated tumor niche formation. Thus, VEGF based therapeutic selective for VEGFR-2 activation would be desirable in this case. In addition, cell specific targeting, *e.g.* to endothelial cells, would be desirable.

In some embodiments, the modified signaling agent has reduced affinity and/or activity (*e.g.* antagonistic) for VEGFR-2 and/or has substantially reduced or ablated affinity and/or activity for VEGFR-1. When targeted to tumor vasculature endothelial cells via a targeting moiety that binds to a tumor endothelial cell marker (*e.g.* PSMA and others), such construct inhibits VEGFR-2 activation specifically on such marker-positive cells, while not activating VEGFR-1 *en route* and on target cells (if activity ablated), thus eliminating induction of inflammatory responses, for example. This would provide a more selective and safe anti-angiogenic therapy for many tumor types as compared to VEGF-A neutralizing therapies.

In some embodiments, the modified signaling agent has reduced affinity and/or activity (*e.g.* agonistic) for VEGFR-2 and/or has substantially reduced or ablated affinity and/or activity for VEGFR-1. Through targeting to vascular endothelial cells, such construct, in some embodiments, promotes angiogenesis without causing VEGFR-1 associated induction of inflammatory responses. Hence, such a construct would have targeted proangiogenic effects with substantially reduced risk of side effects caused by systemic activation of VEGFR-2 as well as VEGFR-1.

In an illustrative embodiment, the modified signaling agent is VEGF₁₆₅, which has the amino acid sequence VEGF 165 (wild type) (SEQ ID NO: 350).

In another illustrative embodiment, the modified signaling agent is VEGF_{165b}, which has the amino acid sequence VEGF 165b (wild type) (SEQ ID NO: 351).

In these embodiments, the modified signaling agent has a mutation at amino acid I83 (*e.g.*, a substitution mutation at I83, *e.g.*, I83K, I83R, or I83H). Without wishing to be bound by theory, it is believed that such mutations may result in reduced receptor binding affinity. See, for example, U.S. Patent No. 9,078,860, the entire contents of which are hereby incorporated by reference.

In an embodiment, the modified signaling agent is TNF- α . TNF is a pleiotropic cytokine with many diverse functions, including regulation of cell growth, differentiation, apoptosis, tumorigenesis, viral replication, autoimmunity, immune cell functions and trafficking, inflammation, and septic shock. It binds to two distinct membrane receptors on target cells: TNFR1 (p55) and TNFR2 (p75). TNFR1 exhibits a very broad expression pattern whereas TNFR2 is expressed preferentially on certain populations of lymphocytes, Tregs, endothelial cells, certain neurons,

microglia, cardiac myocytes and mesenchymal stem cells. Very distinct biological pathways are activated in response to receptor activation, although there is also some overlap. As a general rule, without wishing to be bound by theory, TNFR1 signaling is associated with induction of apoptosis (cell death) and TNFR2 signaling is associated with activation of cell survival signals (e.g. activation of NFkB pathway). Administration of TNF is systemically toxic, and this is largely due to TNFR1 engagement. However, it should be noted that activation of TNFR2 is also associated with a broad range of activities and, as with TNFR1, in the context of developing TNF based therapeutics, control over TNF targeting and activity is important.

In some embodiments, the modified signaling agent has reduced affinity and/or activity for TNFR1 and/or TNFR2. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for TNFR1 and/or TNFR2. TNFR1 is expressed in most tissues, and is involved in cell death signaling while, by contrast, TNFR2 is involved in cell survival signaling. Accordingly, in embodiments directed to methods of treating cancer, the modified signaling agent has reduced affinity and/or activity for TNFR1 and/or substantially reduced or ablated affinity and/or activity for TNFR2. In these embodiments, the chimeric proteins may be targeted to a cell for which apoptosis is desired, e.g. a tumor cell or a tumor vasculature endothelial cell. In embodiments directed to methods of promoting cell survival, for example, in neurogenesis for the treatment of neurodegenerative disorders, the modified signaling agent has reduced affinity and/or activity for TNFR2 and/or substantially reduced or ablated affinity and/or activity for TNFR1. Stated another way, the present chimeric proteins, in some embodiments, comprise modified TNF- α agent that allows of favoring either death or survival signals.

In some embodiments, the chimeric protein has a modified TNF having reduced affinity and/or activity for TNFR1 and/or substantially reduced or ablated affinity and/or activity for TNFR2. Such a chimera, in some embodiments, is a more potent inducer of apoptosis as compared to a wild type TNF and/or a chimera bearing only mutation(s) causing reduced affinity and/or activity for TNFR1. Such a chimera, in some embodiments, finds use in inducing tumor cell death or a tumor vasculature endothelial cell death (e.g. in the treatment of cancers). Also, in some embodiments, these chimeras avoid or reduce activation of T_{reg} cells via TNFR2, for example, thus further supporting TNFR1-mediated antitumor activity *in vivo*.

In some embodiments, the chimeric protein has a modified TNF having reduced affinity and/or activity for TNFR2 and/or substantially reduced or ablated affinity and/or activity for TNFR1. Such a chimera, in some embodiments, is a more potent activator of cell survival in some cell types, which may be a specific therapeutic objective in various disease settings, including without limitation, stimulation of neurogenesis. In addition, such a TNFR2-favoring chimeras also are useful in the treatment of autoimmune diseases (e.g. Crohn's, diabetes, MS, colitis *etc.* and many others described herein). In some embodiments, the chimera is targeted to auto-reactive T cells. In some embodiments, the chimera promotes T_{reg} cell activation and indirect suppression of cytotoxic T cells.

In some embodiments, the chimera causes the death of auto-reactive T cells, e.g. by activation of TNFR2 and/or avoidance of TNFR1 (e.g. a modified TNF having reduced affinity and/or activity for TNFR2 and/or substantially reduced or ablated affinity and/or activity for TNFR1). Without wishing to be bound by theory these auto-reactive

T cells, have their apoptosis/survival signals altered e.g. by NFkB pathway activity/signaling alterations. In some embodiments, the chimera causes the death of autoreactive T cells having lesions or modifications in the NFkB pathway, which underlie an imbalance of their cell death (apoptosis)/survival signaling properties and, optionally, altered susceptibility to certain death-inducing signals (e.g., TNFR2 activation).

In some embodiments, a TNFR2 based chimera has additional therapeutic applications in diseases, including various autoimmune diseases, heart disease, de-myelinating and neurodegenerative disorders, and infectious disease, among others.

In an embodiment, the wild type TNF- α has the amino acid sequence of SEQ ID NO: 352.

In such embodiments, the modified TNF- α agent has mutations at one or more amino acid positions 29, 31, 32, 84, 85, 86, 87, 88, 89, 145, 146 and 147 which produces a modified TNF- α with reduced receptor binding affinity. See, for example, U.S. Patent No. 7,993,636, the entire contents of which are hereby incorporated by reference.

In some embodiments, the modified human TNF- α moiety has mutations at one or more amino acid positions R32, N34, Q67, H73, L75, T77, S86, Y87, V91, I97, T105, P106, A109, P113, Y115, E127, N137, D143, A145, and E146 as described, for example, in WO/2015/007903, the entire contents of which is hereby incorporated by reference (numbering according to the human TNF sequence, Genbank accession number BAG70306, version BAG70306.1 GI: 197692685). In some embodiments, the modified human TNF- α moiety has substitution mutations selected from L29S, R32G, R32W, N34G, Q67G, H73G, L75G, L75A, L75S, T77A, S86G, S86T, Y87Q, Y87L, Y87A, Y87F, Y87H, V91G, V91A, I97A, I97Q, I97S, T105G, P106G, A109Y, P113G, Y115G, Y115A, E127G, N137G, D143N, A145G, A145R, A145T, E146D, E146K, and S147D. In an embodiment, the human TNF- α moiety has a mutation selected from Y87Q, Y87L, Y87A, Y87F, and Y87H. In another embodiment, the human TNF- α moiety has a mutation selected from I97A, I97Q, and I97S. In a further embodiment, the human TNF- α moiety has a mutation selected from Y115A and Y115G. In an embodiment, the human TNF- α moiety has an E146K mutation. In an embodiment, the human TNF- α moiety has an Y87H and an E146K mutation. In an embodiment, the human TNF- α moiety has an Y87H and an A145R mutation. In an embodiment, the human TNF- α moiety has a R32W and a S86T mutation. In an embodiment, the human TNF- α moiety has a R32W and an E146K mutation. In an embodiment, the human TNF- α moiety has a L29S and a R32W mutation. In an embodiment, the human TNF- α moiety has a D143N and an A145R mutation. In an embodiment, the human TNF- α moiety has a D143N and an A145R mutation. In an embodiment, the human TNF- α moiety has an A145T, an E146D, and a S147D mutation. In an embodiment, the human TNF- α moiety has an A145T and a S147D mutation.

In some embodiments, the modified TNF- α agent has one or more mutations selected from N39Y, S147Y, and Y87H, as described in WO2008/124086, the entire contents of which is hereby incorporated by reference.

In some embodiments, the modified human TNF- α moiety has mutations that provide receptor selectivity as described in PCT/IB2016/001668, the entire contents of which are hereby incorporated by reference. In some embodiments, the mutations to TNF are TNF-R1 selective. In some embodiments, the mutations to TNF which are TNF-R1 selective are at one or more of positions R32, S86, and E146. In some embodiments, the mutations to

TNF which are TNF-R1 selective are one or more of R32W, S86T, and E146K. In some embodiments, the mutations to TNF which are TNF-R1 selective are one or more of R32W, R32W/S86T, R32W/E146K and E146K. In some embodiments, the mutations to TNF are TNF-R2 selective. In some embodiments, the mutations to TNF which are TNF-R2 selective are at one or more of positions A145, E146, and S147. In some embodiments, the mutations to TNF which are TNF-R2 selective are one or more of A145T, A145R, E146D, and S147D. In some embodiments, the mutations to TNF which are TNF-R2 selective are one or more of A145R, A145T/S147D, and A145T/E146D/S147D.

In an embodiment, the modified signaling agent is TNF- β . TNF- β can form a homotrimer or a heterotrimer with LT- β (LT- α 1 β 2). In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for TNFR1 and/or TNFR2 and/or herpes virus entry mediator (HEVM) and/or LT- β R.

In an embodiment, the wild type TNF- β has the amino acid sequence of SEQ ID NO: 353.

In such embodiments, the modified soluble agent may comprise mutations at one or more amino acids at positions 106-113, which produce a modified TNF- β with reduced receptor binding affinity to TNFR2. In an embodiment, the modified soluble agent has one or more substitution mutations at amino acid positions 106-113. In illustrative embodiments, the substitution mutations are selected from Q107E, Q107D, S106E, S106D, Q107R, Q107N, Q107E/S106E, Q107E/S106D, Q107D/S106E, and Q107D/S106D. In another embodiment, the modified soluble agent has an insertion of about 1 to about 3 amino acids at positions 106-113.

In some embodiments, the modified agent is a TNF family member (e.g. TNF-alpha, TNF-beta) which can be a single chain trimeric version as described in WO 2015/007903, the entire contents of which are incorporated by reference.

In some embodiments, the modified agent is a TNF family member (e.g. TNF-alpha, TNF-beta) which has reduced affinity and/or activity, *i.e.* antagonistic activity (e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, *see, e.g.*, WO 2015/007520, the entire contents of which are hereby incorporated by reference) at TNFR1. In these embodiments, the modified agent is a TNF family member (e.g. TNF-alpha, TNF-beta) which also, optionally, has substantially reduced or ablated affinity and/or activity for TNFR2. In some embodiments, the modified agent is a TNF family member (e.g. TNF-alpha, TNF-beta) which has reduced affinity and/or activity, *i.e.* antagonistic activity (e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, *see, e.g.*, WO 2015/007520, the entire contents of which are hereby incorporated by reference) at TNFR2. In these embodiments, the modified agent is a TNF family member (e.g. TNF-alpha, TNF-beta) which also, optionally, has substantially reduced or ablated affinity and/or activity for TNFR1. The constructs of such embodiments find use in, for example, methods of dampening TNF response in a cell specific manner. In some embodiments, the antagonistic TNF family member (e.g. TNF-alpha, TNF-beta) is a single chain trimeric version as described in WO 2015/007903.

In an embodiment, the modified signaling agent is TRAIL. In some embodiments, the modified TRAIL agent has reduced affinity and/or activity for DR4 (TRAIL-RI) and/or DR5 (TRAIL-RII) and/or DcR1 and/or DcR2. In some

embodiments, the modified TRAIL agent has substantially reduced or ablated affinity and/or activity for DR4 (TRAIL-R1) and/or DR5 (TRAIL-R2) and/or DcR1 and/or DcR2.

In an embodiment, the wild type TRAIL has the amino acid sequence of SEQ ID NO: 354.

In such embodiments, the modified TRAIL agent may comprise a mutation at amino acid positions T127-R132, E144-R149, E155-H161, Y189-Y209, T214-1220, K224-A226, W231, E236-L239, E249-K251, T261-H264 and H270-E271 (Numbering based on the human sequence, Genbank accession number NP_003801, version 10 NP_003801.1, GI: 4507593; see above).

In some embodiments, the modified TRAIL agent may comprise one or more mutations that substantially reduce its affinity and/or activity for TRAIL-R1. In such embodiments, the modified TRAIL agent may specifically bind to TRIL-R2. Exemplary mutations include mutations at one or more amino acid positions Y189, R191, Q193, H264, I266, and D267. For example, the mutations may be one or more of Y189Q, R191K, Q193R, H264R, I266L and D267Q. In an embodiment, the modified TRAIL agent comprises the mutations Y189Q, R191K, Q193R, H264R, I266L and D267Q.

In some embodiments, the modified TRAIL agent may comprise one or more mutations that substantially reduce its affinity and/or activity for TRAIL-R2. In such embodiments, the modified TRAIL agent may specifically bind to TRIL-R1. Exemplary mutations include mutations at one or more amino acid positions G131, R149, S159, N199, K201, and S215. For example, the mutations may be one or more of G131R, R149I, S159R, N199R, K201H, and S215D. In an embodiment, the modified TRAIL agent comprises the mutations G131R, R149I, S159R, N199R, K201H, and S215D. Additional TRAIL mutations are described in, for example, Trebing et al., (2014) Cell Death and Disease, 5:e1035, the entire disclosure of which is hereby incorporated by reference.

In an embodiment, the modified signaling agent is TGF α . In such embodiments, the modified TGF α agent has reduced affinity and/or activity for the epidermal growth factor receptor (EGFR). In some embodiments, the modified TGF α agent has substantially reduced or ablated affinity and/or activity for the epidermal growth factor receptor (EGFR).

In an embodiment, the modified signaling agent is TGF β . In such embodiments, the modified signaling agent has reduced affinity and/or activity for TGFBR1 and/or TGFBR2. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for TGFBR1 and/or TGFBR2. In some embodiments, the modified signaling agent optionally has reduced or substantially reduced or ablated affinity and/or activity for TGFBR3 which, without wishing to be bound by theory, may act as a reservoir of ligand for TGF-beta receptors. In some embodiments, the TGF β may favor TGFBR1 over TGFBR2 or TGFBR2 over TGFBR1. Similarly, LAP, without wishing to be bound by theory, may act as a reservoir of ligand for TGF-beta receptors. In some embodiments, the modified signaling agent has reduced affinity and/or activity for TGFBR1 and/or TGFBR2 and/or substantially reduced or ablated affinity and/or activity for Latency Associated Peptide (LAP). In some embodiments, such chimeras find use in Camurati-Engelmann disease, or other diseases associated with inappropriate TGF β signaling.

In some embodiments, the modified agent is a TGF family member (e.g. TGF α , TGF β) which has reduced affinity and/or activity, *i.e.* antagonistic activity (e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, see, e.g., WO 2015/007520, the entire contents of which are hereby incorporated by reference) at one or more of TGFBR1, TGFBR2, TGFBR3. In these embodiments, the modified agent is a TGF family member (e.g. TGF α , TGF β) which also, optionally, has substantially reduced or ablated affinity and/or activity at one or more of TGFBR1, TGFBR2, TGFBR3.

In some embodiments, the modified agent is a TGF family member (e.g. TGF α , TGF β) which has reduced affinity and/or activity, *i.e.* antagonistic activity (e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, see, e.g., WO 2015/007520, the entire contents of which are hereby incorporated by reference) at TGFBR1 and/or TGFBR2. In these embodiments, the modified agent is a TGF family member (e.g. TGF α , TGF β) which also, optionally, has substantially reduced or ablated affinity and/or activity at TGFBR3.

In an embodiment, the modified signaling agent is an interleukin. In an embodiment, the modified signaling agent is IL-1. In an embodiment, the modified signaling agent is IL-1 α or IL-1 β . In some embodiments, the modified signaling agent has reduced affinity and/or activity for IL-1R1 and/or IL-1RAcP. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-1R1 and/or IL-1RAcP. In some embodiments, the modified signaling agent has reduced affinity and/or activity for IL-1R2. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-1R2. For instance, in some embodiments, the present modified IL-1 agents avoid interaction at IL-1R2 and therefore substantially reduce its function as a decoy and/or sink for therapeutic agents.

In an embodiment, the wild type IL-1 β has the amino acid sequence of IL-1 beta (mature form, wild type) (SEQ ID NO: 355).

IL1 is a proinflammatory cytokine and an important immune system regulator. It is a potent activator of CD4 T cell responses, increases proportion of Th17 cells and expansion of IFN γ and IL-4 producing cells. IL-1 is also a potent regulator of CD8 $^{+}$ T cells, enhancing antigen-specific CD8 $^{+}$ T cell expansion, differentiation, migration to periphery and memory. IL-1 receptors comprise IL-1R1 and IL-1R2. Binding to and signaling through the IL-1R1 constitutes the mechanism whereby IL-1 mediates many of its biological (and pathological) activities. IL-1R2 can function as a decoy receptor, thereby reducing IL-1 availability for interaction and signaling through the IL-1R1.

In some embodiments, the modified IL-1 has reduced affinity and/or activity (e.g. agonistic activity) for IL-1R1. In some embodiments, the modified IL-1 has substantially reduced or ablated affinity and/or activity for IL-1R2. In such embodiments, there is restorable IL-1/ IL-1R1 signaling and prevention of loss of therapeutic chimeras at IL-1R2 and therefore a reduction in dose of IL-1 that is required (e.g. relative to wild type or a chimera bearing only an attenuation mutation for IL-1R1). Such constructs find use in, for example, methods of treating cancer, including, for example, stimulating the immune system to mount an anti-cancer response.

In some embodiments, the modified IL-1 has reduced affinity and/or activity (e.g. antagonistic activity, e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, see, e.g., WO 2015/007520,

the entire contents of which are hereby incorporated by reference) for IL-1R1. In some embodiments, the modified IL-1 has substantially reduced or ablated affinity and/or activity for IL-1R2. In such embodiments, there is the IL-1/IL-1R1 signaling is not restorable and prevention of loss of therapeutic chimeras at IL-1R2 and therefore a reduction in dose of IL-1 that is required (e.g. relative to wild type or a chimera bearing only an attenuation mutation for IL-1R1). Such constructs find use in, for example, methods of treating autoimmune diseases, including, for example, suppressing the immune system.

In such embodiments, the modified signaling agent has a deletion of amino acids 52-54 which produces a modified human IL-1 β with reduced binding affinity for type I IL-1R and reduced biological activity. See, for example, WO 1994/000491, the entire contents of which are hereby incorporated by reference. In some embodiments, the modified human IL-1 β has one or more substitution mutations selected from A117G/P118G, R120X, L122A, T125G/L126G, R127G, Q130X, Q131G, K132A, S137G/Q138Y, L145G, H146X, L145A/L147A, Q148X, Q148G/Q150G, Q150G/D151A, M152G, F162A, F162A/Q164E, F166A, Q164E/E167K, N169G/D170G, I172A, V174A, K208E, K209X, K209A/K210A, K219X, E221X, E221 S/N224A, N224S/K225S, E244K, N245Q (where X can be any change in amino acid, e.g., a non-conservative change), which exhibit reduced binding to IL-1R, as described, for example, in WO2015/007542 and WO/2015/007536, the entire contents of which is hereby incorporated by reference (numbering base on the human IL-1 β sequence, Genbank accession number NP_000567, version NP-000567.1, GI: 10835145). In some embodiments, the modified human IL-1 β may have one or more mutations selected from R120A, R120G, Q130A, Q130W, H146A, H146G, H146E, H146N, H146R, Q148E, Q148G, Q148L, K209A, K209D, K219S, K219Q, E221S and E221K. In an embodiment, the modified human IL-1 β comprises the mutations Q131G and Q148G. In an embodiment, the modified human IL-1 β comprises the mutations Q148G and K208E. In an embodiment, the modified human IL-1 β comprises the mutations R120G and Q131G. In an embodiment, the modified human IL-1 β comprises the mutations R120G and H146A. In an embodiment, the modified human IL-1 β comprises the mutations R120G and H146N. In an embodiment, the modified human IL-1 β comprises the mutations R120G and H146R. In an embodiment, the modified human IL-1 β comprises the mutations R120G and H146E. In an embodiment, the modified human IL-1 β comprises the mutations R120G and H146G. In an embodiment, the modified human IL-1 β comprises the mutations R120G and K208E. In an embodiment, the modified human IL-1 β comprises the mutations R120G, F162A, and Q164E.

In an embodiment, the modified signaling agent is IL-2. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for IL-2R α and/or IL-2R β and/or IL-2R γ . In some embodiments, the modified signaling agent has reduced affinity and/or activity for IL-2R β and/or IL-2R γ . In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-2R α . Such embodiments may be relevant for treatment of cancer, for instance when the modified IL-2 is agonistic at IL-2R β and/or IL-2R γ . For instance, the present constructs may favor attenuated activation of CD8⁺ T cells (which can provide an anti-tumor effect), which have IL2 receptors β and γ and disfavor T_{regs} (which can provide an immune suppressive, pro-tumor effect), which have IL2 receptors α , β , and γ . Further, in some embodiments, the preferences for IL-2R β and/or IL-2R γ over IL-2R α avoid IL-2 side effects such as pulmonary edema. Also, IL-2-based chimeras are useful for the

treatment of autoimmune diseases, for instance when the modified IL-2 is antagonistic (e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, see, e.g., WO 2015/007520, the entire contents of which are hereby incorporated by reference) at IL-2R β and/or IL-2R γ . For instance, the present constructs may favor attenuated suppression of CD8⁺ T cells (and therefore dampen the immune response), which have IL2 receptors β and γ and disfavor T_{regs} which have IL2 receptors α , β , and γ . Alternatively, in some embodiments, the chimeras bearing IL-2 favor the activation of T_{regs}, and therefore immune suppression, and activation of disfavor of CD8⁺ T cells. For instance, these constructs find use in the treatment of diseases or diseases that would benefit from immune suppression, e.g. autoimmune disorders.

In some embodiments, the chimeric protein has targeting moieties as described herein directed to Clec9A⁺ dendritic cells as well as a modified IL-2 agent having reduced affinity and/or activity for IL-2R β and/or IL-2R γ and/or substantially reduced or ablated affinity and/or activity for IL-2R α . In some embodiments, these constructs provide targeted Clec9A⁺ dendritic cell activity and are generally inactive (or have substantially reduced activity) towards T_{reg} cells. In some embodiments, such constructs have enhanced immune stimulatory effect compared to wild type IL-2 (e.g., without wishing to be bound by theory, by not stimulating Tregs), whilst eliminating or reducing the systemic toxicity associated with IL-2.

In an embodiment, the wild type IL-2 has the amino acid sequence of IL-2 (mature form, wild type) (SEQ ID NO: 356).

In such embodiments, the modified IL-2 agent has one or more mutations at amino acids L72 (L72G, L72A, L72S, L72T, L72Q, L72E, L72N, L72D, L72R, or L72K), F42 (F42A, F42G, F42S, F42T, F42Q, F42E, F42N, F42D, F42R, or F42K) and Y45 (Y45A, Y45G, Y45S, Y45T, Y45Q, Y45E, Y45N, Y45D, Y45R or Y45K). Without wishing to be bound by theory, it is believed that these modified IL-2 agents have reduced affinity for the high-affinity IL-2 receptor and preserves affinity to the intermediate-affinity IL-2 receptor, as compared to the wild-type IL-2. See, for example, US Patent Publication No. 2012/0244112, the entire contents of which are hereby incorporated by reference.

In some embodiments, the modified IL-2 agent has one or more mutations at amino acids R38, F42, Y45, and E62. For example, the modified IL-2 agent may comprise one or more of R38A, F42A, Y45A, and E62A. In some embodiments, the modified IL-2 agent may comprise a mutation at C125. For example, the mutation may be C125S. In such embodiments, the modified IL-2 agent may have substantially reduced affinity and/or activity for IL-2R α , as described in, for example, Carment et al. (2013) The Journal of Immunology, 190:6230-6238, the entire disclosure of which is hereby incorporated by reference. In some embodiments, the modified IL-2 agent with mutations at R38, F42, Y45, and/or E62 is able to induce an expansion of effector cells including CD8⁺ T cells and NK cells but not Treg cells. In some embodiments, the modified IL-2 agent with mutations at R38, F42, Y45, and/or E62 is less toxic than wildtype IL-2 agents. A chimeric protein comprising the modified IL-2 agent with substantially reduced affinity and/or activity for IL-2R α may find application in oncology for example. In other embodiments, the modified IL-2 agent may have substantially reduced affinity and/or activity for IL-2R β , as described in, for example, WO2016/025385, the entire disclosure of which is hereby incorporated by reference. In such embodiments, the

modified IL-2 agent may induce an expansion of Treg cells but not effector cells such as CD8⁺ T cells and NK cells. A chimeric protein comprising the modified IL-2 agent with substantially reduced affinity and/or activity for IL-2R β may find application in the treatment of autoimmune disease for example. In some embodiments, the modified IL-2 agent may comprise one or more mutations at amino acids N88, D20, and/or A126. For example, the modified IL-2 agent may comprise one or more of N88R, N88I, N88G, D20H, Q126L, and Q126F.

In various embodiments, the modified IL-2 agent may comprise a mutation at D109 or C125. For example, the mutation may be D109C or C125S. In some embodiments, the modified IL-2 with a mutation at D109 or C125 may be utilized for attachment to a PEG moiety.

In an embodiment, the modified signaling agent is IL-3. In some embodiments, the modified signaling agent has reduced affinity and/or activity for the IL-3 receptor, which is a heterodimer with a unique alpha chain paired with the common beta (beta c or CD131) subunit. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for the IL-3 receptor, which is a heterodimer with a unique alpha chain paired with the common beta (beta c or CD131) subunit.

In an embodiment, the modified signaling agent is IL-4. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for type 1 and/or type 2 IL-4 receptors. In such an embodiment, the modified signaling agent has substantially reduced or ablated affinity and/or activity for type 1 and/or type 2 IL-4 receptors. Type 1 IL-4 receptors are composed of the IL-4R α subunit with a common γ chain and specifically bind IL-4. Type 2 IL-4 receptors include an IL-4R α subunit bound to a different subunit known as IL-13R α 1. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for the type 2 IL-4 receptors.

In an embodiment, the wild type IL-4 has the amino acid sequence of IL-4 (mature form, wild type) (SEQ ID NO: 357).

In such embodiments, the modified IL-4 agent has one or more mutations at amino acids R121 (R121A, R121D, R121E, R121F, R121H, R121I, R121K, R121N, R121P, R121T, R121W), E122 (E122F), Y124 (Y124A, Y124Q, Y124R, Y124S, Y124T) and S125 (S125A). Without wishing to be bound by theory, it is believed that these modified IL-4 agents maintain the activity mediated by the type I receptor, but significantly reduces the biological activity mediated by the other receptors. See, for example, US Patent No. 6,433,157, the entire contents of which are hereby incorporated by reference.

In an embodiment, the modified signaling agent is IL-6. IL-6 signals through a cell-surface type I cytokine receptor complex including the ligand-binding IL-6R chain (CD126), and the signal-transducing component gp130. IL-6 may also bind to a soluble form of IL-6R (sIL-6R), which is the extracellular portion of IL-6R. The sIL-6R/IL-6 complex may be involved in neurite outgrowth and survival of neurons and, hence, may be important in nerve regeneration through remyelination. Accordingly, in some embodiments, the modified signaling agent has reduced affinity and/or activity for IL-6R/gp130 and/or sIL-6R. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-6R/gp130 and/or sIL-6R.

In an embodiment, the wild type IL-6 has the amino acid sequence of IL-6 (mature form, wild type) (SEQ ID NO: 358).

In such embodiments, the modified signaling agent has one or more mutations at amino acids 58, 160, 163, 171 or 177. Without wishing to be bound by theory, it is believed that these modified IL-6 agents exhibit reduced binding affinity to IL-6R α and reduced biological activity. See, for example, WO 97/10338, the entire contents of which are hereby incorporated by reference.

In an embodiment, the modified signaling agent is IL-10. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for IL-10 receptor-1 and IL-10 receptor-2. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-10 receptor-1 and IL-10 receptor-2

In an embodiment, the modified signaling agent is IL-11. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for IL-11R α and/or IL-11R β and/or gp130. In such an embodiment, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-11R α and/or IL-11R β and/or gp130.

In an embodiment, the modified signaling agent is IL-12. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for IL-12R β 1 and/or IL-12R β 2. In such an embodiment, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-12R β 1 and/or IL-12R β 2.

In an embodiment, the modified signaling agent is IL-13. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for the IL-4 receptor (IL-4R α) and IL-13R α 1. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-4 receptor (IL-4R α) or IL-13R α 1.

In an embodiment, the wild type IL-13 has the amino acid sequence of IL-13 (mature form, wild type) (SEQ ID NO: 359).

In such embodiments, the modified IL-13 agent has one or more mutations at amino acids 13, 16, 17, 66, 69, 99, 102, 104, 105, 106, 107, 108, 109, 112, 113 and 114. Without wishing to be bound by theory, it is believed that these modified IL-13 agents exhibit reduced biological activity. See, for example, WO 2002/018422, the entire contents of which are hereby incorporated by reference.

In an embodiment, the modified signaling agent is IL-18. In some embodiments, the modified signaling agent has reduced affinity and/or activity for IL-18R α and/or IL-18R β . In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-18R α and/or IL-18R β . In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for IL-18R α type II, which is an isoform of IL-18R α that lacks the TIR domain required for signaling.

In an embodiment, the wild type IL-18 has the amino acid sequence of IL-18 (wild type) (SEQ ID NO: 360).

In such embodiments, the modified IL-18 agent may comprise one or more mutations in amino acids or amino acid regions selected from Y37-K44, R49-Q54, D59-R63, E67-C74, R80, M87-A97, N 127-K129, Q139-M149, K165-

K171, R183 and Q190-N191, as described in WO/2015/007542, the entire contents of which are hereby incorporated by reference (numbering based on the human IL-18 sequence, Genbank accession number AAV38697, version AAV38697.1, GI: 54696650).

In an embodiment, the modified signaling agent is IL-33. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for the ST-2 receptor and IL-1RAcP. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for the ST-2 receptor and IL-1RAcP.

In an embodiment, the wild type IL-33 has the amino acid sequence of SEQ ID NO: 361.

In such embodiments, the modified IL-33 agent may comprise one or more mutations in amino acids or amino acid regions selected from I113-Y122, S127-E139, E144-D157, Y163-M183, E200, Q215, L220-C227 and T260-E269, as described in WO/2015/007542, the entire contents of which are hereby incorporated by reference (numbering based on the human sequence, Genbank accession number NP_254274, version NP_254274.1, GI:15559209).

In an embodiment, the modified signaling agent is epidermal growth factor (EGF). EGF is a member of a family of potent growth factors. Members include EGF, HB-EGF, and others such as TGFalpha, amphiregulin, neuregulins, epiregulin, betacellulin. EGF family receptors include EGFR (ErbB1), ErbB2, ErbB3 and ErbB4. These may function as homodimeric and /or heterodimeric receptor subtypes. The different EGF family members exhibit differential selectivity for the various receptor subtypes. For example, EGF associates with ErbB1/ErbB1, ErbB1/ErbB2, ErbB4/ErbB2 and some other heterodimeric subtypes. HB-EGF has a similar pattern, although it also associates with ErbB4/4. Modulation of EGF (EGF-like) growth factor signaling, positively or negatively, is of considerable therapeutic interest. For example, inhibition of EGFRs signaling is of interest in the treatment of various cancers where EGFR signaling constitutes a major growth promoting signal. Alternatively, stimulation of EGFRs signaling is of therapeutic interest in, for example, promoting wound healing (acute and chronic), oral mucositis (a major side-effect of various cancer therapies, including, without limitation radiation therapy).

In some embodiments, the modified signaling agent has reduced affinity and/or activity for ErbB1, ErbB2, ErbB3, and/or ErbB4. Such embodiments find use, for example, in methods of treating wounds. In some embodiments, the modified signaling agent binds to one or more ErbB1, ErbB2, ErbB3, and ErbB4 and antagonizes the activity of the receptor. In such embodiments, the modified signaling agent has reduced affinity and/or activity for ErbB1, ErbB2, ErbB3, and/or ErbB4 which allows for the activity of the receptor to be antagonized in an attenuated fashion. Such embodiments find use in, for example, treatments of cancer. In an embodiment, the modified signaling agent has reduced affinity and/or activity for ErbB1. ErbB1 is the therapeutic target of kinase inhibitors - most have side effects because they are not very selective (e.g., gefitinib, erlotinib, afatinib, brigatinib and icotinib). In some embodiments, attenuated antagonistic ErbB1 signaling is more on-target and has less side effects than other agents targeting receptors for EGF.

In some embodiments, the modified signaling agent has reduced affinity and/or activity (e.g. antagonistic e.g. natural antagonistic activity or antagonistic activity that is the result of one or more mutations, see, e.g., WO 2015/007520, the entire contents of which are hereby incorporated by reference) for ErbB1 and/or substantially

reduced or ablated affinity and/or activity for ErbB4 or other subtypes it may interact with. Through specific targeting via the targeting moiety, cell-selective suppression (antagonism *e.g.* natural antagonistic activity or antagonistic activity that is the result of one or more mutations, *see, e.g.*, WO 2015/007520, the entire contents of which are hereby incorporated by reference) of ErbB1/ErbB1 receptor activation would be achieved – while not engaging other receptor subtypes potentially associated with inhibition-associated side effects. Hence, in contrast to EGFR kinase inhibitors, which inhibit EGFR activity in all cell types in the body, such a construct would provide a cell-selective (*e.g.*, tumor cell with activated EGFR signaling due to amplification of receptor, overexpression *etc.*) anti-EGFR (ErbB1) drug effect with reduced side effects.

In some embodiments, the modified signaling agent has reduced affinity and/or activity (*e.g.* agonistic) for ErbB4 and/or other subtypes it may interact with. Through targeting to specific target cells through the targeting moiety, a selective activation of ErbB1 signaling is achieved (*e.g.* epithelial cells). Such a construct finds use, in some embodiments, in the treatment of wounds (promoting wound healing) with reduced side effects, especially for treatment of chronic conditions and application other than topical application of a therapeutic (*e.g.* systemic wound healing).

In an embodiment, the modified signaling agent is insulin or insulin analogs. In some embodiments, the modified insulin or insulin analog has reduced affinity and/or activity for the insulin receptor and/or IGF1 or IGF2 receptor. In some embodiments, the modified insulin or insulin analog has substantially reduced or ablated affinity and/or activity for the insulin receptor and/or IGF1 or IGF2 receptor. Attenuated response at the insulin receptor allows for the control of diabetes, obesity, metabolic disorders and the like while directing away from IGF1 or IGF2 receptor avoids pro-cancer effects.

In an embodiment, the modified signaling agent is insulin-like growth factor-I or insulin-like growth factor-II (IGF-1 or IGF-2). In an embodiment, the modified signaling agent is IGF-1. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for the insulin receptor and/or IGF1 receptor. In an embodiment, the modified signaling agent may bind to the IGF1 receptor and antagonize the activity of the receptor. In such an embodiment, the modified signaling agent has reduced affinity and/or activity for IGF1 receptor which allows for the activity of the receptor to be antagonized in an attenuated fashion. In some embodiments, the modified signaling agent has substantially reduced or ablated affinity and/or activity for the insulin receptor and/or IGF1 receptor. In some embodiments, the modified signaling agent has reduced affinity and/or activity for IGF2 receptor which allows for the activity of the receptor to be antagonized in an attenuated fashion. In an embodiment, the modified signaling agent has substantially reduced or ablated affinity and/or activity for the insulin receptor and accordingly does not interfere with insulin signaling. In various embodiments, this applies to cancer treatment. In various embodiments, the present agents may prevent IR isoform A from causing resistance to cancer treatments.

In one embodiment, the present chimeric protein has (i) a targeting moiety against Clec9A and (ii) a targeting moiety which is directed against a tumor cell, along with any of the modified or mutant signaling agents described

herein. In an embodiment, the present chimeric protein has a targeting moiety directed against Clec9A on dendritic cells and a second targeting moiety directed against PD-L1 or PD-L2 on tumor cells.

In one embodiment, the present chimeric protein has (i) a targeting moiety against Clec9A and (ii) a targeting moiety which is directed against a checkpoint inhibitor marker, along with any of the modified or mutant interferons described herein. In an embodiment, the present chimeric protein has a targeting moiety directed against Clec9A on dendritic cells and a second targeting moiety directed against PD-1.

In various embodiments, the signaling agent is a toxin or toxic enzyme. In some embodiments, the toxin or toxic enzyme is derived from plants and bacteria. Illustrative toxins or toxic enzymes include, but are not limited to, the diphtheria toxin, Pseudomonas toxin, anthrax toxin, ribosome-inactivating proteins (RIPs) such as ricin and saporin, modeccin, abrin, gelonin, and poke weed antiviral protein. Additional toxins include those disclosed in Mathew et al., (2009) Cancer Sci 100(8): 1359-65, the entire disclosures are hereby incorporated by reference. In such embodiments, the chimeric proteins of the invention may be utilized to induce cell death in cell-type specific manner. In such embodiments, the toxin may be modified, e.g. mutated, to reduce affinity and/or activity of the toxin for an attenuated effect, as described with other signaling agents herein.

Multi-Specific Chimeras and Fusions with Signaling Agents

In various embodiments, the Clec9A binding agent of the invention is part of a chimera or fusion with one or more signaling agents as described herein and/or one or more additional targeting moieties. Accordingly, the present invention provides for chimeric or fusion proteins that include one or more signaling agents and a targeting moiety against Clec9A and/or one or more additional targeting moieties.

In various embodiments, the Clec9A binding agent of the invention is multispecific, *i.e.*, the Clec9A binding agent comprises two or more targeting moieties having recognition domains that recognize and bind two or more targets, e.g. antigens, or receptors, or epitopes. In such embodiments, the Clec9A binding agent of the invention may comprise two or more targeting moieties having recognition domains that recognize and bind two or more epitopes on the same antigen or on different antigens. In various embodiments, such multi-specific Clec9A binding agents exhibit advantageous properties such as increased avidity and/or improved selectivity. In an embodiment, the Clec9A binding agent of the invention comprises two targeting moieties and is bispecific, *i.e.*, binds and recognizes two epitopes on the same antigen or on different antigens.

In various embodiments, the multispecific Clec9A binding agent of the invention comprises two or more targeting moieties with each targeting moiety being an antibody or an antibody derivative as described herein. In an embodiment, the multispecific Clec9A binding agent of the invention comprises at least one VHH comprising an antigen recognition domain against Clec9A and one antibody or antibody derivative comprising an antigen recognition domain against a tumor antigen.

In various embodiments, the present multispecific Clec9A binding agents have two or more targeting moieties that target different antigens or receptors, and one targeting moiety may be attenuated for its antigen or receptor, e.g.

the targeting moiety binds its antigen or receptor with a low affinity or avidity (including, for example, at an affinity or avidity that is less than the affinity or avidity the other targeting moiety has for its antigen or receptor, for instance the difference between the binding affinities may be about 10-fold, or 25-fold, or 50-fold, or 100-fold, or 300-fold, or 500-fold, or 1000-fold, or 5000-fold; for instance the lower affinity or avidity targeting moiety may bind its antigen or receptor at a K_D in the mid- to high-nM or low- to mid- μ M range while the higher affinity or avidity targeting moiety may bind its antigen or receptor at a K_D in the mid- to high-pM or low- to mid-nM range). For instance, in some embodiments, the present multispecific Clec9A binding agents comprises an attenuated targeting moiety that is directed against a promiscuous antigen or receptor, which may improve targeting to a cell of interest (e.g. via the other targeting moiety) and prevent effects across multiple types of cells, including those not being targeted for therapy (e.g. by binding promiscuous antigen or receptor at a higher affinity than what is provided in these embodiments).

The multispecific Clec9A binding agent of the invention may be constructed using methods known in the art, see for example, U.S. Patent No. 9,067,991, U.S. Patent Publication No. 20110262348 and WO 2004/041862, the entire contents of which are hereby incorporated by reference. In an illustrative embodiment, the multispecific Clec9A binding agent of the invention comprising two or more targeting moieties may be constructed by chemical crosslinking, for example, by reacting amino acid residues with an organic derivatizing agent as described by Blattler *et al.*, Biochemistry 24,1517-1524 and EP294703, the entire contents of which are hereby incorporated by reference. In another illustrative embodiment, the multispecific Clec9A binding agent comprising two or more targeting moieties is constructed by genetic fusion, *i.e.*, constructing a single polypeptide which includes the polypeptides of the individual targeting moieties. For example, a single polypeptide construct may be formed which encodes a first VHH with an antigen recognition domain against Clec9A and a second antibody or antibody derivative with an antigen recognition domain against a tumor antigen. A method for producing bivalent or multivalent VHH polypeptide constructs is disclosed in PCT patent application WO 96/34103, the entire contents of which is hereby incorporated by reference. In a further illustrative embodiment, the multispecific Clec9A binding agent of the invention may be constructed by using linkers. For example, the carboxy-terminus of a first VHH with an antigen recognition domain against Clec9A may be linked to the amino-terminus of a second antibody or antibody derivative with an antigen recognition domain against a tumor antigen (or vice versa). Exemplary linkers that may be used are described herein. In some embodiments, the components of the multispecific Clec9A binding agent of the invention are directly linked to each other without the use of linkers.

In various embodiments, the multi-specific Clec9A binding agent of the invention recognizes and binds to Clec9A and one or more antigens found on one or more immune cells, which can include, without limitation, megakaryocytes, thrombocytes, erythrocytes, mast cells, basophils, neutrophils, eosinophils, monocytes, macrophages, natural killer cells, T lymphocytes (e.g., cytotoxic T lymphocytes, T helper cells, natural killer T cells), B lymphocytes, plasma cells, dendritic cells, or subsets thereof. In some embodiments, the Clec9A binding agent specifically binds to an antigen of interest and effectively directly or indirectly recruits one or more immune cells.

In various embodiments, the multi-specific Clec9A binding agent of the invention recognizes and binds to Clec9A and one or more antigens found on tumor cells. In these embodiments, the present Clec9A binding agents may directly or indirectly recruit an immune cell to a tumor cell or the tumor microenvironment. In some embodiments, the present Clec9A binding agents may directly or indirectly recruit an immune cell, *e.g.* an immune cell that can kill and/or suppress a tumor cell (*e.g.*, a CTL), to a site of action (such as, by way of non-limiting example, the tumor microenvironment).

In some embodiments, the present Clec9A binding agents are capable of, or find use in methods involving, shifting the balance of immune cells in favor of immune attack of a tumor. For instance, the present Clec9A binding agents can shift the ratio of immune cells at a site of clinical importance in favor of cells that can kill and/or suppress a tumor (*e.g.* T cells, cytotoxic T lymphocytes, T helper cells, natural killer (NK) cells, natural killer T (NKT) cells, anti-tumor macrophages (*e.g.* M1 macrophages), neutrophils, B cells, dendritic cells or subsets thereof and in opposition to cells that protect tumors (*e.g.* myeloid-derived suppressor cells (MDSCs), regulatory T cells (Tregs); tumor associated neutrophils (TANs), M2 macrophages, tumor associated macrophages (TAMs), or subsets thereof). In some embodiments, the present Clec9A binding agent is capable of increasing a ratio of effector T cells to regulatory T cells.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to an antigen associated with tumor cells. In some embodiments, the targeting moiety directly or indirectly recruits tumor cells. For instance, in some embodiments, the recruitment of the tumor cell is to one or more effector cell (*e.g.* an immune cell as described herein) that can kill and/or suppress the tumor cell. In some embodiments, the targeting moiety directly or indirectly recruits T cells to a tumor cell, for example, by virtue of the two targeting moieties interacting with their respective antigens on a tumor and Clec9A -positive immune cell (*e.g.* dendritic cells).

Tumor cells, or cancer cells refer to an uncontrolled growth of cells or tissues and/or an abnormal increased in cell survival and/or inhibition of apoptosis which interferes with the normal functioning of bodily organs and systems. For example, tumor cells include benign and malignant cancers, polyps, hyperplasia, as well as dormant tumors or micrometastases. Illustrative tumor cells include, but are not limited to cells of: basal cell carcinoma, biliary tract cancer; bladder cancer; bone cancer; brain and central nervous system cancer; breast cancer; cancer of the peritoneum; cervical cancer; choriocarcinoma; colon and rectum cancer; connective tissue cancer; cancer of the digestive system; endometrial cancer; esophageal cancer; eye cancer; cancer of the head and neck; gastric cancer (including gastrointestinal cancer); glioblastoma; hepatic carcinoma; hepatoma; intra-epithelial neoplasm; kidney or renal cancer; larynx cancer; leukemia; liver cancer; lung cancer (*e.g.*, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung); melanoma; myeloma; neuroblastoma; oral cavity cancer (lip, tongue, mouth, and pharynx); ovarian cancer; pancreatic cancer; prostate cancer; retinoblastoma; rhabdomyosarcoma; rectal cancer; cancer of the respiratory system; salivary gland carcinoma; sarcoma; skin cancer; squamous cell cancer; stomach cancer; testicular cancer; thyroid cancer; uterine or endometrial cancer; cancer of the urinary system; vulval cancer; lymphoma including Hodgkin's and non-Hodgkin's

lymphoma, as well as B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia; chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblastic leukemia; as well as other carcinomas and sarcomas; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (e.g. that associated with brain tumors), and Meigs' syndrome.

Tumor cells, or cancer cells also include, but are not limited to, carcinomas, e.g. various subtypes, including, for example, adenocarcinoma, basal cell carcinoma, squamous cell carcinoma, and transitional cell carcinoma), sarcomas (including, for example, bone and soft tissue), leukemias (including, for example, acute myeloid, acute lymphoblastic, chronic myeloid, chronic lymphocytic, and hairy cell), lymphomas and myelomas (including, for example, Hodgkin and non-Hodgkin lymphomas, light chain, non-secretory, MGUS, and plasmacytomas), and central nervous system cancers (including, for example, brain (e.g. gliomas (e.g. astrocytoma, oligodendroglioma, and ependymoma), meningioma, pituitary adenoma, and neuromas, and spinal cord tumors (e.g. meningiomas and neurofibroma).

Illustrative tumor antigens include, but are not limited to, MART-1/Melan-A, gp100, Dipeptidyl peptidase IV (DPPIV), adenosine deaminase-binding protein (ADA bp), cyclophilin b, Colorectal associated antigen (CRC)-0017-1A/GA733, Carcinoembryonic Antigen (CEA) and its immunogenic epitopes CAP-1 and CAP-2, etv6, aml1, Prostate Specific Antigen (PSA) and its immunogenic epitopes PSA-1, PSA-2, and PSA-3, prostate-specific membrane antigen (PSMA), T-cell receptor/CD3-zeta chain, MAGE-family of tumor antigens (e.g., MAGE-A1, MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A7, MAGE-A8, MAGE-A9, MAGE-A10, MAGE-A11, MAGE-A12, MAGE-Xp2 (MAGE-B2), MAGE-Xp3 (MAGE-B3), MAGE-Xp4 (MAGE-B4), MAGE-C1, MAGE-C2, MAGE-C3, MAGE-C4, MAGE-C5), GAGE-family of tumor antigens (e.g., GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, GAGE-7, GAGE-8, GAGE-9), BAGE, RAGE, LAGE-1, NAG, GnT-V, MUM-1, CDK4, tyrosinase, p53, MUC family, HER2/neu, p21ras, RCAS1, α -fetoprotein, E-cadherin, α -catenin, β -catenin and γ -catenin, p120ctn, gp100 Pmel117, PRAME, NY-ESO-1, cdc27, adenomatous polyposis coli protein (APC), fodrin, Connexin 37, Ig-idiotype, p15, gp75, GM2 and GD2 gangliosides, viral products such as human papilloma virus proteins, Smad family of tumor antigens, Imp-1, NA, EBV-encoded nuclear antigen (EBNA)-1, brain glycogen phosphorylase, SSX-1, SSX-2 (HOM-MEL-40), SSX-1, SSX-4, SSX-5, SCP-1 CT-7, c-erbB-2, CD19, CD20, CD22, CD30, CD33, CD37, CD56, CD70, CD74, CD138, AGS16, MUC1, GPNMB, Ep-CAM, PD-L1, PD-L2, PMSA, and BCMA (TNFRSF17).. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these tumor antigens.

In some embodiments, the present multi-specific Clec9A binding agent recognizes and binds to Clec9A as well as an antigen on a tumor cell. In some embodiments, the multi-specific Clec9A binding agent directly or indirectly recruits CTLs to the tumor cell or tumor microenvironment.

In various embodiments, the present multi-specific Clec9A binding agent has targeting moieties which target two different cells (e.g. to make a synapse) or the same cell (e.g. to get a more concentrated signaling agent effect).

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (e.g. antigen, receptor) associated with T cells. In some embodiments, the targeting moiety recruits directly or indirectly T cells. In an embodiment, the antigen recognition domains specifically bind to effector T cells. In some embodiments, the antigen recognition domain directly or indirectly recruits effector T cells, e.g., in some embodiments, to a therapeutic site (e.g. a locus with one or more disease cell or cell to be modulated for a therapeutic effect). Illustrative effector T cells include cytotoxic T cells (e.g. $\alpha\beta$ TCR, CD3⁺, CD8⁺, CD45RO⁺); CD4⁺ effector T cells (e.g. $\alpha\beta$ TCR, CD3⁺, CD4⁺, CCR7⁺, CD62L^{hi}, IL-7R/CD127⁺); CD8⁺ effector T cells (e.g. $\alpha\beta$ TCR, CD3⁺, CD8⁺, CCR7⁺, CD62L^{hi}, IL-7R/CD127⁺); effector memory T cells (e.g. CD62L^{low}, CD44⁺, TCR, CD3⁺, IL-7R/CD127⁺, IL-15R⁺, CCR7^{low}); central memory T cells (e.g. CCR7⁺, CD62L⁺, CD27⁺; or CCR7^{hi}, CD44⁺, CD62L^{hi}, TCR, CD3⁺, IL-7R/CD127⁺, IL-15R⁺); CD62L⁺ effector T cells; CD8⁺ effector memory T cells (TEM) including early effector memory T cells (CD27⁺ CD62L⁻) and late effector memory T cells (CD27⁻ CD62L⁻) (TemE and TemL, respectively); CD127⁺CD25^(low/-) effector T cells; CD127⁽⁻⁾CD25⁽⁻⁾ effector T cells; CD8⁺ stem cell memory effector cells (TSCM) (e.g. CD44^(low)CD62L^(high)CD122^(high)sca⁽⁺⁾); TH1 effector T-cells (e.g. CXCR3⁺, CXCR6⁺ and CCR5⁺; or $\alpha\beta$ TCR, CD3⁺, CD4⁺, IL-12R⁺, IFN γ R⁺, CXCR3⁺); TH2 effector T cells (e.g. CCR3⁺, CCR4⁺ and CCR8⁺; or $\alpha\beta$ TCR, CD3⁺, CD4⁺, IL-4R⁺, IL-33R⁺, CCR4⁺, IL-17RB⁺, CRTH2⁺); TH9 effector T cells (e.g. $\alpha\beta$ TCR, CD3⁺, CD4⁺); TH17 effector T cells (e.g. $\alpha\beta$ TCR, CD3⁺, CD4⁺, IL-23R⁺, CCR6⁺, IL-1R⁺); CD4⁺CD45RO⁺CCR7⁺ effector T cells, ICOS⁺ effector T cells; CD4⁺CD45RO⁺CCR7⁽⁻⁾ effector T cells; and effector T cells secreting IL-2, IL-4 and/or IFN- γ .

Illustrative T cell antigens of interest include, for example (and inclusive of the extracellular domains, where applicable): CD8, CD3, SLAMF4, IL-2R α , 4-1BB/TNFRSF9, IL-2 R β , ALCAM, B7-1, IL-4 R, B7-H3, BLAME/SLAMFS, CEACAM1, IL-6 R, CCR3, IL-7 R α , CCR4, CXCR1/IL-8 R α , CCR5, CCR6, IL-10R α , CCR 7, IL-10 R β , CCR8, IL-12 R β 1, CCR9, IL-12 R β 2, CD2, IL-13 R α 1, IL-13, CD3, CD4, ILT2/CDS5j, ILT3/CDS5k, ILT4/CDS5d, ILT5/CDS5a, Integrin α 4/CD49d, CDS, Integrin α E/CD103, CD6, Integrin α M/CD 11 b, CDS, Integrin α X/CD11c, Integrin β 2/CD18, KIR/CD15S, CD27/TNFRSF7, KIR2DL1, CD2S, KIR2DL3, CD30/TNFRSF8, KIR2DL4/CD15Sd, CD31/PECAM-1, KIR2DS4, CD40 Ligand/TNFSF5, LAG-3, CD43, LAIR1, CD45, LAIR2, CDS3, Leukotriene B4-R1, CDS4/SLAMF5, NCAM-L1, CD94, NKG2A, CD97, NKG2C, CD229/SLAMF3, NKG2D, CD2F-10/SLAMF9, NT-4, CD69, NTB-A/SLAMF6, Common γ Chain/IL-2 R γ , Osteopontin, CRACC/SLAMF7, PD-1, CRTAM, PSGL-1, CTLA-4, RANK/TNFRSF11A, CX3CR1, CX3CL1, L-Selectin, CXCR3, SIRP β 1, CXCR4, SLAM, CXCR6, TCCR/WSX-1, DNAM-1, Thymopoietin, EMMPRIN/CD147, TIM-1, EphB6, TIM-2, Fas/TNFRSF6, TIM-3, Fas Ligand/TNFSF6, TIM-4, Fc γ RIII/CD16, TIM-6, TNFR1/TNFRSF1A, Granulysin, TNF RIII/TNFRSF1B, TRAIL R1/TNFRSF10A, ICAM-1/CD54, TRAIL R2/TNFRSF10B, ICAM-2/CD102, TRAILR3/TNFRSF10C, IFN- γ R1, TRAILR4/TNFRSF10D, IFN- γ R2, TSLP, IL-1 R1 and TSLP R. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative T cell antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety against CD8 which is a VHH comprising a single amino acid chain having four "framework regions" or FRs and three "complementary determining regions" or CDRs. As used herein, "framework region" or "FR" refers to a region in the variable domain which is located between the CDRs. As used herein, "complementary determining region" or "CDR" refers to variable regions in VHHs that contains the amino acid sequences capable of specifically binding to antigenic targets.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a VHH against CD8 having a variable domain comprising at least one CDR1, CDR2, and/or CDR3 sequences.

In some embodiments, the CDR1 sequence is selected from SEQ ID NO: 362 or (SEQ ID NO: 18).

In some embodiments, the CDR2 sequence is selected from (SEQ ID NO: 363) or (SEQ ID NO: 364).

In some embodiments, the CDR3 sequence is selected from SEQ ID NO: 365) or (SEQ ID NO: 366) or (SEQ ID NO: 367).

In various embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from the following sequences R3HCD27 (SEQ ID NO: 368) or R3HCD129 (SEQ ID NO: 369) or R2HCD26 (SEQ ID NO: 370).

In various embodiments, the CD8 targeting moiety comprises a VHH having a variable domain comprising at least one CDR1, CDR2, and/or CDR3 sequences as described below.

In some embodiments, the CDR1 sequence is selected from SEQ ID NO: 371 to SEQ ID NO: 438 or SEQ ID NO: 52.

In some embodiments, the CDR2 sequence is selected from SEQ ID NO: 439 to SEQ ID NO: 507.

In some embodiments, the CDR3 sequence is selected from SEQ ID NO: 508 to SEQ ID NO: 576.

In various embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from the following sequences 1CDA 7 (SEQ ID NO: 577) or 1CDA 12 (SEQ ID NO: 578) or 1CDA 14 (SEQ ID NO: 579) or 1CDA 15 (SEQ ID NO: 580) or 1CDA 17 (SEQ ID NO: 581) or 1CDA 18 (SEQ ID NO: 582) or 1CDA 19 (SEQ ID NO: 583) or 1CDA 24 (SEQ ID NO: 584) or 1CDA 26 (SEQ ID NO: 585) or 1CDA 28 (SEQ ID NO: 586) or 1CDA 37 (SEQ ID NO: 587) or 1CDA 43 (SEQ ID NO: 588) or 1CDA 45 (SEQ ID NO: 589) or 1CDA 47 (SEQ ID NO: 590) or 1CDA 48 (SEQ ID NO: 591) or 1CDA 58 (SEQ ID NO: 592) or 1CDA 65 (SEQ ID NO: 593) or 1CDA 68 (SEQ ID NO: 594) or 1CDA 73 (SEQ ID NO: 595) or 1CDA 75 (SEQ ID NO: 596) or 1CDA 86 (SEQ ID NO: 597) or 1CDA 87 (SEQ ID NO: 598) or 1CDA 88 (SEQ ID NO: 599) or 1CDA 89 (SEQ ID NO: 600) or 1CDA 92 (SEQ ID NO: 601) or 1CDA 93 (SEQ ID NO: 602) or 2CDA 1 (SEQ ID NO: 603) or 2CDA 5 (SEQ ID NO: 604) or 2CDA 22 (SEQ ID NO: 605) or 2CDA 28 (SEQ ID NO: 606) or 2CDA 62 (SEQ ID NO: 607) or 2CDA 68 (SEQ ID NO: 608) or 2CDA 73 (SEQ ID NO: 609) or 2CDA 74 (SEQ ID NO: 610) or 2CDA 75 (SEQ ID NO: 611) or 2CDA 77 (SEQ ID NO: 612) or 2CDA 81 (SEQ ID NO: 613) or 2CDA 87 (SEQ ID NO: 614) or 2CDA 88 (SEQ ID NO: 615) or 2CDA 89 (SEQ ID NO: 616) or 2CDA 91 (SEQ ID NO: 617) or 2CDA 92 (SEQ ID NO: 618) or 2CDA 93 (SEQ ID NO: 619) or 2CDA 94 (SEQ ID NO: 620) or 2CDA 95 (SEQ ID NO: 621) or 3CDA 3 (SEQ ID NO: 622) or 3CDA 8 (SEQ ID

NO: 623) or 3CDA 11 (SEQ ID NO: 624) or 3CDA 18 (SEQ ID NO: 625) or 3CDA 19 (SEQ ID NO: 626) or 3CDA 21 (SEQ ID NO: 627) or 3CDA 24 (SEQ ID NO: 628) or 3CDA 28 (SEQ ID NO: 629) or 3CDA 29 (SEQ ID NO: 630) or 3CDA 31 (SEQ ID NO: 631) or 3CDA 32 (SEQ ID NO: 632) or 3CDA 33 (SEQ ID NO: 633) or 3CDA 37 (SEQ ID NO: 634) or 3CDA 40 (SEQ ID NO: 635) or 3CDA 41 (SEQ ID NO: 636) or 3CDA 48 (SEQ ID NO: 637) or 3CDA 57 (SEQ ID NO: 638) or 3CDA 65 (SEQ ID NO: 639) or 3CDA 70 (SEQ ID NO: 640) or 3CDA 73 (SEQ ID NO: 641) or 3CDA 83 (SEQ ID NO: 642) or 3CDA 86 (SEQ ID NO: 643) or 3CDA 88 (SEQ ID NO: 644) or 3CDA 90 (SEQ ID NO: 645). In various exemplary embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from any one of the above sequences without the terminal histidine tag sequence (*i.e.*, HHHHHH; SEQ ID NO: 324).

In some embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 577-645 (provided above) without the HA tag (*i.e.*, YPYDVPDYGS; SEQ ID NO: 325).

In some embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 577-645 (provided above) without the AAA linker (*i.e.*, AAA).

In some embodiments, the CD8 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 577-645 (provided above) without the the AAA linker, HA tag, and terminal histidine tag sequence (*i.e.*, AAAYPYDVPDYGSHHHHHH; SEQ ID NO: 326). In various embodiments, the CD8 targeting moiety comprises an amino acid sequence described in US Patent Publication No. 2014/0271462, the entire contents of which are incorporated by reference. In various embodiments, the CD8 targeting moiety comprises an amino acid sequence described in Table 0.1, Table 0.2, Table 0.3, and/or Figures 1A-12I of US Patent Publication No. 2014/0271462, the entire contents of which are incorporated by reference. In various embodiments, the CD8 targeting moiety comprises a HCDR1 of a HCDR1 of SEQ ID NO: 646 or 647 and/or a HCDR2 of HCDR1 of SEQ ID NO: 646 or 647 and/or a HCDR3 of HCDR1 of SEQ ID NO: 646 or 647 and/or a LCDR1 of LCDR1 of SEQ ID NO: 648 and/or a LCDR2 of LCDR1 of SEQ ID NO: 648 and/or a LCDR3 of LCDR1 of SEQ ID NO: 648, as provided below.

In various embodiments, the present invention contemplates the use of any natural or synthetic analogs, mutants, variants, alleles, homologs and orthologs (herein collectively referred to as "analogs") of the targeting moiety directed against CD8 as described herein. In various embodiments, the amino acid sequence of the targeting moiety directed against CD8 further includes an amino acid analog, an amino acid derivative, or other non-classical amino acids.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with B cells. In some embodiments, the targeting moiety directly or indirectly recruits B cells, *e.g.*, in some embodiments, to a therapeutic site (*e.g.* a locus with one or more disease cell or cell to be modulated for a therapeutic effect). Illustrative B cell antigens of interest include, for example, CD10, CD19, CD20, CD21, CD22, CD23, CD24, CD37, CD38, CD39, CD40, CD70, CD72, CD73, CD74, CDw75, CDw76, CD77, CD78, CD79a/b, CD80, CD81, CD82, CD83, CD84, CD85, CD86, CD89, CD98, CD126, CD127, CDw130, CD138, CDw150, and B-cell maturation

antigen (BCMA). In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative B cell antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically bind to a target (e.g. antigen, receptor) associated with Natural Killer cells. In some embodiments, the targeting moiety directly or indirectly recruits Natural Killer cells, e.g., in some embodiments, to a therapeutic site (e.g. a locus with one or more disease cell or cell to be modulated for a therapeutic effect). Illustrative Natural Killer cell antigens of interest include, for example TIGIT, 2B4/SLAMF4, KIR2DS4, CD155/PVR, KIR3DL1, CD94, LMIR1/CD300A, CD69, LMIR2/CD300c, CRACC/SLAMF7, LMIR3/CD300LF, Kir1alpha, DNAM-1, LMIR5/CD300LB, Fc-epsilon RII, LMIR6/CD300LE, Fc-gamma RI/CD64, MICA, Fc-gamma RIIb/CD32b, MICB, Fc-gamma RIIC/CD32c, MULT-1, Fc-gamma RIIA/CD32a, Nectin-2/CD112, Fc-gamma RIII/CD16, NKG2A, FcRH1/IRTA5, NKG2C, FcRH2/IRTA4, NKG2D, FcRH4/IRTA1, NKp30, FcRH5/IRTA2, NKp44, Fc-Receptor-like 3/CD16-2, NKp46/NCR1, NKp80/KLRF1, NTB-A/SLAMF6, Rae-1, Rae-1 α , Rae-1 β , Rae-1 delta, H60, Rae-1 epsilon, ILT2/CD85j, Rae-1 γ , ILT3/CD85k, TREM-1, ILT4/CD85d, TREM-2, ILT5/CD85a, TREM-3, KIR/CD158, TREML1/TLT-1, KIR2DL1, ULBP-1, KIR2DL3, ULBP-2, KIR2DL4/CD158d and ULBP-3. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative NK cell antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (e.g. antigen, receptor) associated with macrophages/monocytes. In some embodiments, the targeting moiety directly or indirectly recruits macrophages/monocytes, e.g., in some embodiments, to a therapeutic site (e.g. a locus with one or more disease cell or cell to be modulated for a therapeutic effect). Illustrative macrophages/monocyte antigens of interest include, for example SIRP1a, B7-1/CD80, ILT4/CD85d, B7-H1, ILT5/CD85a, Common β Chain, Integrin α 4/CD49d, BLAME/SLAMF8, Integrin α X/CD11c, CCL6/C10, Integrin β 2/CD18, CD155/PVR, Integrin β 3/CD61, CD31/PECAM-1, Latexin, CD36/SR-B3, Leukotriene B4 R1, CD40/TNFRSF5, LIMP1/CD300A, CD45, LMIR2/CD300c, CD68, LMIR3/CD300LF, CD84/SLAMF5, LMIR5/CD300LB, CD97, LMIR6/CD300LE, CD163, LRP-1, CD2F-10/SLAMF9, MARCO, CRACC/SLAMF7, MD-1, ECF-L, MD-2, EMMPRIN/CD147, MGL2, Endoglin/CD105, Osteoactivin/GPNMB, Fc-gamma RI/CD64, Osteopontin, Fc-gamma RIIb/CD32b, PD-L2, Fc-gamma RIIC/CD32c, Siglec-3/CD33, Fc-gamma RIIA/CD32a, SIGNR1/CD209, Fc-gamma RIII/CD16, SLAM, GM-CSF R α , TCCRWSX-1, ICAM-2/CD102, TLR3, IFN-gamma R1, TLR4, IFN-gamma R2, TREM-1, IL-1 RII, TREM-2, ILT2/CD85j, TREM-3, ILT3/CD85k, TREML1/TLT-1, 2B4/SLAMF 4, IL-10 R α , ALCAM, IL-10 R β , AminopeptidaseN/ANPEP, ILT2/CD85j, Common β Chain, ILT3/CD85k, Clq R1/CD93, ILT4/CD85d, CCR1, ILT5/CD85a, CCR2, CD206, Integrin α 4/CD49d, CCR5, Integrin α M/CD11b, CCR8, Integrin α X/CD11c, CD155/PVR, Integrin β 2/CD18, CD14, Integrin β 3/CD61, CD36/SR-B3, LAIR1, CD43, LAIR2, CD45, Leukotriene B4-R1, CD68, LIMP1/CD300A, CD97, LMIR2/CD300c, CD163, LMIR3/CD300LF, Coagulation Factor III/Tissue Factor, LMIR5/CD300LB, CX3CR1, CX3CL1, LMIR6/CD300LE, CXCR4, LRP-1, CXCR6, M-CSF R, DEP-1/CD148, MD-1, DNAM-1, MD-2, EMMPRIN/CD147, MMR, Endoglin/CD105, NCAM-L1, Fc-gamma RI/CD64, PSGL-1, Fc-gamma RIIIC/CD16, RP105, G-CSF R, L-Selectin, GM-CSF R α , Siglec-3/CD33, HVEM/TNFRSF14, SLAM, ICAM-

1/CD54, TCCR/WSX-1, ICAM-2/CD102, TREM-1, IL-6 R, TREM-2, CXCR1/IL-8 RA, TREM-3 and TREML1/TLT-1. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative macrophage/monocyte antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (e.g. antigen, receptor) associated with dendritic cells. In some embodiments, the targeting moiety directly or indirectly recruits dendritic cells, e.g., in some embodiments, to a therapeutic site (e.g. a locus with one or more disease cell or cell to be modulated for a therapeutic effect). Illustrative dendritic cell antigens of interest include, for example, CLEC9A, XCR1, RANK, CD36/SRB3, LOX-1/SR-E1, CD68, MARCO, CD163, SR-A1/MSR, CD5L, SREC-1, CL-PI/COLEC12, SREC-II, LIMP1/SRB2, RP105, TLR4, TLR1, TLR5, TLR2, TLR6, TLR3, TLR9, 4-1BB Ligand/TNFSF9, IL-12/IL-23 p40, 4-Amino-1,8-naphthalimide, ILT2/CD85j, CCL21/6CKine, ILT3/CD85k, 8-oxo-dG, ILT4/CD85d, 8D6A, ILT5/CD85a, A2B5, Integrin α 4/CD49d, A α g, Integrin β 2/CD18, AMICA, Langerin, B7-2/CD86, Leukotriene B4 RI, B7-H3, LMIR1/CD300A, BLAME/SLAMF8, LMIR2/CD300c, Clq R1/CD93, LMIR3/CD300LF, CCR6, LMIR5/CD300LB, CCR7, LMIR6/CD300LE, CD40/TNFRSF5, MAG/Siglec-4-a, CD43, MCAM, CD45, MD-1, CD68, MD-2, CD83, MDL-1/CLEC5A, CD84/SLAMF5, MMR, CD97, NCAM1, CD2F-10/SLAMF9, Osteoactivin GPNMB, Chem 23, PD-L2, CLEC-1, RP105, CLEC-2, CLEC-8, Siglec-2/CD22, CRACC/SLAMF7, Siglec-3/CD33, DC-SIGN, DEC-205, Siglec-5, DC-SIGNR/CD299, Siglec-6, DCAR, Siglec-7, DCIR/CLEC4A, Siglec-9, DEC-205, Siglec-10, Dectin-1/CLEC7A, Siglec-F, Dectin-2/CLEC6A, SIGNR1/CD209, DEP-1/CD148, SIGNR4, DLEC, SLAM, EMMPRIN/CD147, TCCR/WSX-1, Fc- γ R1/CD64, TLR3, Fc- γ RIIB/CD32b, TREM-1, Fc- γ RIIC/CD32c, TREM-2, Fc- γ RIIA/CD32a, TREM-3, Fc- γ RIIC/CD16, TREML1/TLT-1, ICAM-2/CD102, DEC205, and Vanilloid R1. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative DC antigens.

In various embodiments, the present chimeric protein comprises a targeting moiety comprising an amino acid sequence that is at least 60% identical to any one of the sequences disclosed herein. For example, the chimeric protein may comprise a targeting moiety comprising an amino acid sequence that is at least about 60%, at least about 61%, at least about 62%, at least about 63%, at least about 64%, at least about 65%, at least about 66%, at least about 67%, at least about 68%, at least about 69%, at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to any one of the sequences disclosed herein (e.g. about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about

87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, about 99% or about 100% sequence identity to any one of the sequences disclosed herein).

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds a target (*e.g.* antigen, receptor) on immune cells selected from, but not limited to, megakaryocytes, thrombocytes, erythrocytes, mast cells, basophils, neutrophils, and eosinophils. In some embodiments, the antigen recognition domains directly or indirectly recruit megakaryocytes, thrombocytes, erythrocytes, mast cells, basophils, neutrophils, and eosinophil, *e.g.*, in some embodiments, to a therapeutic site (*e.g.* a locus with one or more disease cell or cell to be modulated for a therapeutic effect).

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with megakaryocytes and/or thrombocytes. Illustrative megakaryocyte and/or thrombocyte antigens of interest include, for example, GP IIb/IIIa, GPIb, vWF, PF4, and TSP. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative megakaryocyte and/or thrombocyte antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with erythrocytes. Illustrative erythrocyte antigens of interest include, for example, CD34, CD36, CD38, CD41a (platelet glycoprotein IIb/IIIa), CD41b (GPIIb), CD71 (transferrin receptor), CD105, glycophorin A, glycophorin C, c-kit, HLA-DR, H2 (MHC-II), and Rhesus antigens. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these illustrative erythrocyte antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with mast cells. Illustrative mast cells antigens of interest include, for example, SCFR/CD117, Fc ϵ RI, CD2, CD25, CD35, CD88, CD203c, C5R1, CMAI, FCER1A, FCER2, TPSAB1. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these mast cell antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with basophils. Illustrative basophils antigens of interest include, for example, Fc ϵ RI, CD203c, CD123, CD13, CD107a, CD107b, and CD164. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these basophil antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (*e.g.* antigen, receptor) associated with neutrophils. Illustrative neutrophils antigens of interest include, for example, 7D5, CD10/CALLA, CD13, CD16 (FcRIII), CD18 proteins (LFA-1, CR3, and p150, 95), CD45, CD67, and CD177. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these neutrophil antigens.

In some embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a target (e.g. antigen, receptor) associated with eosinophils. Illustrative eosinophils antigens of interest include, for example, CD35, CD44 and CD69. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these eosinophil antigens.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to any appropriate antigen or receptor or cell surface markers known by the skilled artisan. In some embodiments, the antigen or cell surface marker is a tissue-specific marker. Illustrative tissue-specific markers include, but are not limited to, endothelial cell surface markers such as ACE, CD14, CD34, CDH5, ENG, ICAM2, MCAM, NOS3, PECAMI, PROCR, SELE, SELP, TEK, THBD, VCAMI, VWF; smooth muscle cell surface markers such as ACTA2, MYH10, MYH11, MYH9, MYOCD; fibroblast (stromal) cell surface markers such as ALCAM, CD34, COL1A1, COL1A2, COL3A1, FAP, PH-4; epithelial cell surface markers such as CDID, K6IRS2, KRT10, KRT13, KRT17, KRT18, KRT19, KRT4, KRT5, KRT8, MUC1, TACSTD1; neovasculture markers such as CD13, TFNA, Alpha-v beta-3 ($\alpha_v\beta_3$), E-selectin; and adipocyte surface markers such as ADIPOQ, FABP4, and RETN. In various embodiments, the Clec9A binding agent comprises a targeting moiety that binds one or more of these antigens.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a checkpoint marker expressed on a T cell, e.g. one or more of PD-1, CD28, CTLA4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD40L, TIM3, and A2aR.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to a checkpoint marker, e.g. one or more of PD-1/PD-L1 or PD-L2, CD28/CD80 or CD86, CTLA4/ CD80 or CD86, ICOS/ICOSL or B7RP1, BTLA/HVEM, KIR, LAG3, CD137/CD137L, OX40/OX40L, CD27, CD40L, TIM3/Ga19, and A2aR.

By way of non-limiting example, in various embodiments, the present multispecific Clec9A binding agent comprises a targeting moiety directed against (i) CD8; (ii) a checkpoint marker expressed on a T cell, e.g. one or more of PD-1, CD28, CTLA4, ICOS, BTLA, KIR, LAG3, CD137, OX40, Cd27, CD40L, TIM3, and A2aR and/or (iii) a targeting moiety is directed against a tumor cell, along with any of the modified (e.g. mutant) signaling agents described herein.

In various embodiments, the present multi-specific Clec9A binding agent has one or more targeting moieties directed against PD-1. In some embodiments, the Clec9A binding agent has one or more targeting moieties which selectively bind a PD-1 polypeptide. In some embodiments, the Clec9A binding agent comprises one or more antibodies, antibody derivatives or formats, peptides or polypeptides, or fusion proteins that selectively bind a PD-1 polypeptide.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a VHH against PD1 having a variable domain comprising at least one CDR1, CDR2, and/or CDR3 sequences.

In some embodiments, the PD1 CDR1 sequence is selected from SEQ ID NO: 649 to SEQ ID NO: 662.

In some embodiments, the PD1 CDR2 sequence is selected from SEQ ID NO: 663 to SEQ ID NO: 676.

In some embodiments, the PD1 CDR3 sequence is selected from SEQ ID NO: 677 to SEQ ID NO: 689.

In various exemplary embodiments, the PD1 targeting moiety comprises an amino acid sequence selected from the following sequences: 2PD23 (SEQ ID NO: 690) or 2PD26 (SEQ ID NO: 691) or 2PD90 (SEQ ID NO: 692) or 2PD106 (SEQ ID NO: 693) or 2PD16 (SEQ ID NO: 694) or 2PD71 (SEQ ID NO: 695) or 2PD152 (SEQ ID NO: 696) or 2PD12 (SEQ ID NO: 697) or 3PD55 (SEQ ID NO: 698) or 3PD82 (SEQ ID NO: 699) or 2PD8 (SEQ ID NO: 700) or 2PD27 (SEQ ID NO: 701) or 2PD82 (SEQ ID NO: 702) or 3PD36 (SEQ ID NO: 703).

In various exemplary embodiments, the PD1 targeting moiety comprises an amino acid sequence selected from any one of the above without the terminal histidine tag sequence (*i.e.*, HHHHHH; SEQ ID NO: 324).

In some embodiments, the PD1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 690-703 (provided above) without the HA tag (*i.e.*, YPYDVPDYGS; SEQ ID NO: 325).

In some embodiments, the PD1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 690-703 (provided above) without the AAA linker (*i.e.*, AAA).

In some embodiments, the PD1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 690-703 (provided above) without the the AAA linker, HA tag, and terminal histidine tag sequence (*i.e.*, AAAYPYDVPDYGSHHHHHH; SEQ ID NO: 326). In an embodiment, the targeting moiety comprises the anti-PD-1 antibody pembrolizumab (aka MK-3475, KEYTRUDA), or fragments thereof. Pembrolizumab and other humanized anti-PD-1 antibodies are disclosed in Hamid, et al. (2013) New England Journal of Medicine 369 (2): 134-44, US 8,354,509, and WO 2009/114335, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, pembrolizumab or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 704 and/or a light chain comprising the amino acid sequence of SEQ ID NO: 705.

In an embodiment, the targeting moiety comprises the anti-PD-1 antibody, nivolumab (aka BMS-936558, MDX-1106, ONO-4538, OPDIVO), or fragments thereof. Nivolumab (clone 5C4) and other human monoclonal antibodies that specifically bind to PD-1 are disclosed in US 8,008,449 and WO 2006/121168, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, nivolumab or an antigen-binding fragment thereof comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 706 and/or a light chain comprising the amino acid sequence of SEQ ID NO: 707.

In an embodiment, the targeting moiety comprises the anti-PD-1 antibody pidilizumab (aka CT-011, hBAT or hBAT-1), or fragments thereof. Pidilizumab and other humanized anti-PD-1 monoclonal antibodies are disclosed in US 2008/0025980 and WO 2009/101611, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, the anti-PD-1 antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a light chain variable regions comprising an amino acid sequence selected from SEQ

ID NOS: 15-18 of US 2008/0025980: SEQ ID No: 15 of US 2008/0025980 (SEQ ID NO: 708); SEQ ID No: 16 of US 2008/0025980 (SEQ ID NO: 709); SEQ ID No: 17 of US 2008/0025980 (SEQ ID NO: 710); SEQ ID No: 18 of US 2008/0025980 (SEQ ID NO: 711); and/or a heavy chain comprising an amino acid sequence selected from SEQ ID NOS: 20-24 of US 2008/0025980: SEQ ID No: 20 of US 2008/0025980 (SEQ ID NO: 712); SEQ ID No: 21 of US 2008/0025980 (SEQ ID NO: 713); SEQ ID No: 22 of US 2008/0025980 (SEQ ID NO: 714); SEQ ID No: 23 of US 2008/0025980 (SEQ ID NO: 715); SEQ ID No: 24 of US 2008/0025980 (SEQ ID NO: 716).

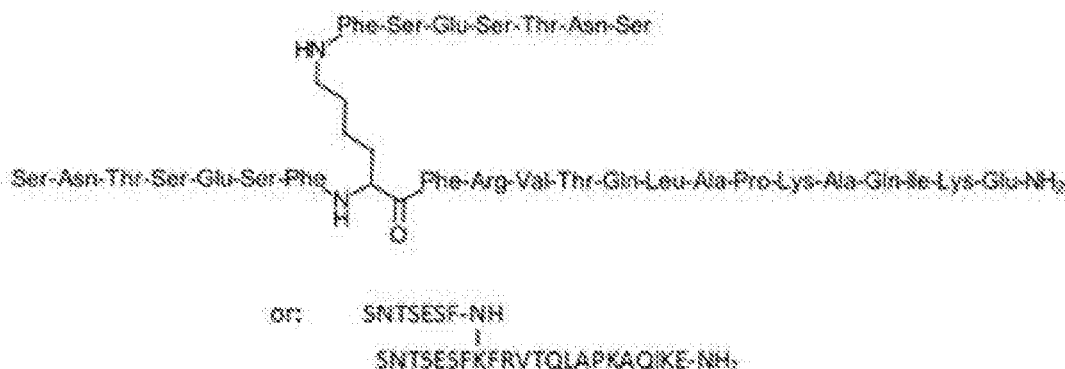
In an embodiment, the targeting moiety comprises a light chain comprising SEQ ID NO:18 of US 2008/0025980 and a heavy chain comprising SEQ ID NO:22 of US 2008/0025980.

In an embodiment, the targeting moiety comprises AMP-514 (aka MEDI-0680).

In an embodiment, the targeting moiety comprises the PD-L2-Fc fusion protein AMP-224, which is disclosed in WO2010/027827 and WO 2011/066342, the entire disclosures of which are hereby incorporated by reference. In such an embodiment, the targeting moiety may include a targeting domain which comprises SEQ ID NO:4 of WO2010/027827 (SEQ ID NO: 717) and/or the B7-DC fusion protein which comprises SEQ ID NO:83 of WO2010/027827 (SEQ ID NO: 718).

In an embodiment, the targeting moiety comprises the peptide AUNP 12 or any of the other peptides disclosed in US 2011/0318373 or 8,907,053. For example, the targeting moiety may comprise AUNP 12 (*i.e.*, Compound 8 or SEQ ID NO:49 of US 2011/0318373) which has the sequence of SEQ ID NO: 719:

SNTSESEFK (SNTSESF) FRVTQLAPKAQIKE-NH₂



In an embodiment, the targeting moiety comprises the anti-PD-1 antibody 1E3, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1E3 or an antigen-binding fragment thereof for use in the methods provided herein comprises a

heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 720; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 721.

In an embodiment, the targeting moiety comprises the anti-PD-1 antibody 1E8, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1E8 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 722; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 723.

In an embodiment, the targeting moiety comprises the anti-PD-1 antibody 1H3, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1H3 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 724; and/or light chain variable region comprising the amino acid sequence of SEQ ID NO: 725.

In an embodiment, the targeting moiety comprises a VHH directed against PD-1 as disclosed, for example, in US 8,907,065 and WO 2008/071447, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, the VHHs against PD-1 comprise SEQ ID NOS: 347-351 of US 8,907,065: SEQ ID No: 347 of US 8,907,065 (SEQ ID NO: 726); SEQ ID No: 348 of US 8,907,065 (SEQ ID NO: 727); SEQ ID No: 349 of US 8,907,065 (SEQ ID NO: 728); SEQ ID No: 350 of US 8,907,065 (SEQ ID NO: 729); SEQ ID No: 351 of US 8,907,065 (SEQ ID NO: 730).

In an embodiment, the targeting moiety comprises any one of the anti-PD-1 antibodies, or fragments thereof, as disclosed in US2011/0271358 and WO2010/036959, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID NOS: 25-29 of US2011/0271358: SEQ ID No: 25 of US2011/0271358 (SEQ ID NO: 731); SEQ ID No: 26 of US2011/0271358 (SEQ ID NO: 732); SEQ ID No: 27 of US2011/0271358 (SEQ ID NO: 733); SEQ ID No: 28 of US2011/0271358 (SEQ ID NO: 734); SEQ ID No: 29 of US2011/0271358 (SEQ ID NO: 735); and/or a light chain comprising an amino acid sequence selected from SEQ ID NOS: 30-33 of US2011/0271358: SEQ ID No: 30 of US2011/0271358 (SEQ ID NO: 736); SEQ ID No: 31 of US2011/0271358 (SEQ ID NO: 737); SEQ ID No: 32 of US2011/0271358 (SEQ ID NO: 738); SEQ ID No: 33 of US2011/0271358 (SEQ ID NO: 739).

In various embodiments, the present multi-specific Clec9A binding agent comprises one or more antibodies directed against PD-1, or antibody fragments thereof, selected from TSR-042 (Tesar, Inc.), REGN2810 (Regeneron Pharmaceuticals, Inc.), PDR001 (Novartis Pharmaceuticals), and BGB-A317 (BeiGene Ltd.)

In various embodiments, the present multi-specific Clec9A binding agent has one or more targeting moieties directed against PD-L1. In some embodiments, the Clec9A binding agent has one or more targeting moieties which

selectively bind a PD-L1 polypeptide. In some embodiments, the Clec9A binding agent comprises one or more antibodies, antibody derivatives or formats, peptides or polypeptides, or fusion proteins that selectively bind a PD-L1 polypeptide.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a VHH against PD-L1 having a variable domain comprising at least one CDR1, CDR2, and/or CDR3 sequences.

In some embodiments, the PD-L1 CDR1 sequence is selected from SEQ ID NO: 740 to SEQ ID NO: 770.

In some embodiments, the PD-L1 CDR2 sequence is selected from SEQ ID NO: 771 to SEQ ID NO: 801.

In some embodiments, the PD-L1 CDR3 sequence is selected from SEQ ID NO: 802 to SEQ ID NO: 832.

In various exemplary embodiments, the PD-L1 targeting moiety comprises an amino acid sequence selected from the following sequences: 2LIG2 (SEQ ID NO: 833) or 2LIG3 (SEQ ID NO: 834) or 2LIG16 (SEQ ID NO: 835) or 2LIG22 (SEQ ID NO: 836) or 2LIG27 (SEQ ID NO: 837) or 2LIG29 (SEQ ID NO: 838) or 2LIG30 (SEQ ID NO: 839) or 2LIG34 (SEQ ID NO: 840) or 2LIG35 (SEQ ID NO: 841) or 2LIG48 (SEQ ID NO: 842) or 2LIG65 (SEQ ID NO: 843) or 2LIG85 (SEQ ID NO: 844) or 2LIG86 (SEQ ID NO: 845) or 2LIG89 (SEQ ID NO: 846) or 2LIG97 (SEQ ID NO: 847) or 2LIG99 (SEQ ID NO: 848) or 2LIG109 (SEQ ID NO: 849) or 2LIG127 (SEQ ID NO: 850) or 2LIG139 (SEQ ID NO: 851) or 2LIG176 (SEQ ID NO: 852) or 2LIG189 (SEQ ID NO: 853) or 3LIG3 (SEQ ID NO: 854) or 3LIG7 (SEQ ID NO: 855) or 3LIG8 (SEQ ID NO: 856) or 3LIG9 (SEQ ID NO: 857) or 3LIG18 (SEQ ID NO: 858) or 3LIG20 (SEQ ID NO: 859) or 3LIG28 (SEQ ID NO: 860) or 3LIG29 (SEQ ID NO: 861) or 3LIG30 (SEQ ID NO: 862) or 3LIG33 (SEQ ID NO: 863).

In various exemplary embodiments, the PD-L1 targeting moiety comprises an amino acid sequence selected from any one of the above sequences without the terminal histidine tag sequence (*i.e.*, HHHHHH; SEQ ID NO: 324).

In some embodiments, the PD-L1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 833-863 (provided above) without the HA tag (*i.e.*, YPYDVPDYGS; SEQ ID NO: 325).

In some embodiments, the PD-L1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 833-863 (provided above) without the AAA linker (*i.e.*, AAA).

In some embodiments, the PD-L1 targeting moiety comprises an amino acid sequence selected from SEQ ID Nos: 833-863 (provided above) without the the AAA linker, HA tag, and terminal histidine tag sequence (*i.e.*, AAAPYDVPDYGSHHHHHH; SEQ ID NO: 326). In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody MEDI4736 (aka durvalumab), or fragments thereof. MEDI4736 is selective for PD-L1 and blocks the binding of PD-L1 to the PD-1 and CD80 receptors. MEDI4736 and antigen-binding fragments thereof for use in the methods provided herein comprises a heavy chain and a light chain or a heavy chain variable region and a light chain variable region. The sequence of MEDI4736 is disclosed in WO/2016/06272, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, MEDI4736 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising the amino acid sequence of (SEQ ID NO: 864); and/or a light chain comprising the amino acid sequence of SEQ ID NO: 865.

In illustrative embodiments, the MEDI4736 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:4 of WO/2016/06272 (SEQ ID NO: 866); and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO:3 of WO/2016/06272 (SEQ ID NO: 867).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody atezolizumab (aka MPDL3280A, RG7446), or fragments thereof. In illustrative embodiments, atezolizumab or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising the amino acid sequence of: SEQ ID NO: 868; and/or a light chain comprising the amino acid sequence of: SEQ ID NO: 869.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody avelumab (aka MSB0010718C), or fragments thereof. In illustrative embodiments, avelumab or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 870; and/or a light chain comprising the amino acid sequence of SEQ ID NO: 871.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody BMS-936559 (aka 12A4, MDX-1105), or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, BMS-936559 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 872; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 873.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 3G10, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 3G10 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 874; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 875.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 10A5, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 10A5 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 876; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 877.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 5F8, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 5F8 or an antigen-binding fragment thereof for use in the methods provided herein

comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 878; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 879.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 10H10, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 10H10 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 880; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 881.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 1B12, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1B12 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 882; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 883.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 7H1, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 7H1 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 884; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 885.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 11E6, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 11E6 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 886; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 887.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 12B7, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 12B7 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 888; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 889.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 13G4, or fragments thereof, as disclosed in US 2013/0309250 and WO2007/005874, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 13G4 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 890; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 891.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 1E12, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1E12 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 892; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 893.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 1F4, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 1F4 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 894; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 895.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2G11, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2G11 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 896; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 897.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 3B6, or fragments thereof, as disclosed in US 2014/0044738, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 3B6 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 898; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 899.

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 3D10, or fragments thereof, as disclosed in US 2014/0044738 and WO2012/145493, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 3D10 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 900; and/or a light chain variable region comprising the amino acid sequence of SEQ ID NO: 901.

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies disclosed in US2011/0271358 and WO2010/036959, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 34-38 of US2011/0271358: SEQ ID No: 34 of US2011/0271358 (SEQ ID NO: 902); SEQ ID No: 35 of US2011/0271358 (SEQ ID NO: 903); SEQ ID No: 36 of US2011/0271358 (SEQ ID NO: 904); SEQ ID No: 37 of US2011/0271358 (SEQ ID NO: 905); SEQ ID No: 38 of US2011/0271358 (SEQ ID NO: 906); and/or a light chain comprising an amino acid sequence selected from SEQ ID Nos: 39-42 of US2011/0271358: SEQ ID No: 39 of US2011/0271358

(SEQ ID NO: 907); SEQ ID No: 40 of US2011/0271358 (SEQ ID NO: 908); SEQ ID No: 41 of US2011/0271358 (SEQ ID NO: 909); SEQ ID No: 42 of US2011/0271358 (SEQ ID NO: 910).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.7A4, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.7A4 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 2 of WO 2011/066389 (SEQ ID NO: 911); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 7 of WO 2011/066389 (SEQ ID NO: 912).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.9D10, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.9D10 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 12 of WO 2011/066389 (SEQ ID NO: 913); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 17 of WO 2011/066389 (SEQ ID NO: 914).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.14H9, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.14H9 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 22 of WO 2011/066389 (SEQ ID NO: 915); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 27 of WO 2011/066389 (SEQ ID NO: 916).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.20A8, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.20A8 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 32 of WO 2011/066389 (SEQ ID NO: 917); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 37 of WO 2011/066389 (SEQ ID NO: 918).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 3.15G8, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 3.15G8 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 42 of WO 2011/066389 (SEQ ID NO: 919); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 47 of WO 2011/066389 (SEQ ID NO: 920).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 3.18G1, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 3.18G1 or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 52 of WO 2011/066389 (SEQ ID NO: 921); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 57 of WO 2011/066389 (SEQ ID NO: 922).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.7A4OPT, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.7A4OPT or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 62 of WO 2011/066389 (SEQ ID NO: 923); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 67 of WO 2011/066389 (SEQ ID NO: 924).

In an embodiment, the targeting moiety comprises the anti-PD-L1 antibody 2.14H9OPT, or fragments thereof, as disclosed in WO 2011/066389, US8,779,108, and US2014/0356353, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, 2.14H9OPT or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain variable region comprising the amino acid sequence of: SEQ ID No: 72 of WO 2011/066389 (SEQ ID NO: 925); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 77 of WO 2011/066389 (SEQ ID NO: 926).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies disclosed in WO2016/061142, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 18, 30, 38, 46, 50, 54, 62, 70, and 78 of WO2016/061142: SEQ ID No: 18 of WO2016/061142 (SEQ ID NO: 927); SEQ ID No: 30 of WO2016/061142 (SEQ ID NO: 928); SEQ ID No: 38 of WO2016/061142 (SEQ ID NO: 929); SEQ ID No: 46 of WO2016/061142 (SEQ ID NO: 930); SEQ ID No: 50 of WO2016/061142 (SEQ ID NO: 931); SEQ ID No: 54 of WO2016/061142 (SEQ ID NO: 932); SEQ ID No: 62 of WO2016/061142 (SEQ ID NO: 933); SEQ ID No: 70 of WO2016/061142 (SEQ ID NO: 934); SEQ ID No: 78 of WO2016/061142 (SEQ ID NO: 935); and/or a light chain comprising an amino acid sequence selected from SEQ ID Nos: 22, 26, 34, 42, 58, 66, 74, 82, and 86 of WO2016/061142: SEQ ID No: 22 of WO2016/061142 (SEQ ID NO: 936); SEQ ID No: 26 of WO2016/061142 (SEQ ID NO: 937); SEQ ID No: 34 of WO2016/061142 (SEQ ID NO: 938); SEQ ID No: 42 of WO2016/061142 (SEQ ID NO: 939); SEQ ID No: 58 of WO2016/061142 (SEQ ID NO: 940); SEQ ID No: 66 of WO2016/061142 (SEQ ID NO: 941); SEQ ID No: 74 of WO2016/061142 (SEQ ID NO: 942); SEQ ID No: 82 of WO2016/061142 (SEQ ID NO: 943); SEQ ID No: 86 of WO2016/061142 (SEQ ID NO: 944).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies disclosed in WO2016/022630, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, and 46 of WO2016/022630: SEQ ID No: 2 of WO2016/022630 (SEQ ID NO: 945); SEQ ID No: 6 of WO2016/022630 (SEQ ID NO: 946); SEQ ID No: 10 of WO2016/022630 (SEQ ID NO: 947); SEQ ID No: 14 of WO2016/022630 (SEQ ID NO: 948); SEQ ID No: 18 of WO2016/022630 (SEQ ID NO: 949); SEQ ID No: 22 of WO2016/022630 (SEQ ID NO: 950); SEQ ID No: 26 of WO2016/022630 (SEQ ID NO: 951); SEQ ID No: 30 of WO2016/022630 (SEQ ID NO: 952); SEQ ID No: 34 of WO2016/022630 (SEQ ID NO: 953); SEQ ID No: 38 of WO2016/022630 (SEQ ID NO: 954); SEQ ID No: 42 of WO2016/022630 (SEQ ID NO: 955); SEQ ID No: 46 of WO2016/022630 (SEQ ID NO: 956); and/or a light chain comprising an amino acid sequence selected from SEQ ID Nos: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, and 48 of WO2016/022630: SEQ ID No: 4 of WO2016/022630 (SEQ ID NO: 957); SEQ ID No: 8 of WO2016/022630 (SEQ ID NO: 958); SEQ ID No: 12 of WO2016/022630 (SEQ ID NO: 959); SEQ ID No: 16 of WO2016/022630 (SEQ ID NO: 960); SEQ ID No: 20 of WO2016/022630 (SEQ ID NO: 961); SEQ ID No: 24 of WO2016/022630 (SEQ ID NO: 962); SEQ ID No: 28 of WO2016/022630 (SEQ ID NO: 963); SEQ ID No: 32 of WO2016/022630 (SEQ ID NO: 964); SEQ ID No: 36 of WO2016/022630 (SEQ ID NO: 965); SEQ ID No: 40 of WO2016/022630 (SEQ ID NO: 966); SEQ ID No: 44 of WO2016/022630 (SEQ ID NO: 967); SEQ ID No: 48 of WO2016/022630 (SEQ ID NO: 968).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies disclosed in WO2015/112900, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 38, 50, 82, and 86 of WO 2015/112900: SEQ ID No: 38 of WO2015/112900 (SEQ ID NO: 969); SEQ ID No: 50 of WO 2015/112900 (SEQ ID NO: 970); SEQ ID No: 82 of WO 2015/112900 (SEQ ID NO: 971); SEQ ID No: 86 of WO 2015/112900 (SEQ ID NO: 972); and/or a light chain comprising an amino acid sequence selected from SEQ ID Nos: 42, 46, 54, 58, 62, 66, 70, 74, and 78 of WO 2015/112900: SEQ ID No: 42 of WO2015/112900 (SEQ ID NO: 973); SEQ ID No: 46 of WO 2015/112900 (SEQ ID NO: 974); SEQ ID No: 54 of WO 2015/112900 (SEQ ID NO: 975); SEQ ID No: 58 of WO 2015/112900 (SEQ ID NO: 976); SEQ ID No: 62 of WO 2015/112900 (SEQ ID NO: 977); SEQ ID No: 66 of WO 2015/112900 (SEQ ID NO: 978); SEQ ID No: 70 of WO 2015/112900 (SEQ ID NO: 979); SEQ ID No: 74 of WO 2015/112900 (SEQ ID NO: 980); SEQ ID No: 78 of WO 2015/112900 (SEQ ID NO: 981).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies disclosed in WO 2010/077634 and US 8,217,149, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, the anti-PD-L1 antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain region comprising the amino acid sequence of: SEQ ID No: 20 of WO 2010/077634

(SEQ ID NO: 982); and/or a light chain variable region comprising the amino acid sequence of: SEQ ID No: 21 of WO 2010/077634 (SEQ ID NO: 983).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L1 antibodies obtainable from the hybridoma accessible under CNCM deposit numbers CNCM I-4122, CNCM I-4080 and CNCM I-4081 as disclosed in US 20120039906, the entire disclosures of which are hereby incorporated by reference.

In an embodiment, the targeting moiety comprises a VHH directed against PD-L1 as disclosed, for example, in US 8,907,065 and WO 2008/071447, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, the VHHs against PD-L1 comprise SEQ ID NOS: 394-399 of US 8,907,065: SEQ ID No: 394 of US 8,907,065 (SEQ ID NO: 984); SEQ ID No: 395 of US 8,907,065 (SEQ ID NO: 985); SEQ ID No: 396 of US 8,907,065 (SEQ ID NO: 986); SEQ ID No: 397 of US 8,907,065 (SEQ ID NO: 987); SEQ ID No: 398 of US 8,907,065 (SEQ ID NO: 988); SEQ ID No: 399 of US 8,907,065 (SEQ ID NO: 989).

In various embodiments, the present multi-specific Clec9A binding agent has one or more targeting moieties directed against PD-L2. In some embodiments, the Clec9A binding agent has one or more targeting moieties which selectively bind a PD-L2 polypeptide. In some embodiments, the Clec9A binding agent comprises one or more antibodies, antibody derivatives or formats, peptides or polypeptides, or fusion proteins that selectively bind a PD-L2 polypeptide.

In an embodiment, the targeting moiety comprises a VHH directed against PD-L2 as disclosed, for example, in US 8,907,065 and WO 2008/071447, the entire disclosures of which are hereby incorporated by reference. In illustrative embodiments, the VHHs against PD-1 comprise SEQ ID Nos: 449-455 of US 8,907,065: SEQ ID No: 449 of US 8,907,065 (SEQ ID NO: 990); SEQ ID No: 450 of US 8,907,065 (SEQ ID NO: 991); SEQ ID No: 451 of US 8,907,065 (SEQ ID NO: 992); SEQ ID No: 452 of US 8,907,065 (SEQ ID NO: 993); SEQ ID No: 453 of US 8,907,065 (SEQ ID NO: 994); SEQ ID No: 454 of US 8,907,065 (SEQ ID NO: 995); SEQ ID No: 455 of US 8,907,065 (SEQ ID NO: 996).

In an embodiment, the targeting moiety comprises any one of the anti-PD-L2 antibodies disclosed in US2011/0271358 and WO2010/036959, the entire contents of which are hereby incorporated by reference. In illustrative embodiments, the antibody or an antigen-binding fragment thereof for use in the methods provided herein comprises a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 43-47 of US2011/0271358: SEQ ID No: 43 of US2011/0271358 (SEQ ID NO: 997); SEQ ID No: 44 of US2011/0271358 (SEQ ID NO: 998); SEQ ID No: 45 of US2011/0271358 (SEQ ID NO: 999); SEQ ID No: 46 of US2011/0271358 (SEQ ID NO: 1000); SEQ ID No: 47 of US2011/0271358 (SEQ ID NO: 1001); and/or a light chain comprising an amino acid sequence selected from SEQ ID Nos: 48-51 of US2011/0271358: SEQ ID No: 48 of US2011/0271358 (SEQ ID NO: 1002); SEQ ID No: 49 of US2011/0271358 (SEQ ID NO: 1003); SEQ ID No: 50 of US2011/0271358 (SEQ ID NO: 1004); SEQ ID No: 51 of US2011/0271358 (SEQ ID NO: 1005).

In various embodiments, the targeting moieties of the invention may comprise a sequence that targets PD-1, PD-L1, and/or PD-L2 which is at least about 60%, at least about 61%, at least about 62%, at least about 63%, at least about 64%, at least about 65%, at least about 66%, at least about 67%, at least about 68%, at least about 69%, at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to any of the sequences disclosed herein (e.g. about 60%, or about 61%, or about 62%, or about 63%, or about 64%, or about 65%, or about 66%, or about 67%, or about 68%, or about 69%, or about 70%, or about 71%, or about 72%, or about 73%, or about 74%, or about 75%, or about 76%, or about 77%, or about 78%, or about 79%, or about 80%, or about 81%, or about 82%, or about 83%, or about 84%, or about 85%, or about 86%, or about 87%, or about 88%, or about 89%, or about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, about 99% or about 100% sequence identity with any of the sequences disclosed herein).

In various embodiments, the targeting moieties of the invention may comprise any combination of heavy chain, light chain, heavy chain variable region, light chain variable region, complementarity determining region (CDR), and framework region sequences that target PD-1, PD-L1, and/or PD-L2 as disclosed herein.

Additional antibodies, antibody derivatives or formats, peptides or polypeptides, or fusion proteins that selectively bind or target PD-1, PD-L1 and/or PD-L2 are disclosed in WO 2011/066389, US 2008/0025980, US 2013/0034559, US 8,779,108, US 2014/0356353, US 8,609,089, US 2010/028330, US 2012/0114649, WO 2010/027827, WO 2011/066342, US 8,907,065, WO 2016/062722, WO 2009/101611, WO2010/027827, WO 2011/066342, WO 2007/005874, WO 2001/014556, US2011/0271358, WO 2010/036959, WO 2010/077634, US 8,217,149, US 2012/0039906, WO 2012/145493, US 2011/0318373, U.S. Patent No. 8,779,108, US 20140044738, WO 2009/089149, WO 2007/00587, WO 2016061142, WO 2016,02263, WO 2010/077634, and WO 2015/112900, the entire disclosures of which are hereby incorporated by reference.

In various embodiments, the multispecific Clec9A binding agent of the present technology comprises a targeting moiety against signal regulatory protein α -1 (SIRP α). SIRP α (also known as SIRP α) belongs to a family of cell immune receptors encompassing inhibitory (SIRP α), activating (SIRP β), nonsignaling (SIRP γ) and soluble (SIRP δ) members. SIRP α is expressed primarily on myeloid cells, including macrophages, granulocytes, myeloid dendritic cells (DCs), mast cells, and their precursors, including hematopoietic stem cells. SIRP α acts as an inhibitory receptor that interacts with a broadly expressed transmembrane glycoprotein CD47 to regulate phagocytosis. In particular, the binding of SIRP α on macrophages by CD47 expressed on target cells, generates an inhibitory signal that negatively regulates phagocytosis of the target cell.

In various embodiments, the SIRP1 α targeting moiety is a targeting moiety that specifically recognizes and binds SIRP1 α on macrophages.

In various embodiments, the SIRP1 α targeting moiety is a targeting moiety that specifically recognizes and binds SIRP1 α on monocytes.

In various embodiments, the SIRP1 α targeting moiety is a targeting moiety that specifically recognizes and binds SIRP1 α on TAMs (Tumor Associated Macrophages).

In various embodiments, the SIRP1 α targeting moiety is a targeting moiety that specifically recognizes and binds SIRP1 α on dendritic cells, including without limitation cDC2 and pDC.

In various embodiments, the SIRP1 α targeting moiety comprises a targeting moiety having a recognition domain that recognizes SIRP1 α . In an embodiment, the recognition domain recognizes one or more linear epitopes present on SIRP1 α . As used herein, a linear epitope refers to any continuous sequence of amino acids present on SIRP1 α . In another embodiment, the recognition domain recognizes one or more conformational epitopes present on SIRP1 α . As used herein, a conformation epitope refers to one or more sections of amino acids (which may be discontinuous) which form a three-dimensional surface with features and/or shapes and/or tertiary structures capable of being recognized by an antigen recognition domain.

In some embodiments, the SIRP1 α targeting moiety may bind to the full-length and/or mature forms and/or isoforms and/or splice variants and/or fragments and/or any other naturally occurring or synthetic analogs, variants, or mutants of SIRP1 α . In an embodiment, the SIRP1 α is human SIRP1 α . In various embodiments, the SIRP1 α targeting moiety may bind to any forms of the human SIRP1 α , including monomeric, dimeric, heterodimeric, multimeric and associated forms. In an embodiment, the SIRP1 α targeting moiety binds to the monomeric form of SIRP1 α . In another embodiment, the SIRP1 α targeting moiety binds to a dimeric form of SIRP1 α .

In an embodiment, the SIRP1 α targeting moiety comprises a recognition domain that recognizes one or more epitopes present on human SIRP1 α . In an embodiment, the SIRP1 α targeting moiety comprises a recognition domain that recognizes human SIRP1 α with a signal peptide sequence. An exemplary human SIRP1 α polypeptide is SEQ ID NO: 1006.

In an embodiment, the SIRP1 α targeting moiety comprises a recognition domain that recognizes human SIRP1 α without a signal peptide sequence. An exemplary human SIRP1 α polypeptide without a signal peptide sequence is SEQ ID NO: 1007.

In an embodiment, the SIRP1 α targeting moiety comprises a recognition domain that recognizes a polypeptide encoding human SIRP1 α isoform 2 (SEQ ID NO: 1008).

In an embodiment, the SIRP1 α targeting moiety comprises a recognition domain that recognizes a polypeptide encoding human SIRP1 α isoform 4 (SEQ ID NO: 1009).

In various embodiments, the SIRP1 α targeting moieties may be any protein-based agent capable of specific binding, such as an antibody or derivatives thereof. In an embodiment, the SIRP1 α targeting moiety comprises an

antibody. In various embodiments, the antibody is a full-length multimeric protein that includes two heavy chains and two light chains. Each heavy chain includes one variable region (e.g., V_H) and at least three constant regions (e.g., CH_1 , CH_2 and CH_3), and each light chain includes one variable region (V_L) and one constant region (C_L). The variable regions determine the specificity of the antibody. Each variable region comprises three hypervariable regions also known as complementarity determining regions (CDRs) flanked by four relatively conserved framework regions (FRs). The three CDRs, referred to as CDR1, CDR2, and CDR3, contribute to the antibody binding specificity. In some embodiments, the antibody is a chimeric antibody. In some embodiments, the antibody is a humanized antibody.

In some embodiments, the SIRP1 α targeting moiety comprises antibody derivatives or formats. In some embodiments, the SIRP1 α targeting moiety is a single-domain antibody, a recombinant heavy-chain-only antibody (VHH), a single-chain antibody (scFv), a shark heavy-chain-only antibody (VNAR), a microprotein (cysteine knot protein, knottin), a DARPin; a Tetranectin; an Affibody; a Transbody; an Anticalin; an AdNectin; an Affilin; a Microbody; a peptide aptamer; an alterase; a plastic antibodies; a phylomer; a stradobody; a maxibody; an evibody; a fynomer, an armadillo repeat protein, a Kunitz domain, an avimer, an atrimer, a probody, an immunobody, a triomab, a troybody; a pepbody; a vaccibody, a UniBody; Affimers, a DuoBody, a Fv, a Fab, a Fab', a F(ab')₂, a peptide mimetic molecule, or a synthetic molecule, as described in US Patent Nos. or Patent Publication Nos. US 7,417,130, US 2004/132094, US 5,831,012, US 2004/023334, US 7,250,297, US 6,818,418, US 2004/209243, US 7,838,629, US 7,186,524, US 6,004,746, US 5,475,096, US 2004/146938, US 2004/157209, US 6,994,982, US 6,794,144, US 2010/239633, US 7,803,907, US 2010/119446, and/or US 7,166,697, the contents of which are hereby incorporated by reference in their entireties. See also, Storz MABs. 2011 May-Jun; 3(3): 310–317.

In one embodiment, the SIRP1 α targeting comprises a single-domain antibody, such as VHH from, for example, an organism that produces VHH antibody such as a camelid, a shark, or a designed VHH. VHHs are antibody-derived therapeutic proteins that contain the unique structural and functional properties of naturally-occurring heavy-chain antibodies. VHH technology is based on fully functional antibodies from camelids that lack light chains. These heavy-chain antibodies contain a single variable domain (VHH) and two constant domains (CH_2 and CH_3).

In an embodiment, the SIRP1 α targeting moiety comprises a VHH. In some embodiments, the VHH is a humanized VHH or camelized VHH.

In some embodiments, the VHH comprises a fully human V_H domain, e.g. a HUMABODY (Crescendo Biologics, Cambridge, UK). In some embodiments, fully human V_H domain, e.g. a HUMABODY is monovalent, bivalent, or trivalent. In some embodiments, the fully human V_H domain, e.g. a HUMABODY is mono- or multi-specific such as monospecific, bispecific, or trispecific. Illustrative fully human V_H domains, e.g. a HUMABODIES are described in, for example, WO 2016/113555 and WO2016/113557, the entire disclosure of which is incorporated by reference.

For example, in some embodiments, the SIRP1 α targeting moiety comprises one or more antibodies, antibody derivatives or formats, peptides or polypeptides, VHHs, or fusion proteins that selectively bind SIRP1 α . In some embodiments, the SIRP1 α targeting moiety comprises an antibody or derivative thereof that specifically binds to

SIRP1 α . In some embodiments, the SIRP1 α targeting moiety is a camelid heavy chain antibody (VHH) that specifically binds to SIRP1 α .

In various embodiments, the SIRP1 α targeting moieties may comprise any combination of heavy chain, light chain, heavy chain variable region, light chain variable region, complementarity determining region (CDR), and framework region sequences that is known to recognize and bind to SIRP1 α .

In various embodiments, the present technology contemplates the use of any natural or synthetic analogs, mutants, variants, alleles, homologs and orthologs (herein collectively referred to as "analogs") of the SIRP1 α targeting moiety described herein. In various embodiments, the amino acid sequence of the SIRP1 α targeting moiety further includes an amino acid analog, an amino acid derivative, or other non-classical amino acids.

In various embodiments, the SIRP1 α targeting moieties comprise an amino acid sequence having one or more amino acid mutations with respect to any targeting moiety sequence that is known to recognize and bind to SIRP1 α . In various embodiments, the SIRP1 α targeting moiety comprises an amino acid sequence having one, or two, or three, or four, or five, or six, or seven, or eight, or nine, or ten, or fifteen, twenty, thirty, forty, or fifty amino acid mutations with respect to any targeting moiety sequence, which is known to recognize and bind to SIRP1 α . In some embodiments, the one or more amino acid mutations may be independently selected from substitutions, insertions, deletions, and truncations.

In some embodiments, the amino acid mutations are amino acid substitutions, and may include conservative and/or non-conservative substitutions.

"Conservative substitutions" may be made, for instance, on the basis of similarity in polarity, charge, size, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the amino acid residues involved. The 20 naturally occurring amino acids can be grouped into the following six standard amino acid groups: (1) hydrophobic: Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; and (6) aromatic: Trp, Tyr, Phe.

As used herein, "conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed within the same group of the six standard amino acid groups shown above. For example, the exchange of Asp by Glu retains one negative charge in the so modified polypeptide. In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices.

As used herein, "non-conservative substitutions" are defined as exchanges of an amino acid by another amino acid listed in a different group of the six standard amino acid groups (1) to (6) shown above.

In various embodiments, the substitutions may also include non-classical amino acids. Exemplary non-classical amino acids include, but are not limited to, selenocysteine, pyrrolysine, *N*-formylmethionine β -alanine, GABA and δ -Aminolevulinic acid, 4-aminobenzoic acid (PABA), D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine,

citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general.

In various embodiments, the amino acid mutation may be in the CDRs of the targeting moiety (e.g., the CDR1, CDR2 or CDR3 regions). In another embodiment, amino acid alteration may be in the framework regions (FRs) of the targeting moiety (e.g., the FR1, FR2, FR3, or FR4 regions).

Modification of the amino acid sequences may be achieved using any known technique in the art e.g., site-directed mutagenesis or PCR based mutagenesis. Such techniques are described, for example, in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., 1989 and Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y., 1989.

In various embodiments, the mutations do not substantially reduce the SIRP1 α targeting moiety's capability to specifically recognize and bind to SIRP1 α . In various embodiments, the mutations do not substantially reduce the SIRP1 α targeting moiety's capability to specifically bind to SIRP1 α and without functionally modulating (e.g., partially or fully neutralizing) SIRP1 α .

In various embodiments, the SIRP1 α targeting moiety binds but does not functionally modulate the antigen of interest, i.e., SIRP1 α . For instance, in various embodiments, the SIRP1 α targeting moiety simply targets the antigen but does not substantially functionally modulate (e.g. substantially inhibit, reduce or neutralize) a biological effect that the antigen has. In various embodiments, the SIRP1 α targeting moiety binds an epitope that is physically separate from an antigen site that is important for its biological activity (e.g. an antigen's active site).

In other embodiments, the SIRP1 α targeting moiety binds and functionally modulates the antigen of interest, i.e., SIRP1 α . For instance, in various embodiments, the SIRP1 α targeting moiety targets the antigen, i.e., SIRP1 α , and functionally modulates (e.g. inhibit, reduce or neutralize) a biological effect that the antigen has. Such binding along with functional modulation may find use in various embodiments of the present invention including methods in which the present chimeric protein is used to directly or indirectly recruit active immune cells to a site of need via an effector antigen.

In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that specifically binds to XCR1, e.g. on DCs. In various embodiments, the multi-specific Clec9A binding agent of the invention comprises a targeting moiety having an antigen recognition domain that comprise all of or part of XCL1.

In various embodiments, the multi-specific Clec9A binding agents have targeting moieties having recognition domains which specifically bind to a target (e.g. antigen, receptor) which is part of a non-cellular structure. In some embodiments, the antigen or receptor is not an integral component of an intact cell or cellular structure. In some embodiments, the antigen or receptor is an extracellular antigen or receptor. In some embodiments, the target is

a non-proteinaceous, non-cellular marker, including, without limitation, nucleic acids, inclusive of DNA or RNA, such as, for example, DNA released from necrotic tumor cells or extracellular deposits such as cholesterol.

In some embodiments, the target (e.g. antigen, receptor) of interest is part of the non-cellular component of the stroma or the extracellular matrix (ECM) or the markers associated therewith. As used herein, stroma refers to the connective and supportive framework of a tissue or organ. Stroma may include a compilation of cells such as fibroblasts/myofibroblasts, glial, epithelia, fat, immune, vascular, smooth muscle, and immune cells along with the extracellular matrix (ECM) and extracellular molecules. In various embodiments, the target (e.g. antigen, receptor) of interest is part of the non-cellular component of the stroma such as the extracellular matrix and extracellular molecules. As used herein, the ECM refers to the non-cellular components present within all tissues and organs. The ECM is composed of a large collection of biochemically distinct components including, without limitation, proteins, glycoproteins, proteoglycans, and polysaccharides. These components of the ECM are usually produced by adjacent cells and secreted into the ECM via exocytosis. Once secreted, the ECM components often aggregate to form a complex network of macromolecules. In various embodiments, the chimeric protein of the invention comprises a targeting moiety that recognizes a target (e.g., an antigen or receptor or non-proteinaceous molecule) located on any component of the ECM. Illustrative components of the ECM include, without limitation, the proteoglycans, the non-proteoglycan polysaccharides, fibers, and other ECM proteins or ECM non-proteins, e.g. polysaccharides and/or lipids, or ECM associated molecules (e.g. proteins or non-proteins, e.g. polysaccharides, nucleic acids and/or lipids).

In some embodiments, the targeting moiety recognizes a target (e.g. antigen, receptor) on ECM proteoglycans. Proteoglycans are glycosylated proteins. The basic proteoglycan unit includes a core protein with one or more covalently attached glycosaminoglycan (GAG) chains. Proteoglycans have a net negative charge that attracts positively charged sodium ions (Na^+), which attracts water molecules via osmosis, keeping the ECM and resident cells hydrated. Proteoglycans may also help to trap and store growth factors within the ECM. Illustrative proteoglycans that may be targeted by the chimeric proteins of the invention include, but are not limited to, heparan sulfate, chondroitin sulfate, and keratan sulfate. In an embodiment, the targeting moiety recognizes a target (e.g. antigen, receptor) on non-proteoglycan polysaccharides such as hyaluronic acid.

In some embodiments, the targeting moiety recognizes a target (e.g. antigen, receptor) on ECM fibers. ECM fibers include collagen fibers and elastin fibers. In some embodiments, the targeting moiety recognizes one or more epitopes on collagens or collagen fibers. Collagens are the most abundant proteins in the ECM. Collagens are present in the ECM as fibrillar proteins and provide structural support to resident cells. In one or more embodiments, the targeting moiety recognizes and binds to various types of collagens present within the ECM including, without limitation, fibrillar collagens (types I, II, III, V, XI), facit collagens (types IX, XII, XIV), short chain collagens (types VIII, X), basement membrane collagens (type IV), and/or collagen types VI, VII, or XIII. Elastin fibers provide elasticity to tissues, allowing them to stretch when needed and then return to their original state. In some embodiments, the target moiety recognizes one or more epitopes on elastins or elastin fibers.

In some embodiments, the targeting moiety recognizes one or more ECM proteins including, but not limited to, a tenascin, a fibronectin, a fibrin, a laminin, or a nidogen/entactin.

In an embodiment, the targeting moiety recognizes and binds to tenascin. The tenascin (TN) family of glycoproteins includes at least four members, tenascin-C, tenascin-R, tenascin-X, and tenascin W. The primary structures of tenascin proteins include several common motifs ordered in the same consecutive sequence: amino-terminal heptad repeats, epidermal growth factor (EGF)-like repeats, fibronectin type III domain repeats, and a carboxyl-terminal fibrinogen-like globular domain. Each protein member is associated with typical variations in the number and nature of EGF-like and fibronectin type III repeats. Isoform variants also exist particularly with respect to tenascin-C. Over 27 splice variants and/or isoforms of tenascin-C are known. In a particular embodiment, the targeting moiety recognizes and binds to tenascin-CA1. Similarly, tenascin-R also has various splice variants and isoforms. Tenascin-R usually exists as dimers or trimers. Tenascin-X is the largest member of the tenascin family and is known to exist as trimers. Tenascin-W exists as trimers. In some embodiments, the targeting moiety recognizes one or more epitopes on a tenascin protein. In some embodiments, the targeting moiety recognizes the monomeric and/or the dimeric and/or the trimeric and/or the hexameric forms of a tenascin protein.

In an embodiment, the targeting moieties recognize and bind to fibronectin. Fibronectins are glycoproteins that connect cells with collagen fibers in the ECM, allowing cells to move through the ECM. Upon binding to integrins, fibronectins unfolds to form functional dimers. In some embodiments, the targeting moiety recognizes the monomeric and/or the dimeric forms of fibronectin. In some embodiments, the targeting moiety recognizes one or more epitopes on fibronectin. In illustrative embodiments, the targeting moiety recognizes fibronectin extracellular domain A (EDA) or fibronectin extracellular domain B (EDB). Elevated levels of EDA are associated with various diseases and disorders including psoriasis, rheumatoid arthritis, diabetes, and cancer. In some embodiments, the targeting moiety recognizes fibronectin that contains the EDA isoform and may be utilized to target the chimeric protein to diseased cells including cancer cells. In some embodiments, the targeting moiety recognizes fibronectin that contains the EDB isoform. In various embodiments, such targeting moieties may be utilized to target the chimeric protein to tumor cells including the tumor neovasculature.

In an embodiment, the targeting moiety recognizes and binds to fibrin. Fibrin is another protein substance often found in the matrix network of the ECM. Fibrin is formed by the action of the protease thrombin on fibrinogen which causes the fibrin to polymerize. In some embodiments, the targeting moiety recognizes one or more epitopes on fibrin. In some embodiments, the targeting moiety recognizes the monomeric as well as the polymerized forms of fibrin.

In an embodiment, the targeting moiety recognizes and binds to laminin. Laminin is a major component of the basal lamina, which is a protein network foundation for cells and organs. Laminins are heterotrimeric proteins that contain an α -chain, a β -chain, and a γ -chain. In some embodiments, the targeting moiety recognizes one or more epitopes on laminin. In some embodiments, the targeting moiety recognizes the monomeric, the dimeric as well as the trimeric forms of laminin.

In an embodiment, the targeting moiety recognizes and binds to a nidogen or entactin. Nidogens/entactins are a family of highly conserved, sulfated glycoproteins. They make up the major structural component of the basement membranes and function to link laminin and collagen IV networks in basement membranes. Members of this family include nidogen-1 and nidogen-2. In various embodiments, the targeting moiety recognizes an epitope on nidogen-1 and/or nidogen-2.

In various embodiments, the targeting moiety comprises an antigen recognition domain that recognizes an epitope present on any of the targets (e.g., ECM proteins) described herein. In an embodiment, the antigen-recognition domain recognizes one or more linear epitopes present on the protein. As used herein, a linear epitope refers to any continuous sequence of amino acids present on the protein. In another embodiment, the antigen-recognition domain recognizes one or more conformational epitopes present on the protein. As used herein, a conformational epitope refers to one or more sections of amino acids (which may be discontinuous) which form a three-dimensional surface with features and/or shapes and/or tertiary structures capable of being recognized by an antigen recognition domain.

In various embodiments, the targeting moiety may bind to the full-length and/or mature forms and/or isoforms and/or splice variants and/or fragments and/or any other naturally occurring or synthetic analogs, variants, or mutants of any of the targets (e.g., ECM proteins) described herein. In various embodiments, the targeting moiety may bind to any forms of the proteins described herein, including monomeric, dimeric, trimeric, tetrameric, heterodimeric, multimeric and associated forms. In various embodiments, the targeting moiety may bind to any post-translationally modified forms of the proteins described herein, such as glycosylated and/or phosphorylated forms.

In various embodiments, the targeting moiety comprises an antigen recognition domain that recognizes extracellular molecules such as DNA. In some embodiments, the targeting moiety comprises an antigen recognition domain that recognizes DNA. In an embodiment, the DNA is shed into the extracellular space from necrotic or apoptotic tumor cells or other diseased cells.

In various embodiments, the targeting moiety comprises an antigen recognition domain that recognizes one or more non-cellular structures associated with atherosclerotic plaques. Two types of atherosclerotic plaques are known. The fibro-lipid (fibro-fatty) plaque is characterized by an accumulation of lipid-laden cells underneath the intima of the arteries. Beneath the endothelium there is a fibrous cap covering the atheromatous core of the plaque. The core includes lipid-laden cells (macrophages and smooth muscle cells) with elevated tissue cholesterol and cholesterol ester content, fibrin, proteoglycans, collagen, elastin, and cellular debris. In advanced plaques, the central core of the plaque usually contains extracellular cholesterol deposits (released from dead cells), which form areas of cholesterol crystals with empty, needle-like clefts. At the periphery of the plaque are younger foamy cells and capillaries. A fibrous plaque is also localized under the intima, within the wall of the artery resulting in thickening and expansion of the wall and, sometimes, spotty localized narrowing of the lumen with some atrophy of the muscular layer. The fibrous plaque contains collagen fibers (eosinophilic), precipitates of calcium

(hematoxylinophilic) and lipid-laden cells. In some embodiments, the targeting moiety recognizes and binds to one or more of the non-cellular components of these plaques such as the fibrin, proteoglycans, collagen, elastin, cellular debris, and calcium or other mineral deposits or precipitates. In some embodiments, the cellular debris is a nucleic acid, e.g. DNA or RNA, released from dead cells.

In various embodiments, the targeting moiety comprises an antigen recognition domain that recognizes one or more non-cellular structures found in the brain plaques associated with neurodegenerative diseases. In some embodiments, the targeting moiety recognizes and binds to one or more non-cellular structures located in the amyloid plaques found in the brains of patients with Alzheimer's disease. For example, the targeting moiety may recognize and bind to the peptide amyloid beta, which is a major component of the amyloid plaques. In some embodiments, the targeting moiety recognizes and binds to one or more non-cellular structures located in the brains plaques found in patients with Huntington's disease. In various embodiments, the targeting moiety recognizes and binds to one or more non-cellular structures found in plaques associated with other neurodegenerative or musculoskeletal diseases such as Lewy body dementia and inclusion body myositis.

Linkers and Functional Groups

In various embodiments, the Clec9A binding agent may include one or more functional groups, residues, or moieties. In various embodiments, the one or more functional groups, residues, or moieties are attached or genetically fused to any of the signaling agents or targeting moieties described herein. In some embodiments, such functional groups, residues or moieties confer one or more desired properties or functionalities to the Clec9A binding agent of the invention. Examples of such functional groups and of techniques for introducing them into the Clec9A binding agent are known in the art, for example, see *Remington's Pharmaceutical Sciences*, 16th ed., Mack Publishing Co., Easton, Pa. (1980).

In various embodiments, the Clec9A binding agent may be conjugated and/or fused with another agent to extend half-life or otherwise improve pharmacodynamic and pharmacokinetic properties. In some embodiments, the Clec9A binding agent may be fused or conjugated with one or more of PEG, XTEN (e.g., as rPEG), polysialic acid (POLYXEN), albumin (e.g., human serum albumin or HAS), elastin-like protein (ELP), PAS, HAP, GLK, CTP, transferrin, and the like. In some embodiments, the Clec9A binding agent may be fused or conjugated with an antibody or an antibody fragment such as an Fc fragment. For example, the chimeric protein may be fused to either the N-terminus or the C-terminus of the Fc domain of human immunoglobulin (Ig) G. In various embodiments, each of the individual chimeric proteins is fused to one or more of the agents described in BioDrugs (2015) 29:215–239, the entire contents of which are hereby incorporated by reference.

In some embodiments, the functional groups, residues, or moieties comprise a suitable pharmacologically acceptable polymer, such as poly(ethyleneglycol) (PEG) or derivatives thereof (such as methoxypoly(ethyleneglycol) or mPEG). In some embodiments, attachment of the PEG moiety increases the half-life and/or reduces the immunogenicity of the Clec9A binding protein. Generally, any suitable form of pegylation can be used, such as the pegylation used in the art for antibodies and antibody fragments (including but not limited

to single domain antibodies such as VHHs); see, for example, Chapman, *Nat. Biotechnol.*, 54, 531-545 (2002); by Veronese and Harris, *Adv. Drug Deliv. Rev.* 54, 453-456 (2003), by Harris and Chess, *Nat. Rev. Drug. Discov.*, 2, (2003) and in WO/04060965, the entire contents of which are hereby incorporated by reference. Various reagents for pegylation of proteins are also commercially available, for example, from Nektar Therapeutics, USA. In some embodiments, site-directed pegylation is used, in particular via a cysteine-residue (see, for example, Yang *et al.*, *Protein Engineering*, 16, 10, 761-770 (2003), the entire contents of which is hereby incorporated by reference). For example, for this purpose, PEG may be attached to a cysteine residue that naturally occurs in the Clec9A binding agent of the invention. In some embodiments, the Clec9A binding agent of the invention is modified so as to suitably introduce one or more cysteine residues for attachment of PEG, or an amino acid sequence comprising one or more cysteine residues for attachment of PEG may be fused to the amino- and/or carboxy-terminus of the Clec9A binding agent, using techniques known in the art.

In some embodiments, the functional groups, residues, or moieties comprise N-linked or O-linked glycosylation. In some embodiments, the N-linked or O-linked glycosylation is introduced as part of a co-translational and/or post-translational modification.

In some embodiments, the functional groups, residues, or moieties comprise one or more detectable labels or other signal-generating groups or moieties. Suitable labels and techniques for attaching, using and detecting them are known in the art and, include, but are not limited to, fluorescent labels (such as fluorescein, isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde, and fluorescamine and fluorescent metals such as Eu or others metals from the lanthanide series), phosphorescent labels, chemiluminescent labels or bioluminescent labels (such as luminal, isoluminol, thermotropic acridinium ester, imidazole, acridinium salts, oxalate ester, dioxetane or GFP and its analogs), radio-isotopes, metals, metals chelates or metallic cations or other metals or metallic cations that are particularly suited for use in in vivo, in vitro or in situ diagnosis and imaging, as well as chromophores and enzymes (such as malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, biotinavidin peroxidase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholine esterase). Other suitable labels include moieties that can be detected using NMR or ESR spectroscopy. Such labeled VHHs and polypeptides of the invention may, for example, be used for in vitro, in vivo or in situ assays (including immunoassays known per se such as ELISA, RIA, EIA and other "sandwich assays," *etc.*) as well as in vivo diagnostic and imaging purposes, depending on the choice of the specific label.

In some embodiments, the functional groups, residues, or moieties comprise a tag that is attached or genetically fused to the Clec9A binding agent. In some embodiments, the Clec9A binding agent may include a single tag or multiple tags. The tag for example is a peptide, sugar, or DNA molecule that does not inhibit or prevent binding of the Clec9A binding agent to Clec9A or any other antigen of interest such as tumor antigens. In various embodiments, the tag is at least about: three to five amino acids long, five to eight amino acids long, eight to twelve amino acids long, twelve to fifteen amino acids long, or fifteen to twenty amino acids long. Illustrative tags are

described for example, in U.S. Patent Publication No. US2013/0058962. In some embodiment, the tag is an affinity tag such as glutathione-S-transferase (GST) and histidine (His) tag. In an embodiment, the Clec9A binding agent comprises a His tag.

In some embodiments, the functional groups, residues, or moieties comprise a chelating group, for example, to chelate one of the metals or metallic cations. Suitable chelating groups, for example, include, without limitation, diethyl-enetriaminepentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

In some embodiments, the functional groups, residues, or moieties comprise a functional group that is one part of a specific binding pair, such as the biotin-(strept)avidin binding pair. Such a functional group may be used to link the Clec9A binding agent of the invention to another protein, polypeptide or chemical compound that is bound to the other half of the binding pair, *i.e.*, through formation of the binding pair. For example, a Clec9A binding agent of the invention may be conjugated to biotin, and linked to another protein, polypeptide, compound or carrier conjugated to avidin or streptavidin. For example, such a conjugated Clec9A binding agent may be used as a reporter, for example, in a diagnostic system where a detectable signal-producing agent is conjugated to avidin or streptavidin. Such binding pairs may, for example, also be used to bind the Clec9A binding agent to a carrier, including carriers suitable for pharmaceutical purposes. One non-limiting example are the liposomal formulations described by Cao and Suresh, *Journal of Drug Targeting*, 8, 4, 257 (2000). Such binding pairs may also be used to link a therapeutically active agent to the Clec9A binding agent of the invention.

In some embodiments, the present Clec9A binding agent optionally comprises one or more linkers. In some embodiments, the Clec9A binding agent includes a linker that connects each binding region and/or targeting moieties. In some embodiments, the Clec9A binding agent includes a linker that connects each signaling agent and targeting moiety (or, if more than one targeting moiety, a signaling agent to one of the targeting moieties). In some embodiments, the linker may be utilized to link various functional groups, residues, or moieties as described herein to the Clec9A binding agent. In some embodiments, the linker is a single amino acid or a plurality of amino acids that does not affect or reduce the stability, orientation, binding, neutralization, and/or clearance characteristics of the binding regions and the binding protein. In various embodiments, the linker is selected from a peptide, a protein, a sugar, or a nucleic acid.

In some embodiments, the present Clec9A binding agent comprises a linker connecting the targeting moiety and the signaling agent. In some embodiments, the present chimeric protein comprises a linker within the signaling agent (*e.g.* in the case of single chain TNF, which can comprise two linkers to yield a trimer).

The invention contemplates the use of a variety of linker sequences. In various embodiments, the linker may be derived from naturally-occurring multi-domain proteins or are empirical linkers as described, for example, in Chichili *et al.*, (2013), *Protein Sci.* 22(2):153-167, Chen *et al.*, (2013), *Adv Drug Deliv Rev.* 65(10):1357-1369, the entire contents of which are hereby incorporated by reference. In some embodiments, the linker may be designed using linker designing databases and computer programs such as those described in Chen *et al.*, (2013), *Adv Drug Deliv Rev.* 65(10):1357-1369 and Crasto *et al.*, (2000), *Protein Eng.* 13(5):309-312, the entire contents of which are

hereby incorporated by reference. In various embodiments, the linker may be functional. For example, without limitation, the linker may function to improve the folding and/or stability, improve the expression, improve the pharmacokinetics, and/or improve the bioactivity of the present Clec9A binding agent.

In some embodiments, the linker is a polypeptide. In some embodiments, the linker is less than about 100 amino acids long. For example, the linker may be less than about 100, about 95, about 90, about 85, about 80, about 75, about 70, about 65, about 60, about 55, about 50, about 45, about 40, about 35, about 30, about 25, about 20, about 19, about 18, about 17, about 16, about 15, about 14, about 13, about 12, about 11, about 10, about 9, about 8, about 7, about 6, about 5, about 4, about 3, or about 2 amino acids long. In some embodiments, the linker is a polypeptide. In some embodiments, the linker is greater than about 100 amino acids long. For example, the linker may be greater than about 100, about 95, about 90, about 85, about 80, about 75, about 70, about 65, about 60, about 55, about 50, about 45, about 40, about 35, about 30, about 25, about 20, about 19, about 18, about 17, about 16, about 15, about 14, about 13, about 12, about 11, about 10, about 9, about 8, about 7, about 6, about 5, about 4, about 3, or about 2 amino acids long. In some embodiments, the linker is flexible. In another embodiment, the linker is rigid.

In some embodiments, the linker length allows for efficient binding of a targeting moiety and the signaling agent to their receptors. For instance, in some embodiments, the linker length allows for efficient binding of one of the targeting moieties and the signaling agent to receptors on the same cell as well as the efficient binding of the other targeting moiety to another cell. Illustrative pairs of cells are provided elsewhere herein.

In some embodiments the linker length is at least equal to the minimum distance between the binding sites of one of the targeting moieties and the signaling agent to receptors on the same cell. In some embodiments the linker length is at least twice, or three times, or four times, or five times, or ten times, or twenty times, or 25 times, or 50 times, or one hundred times, or more the minimum distance between the binding sites of one of the targeting moieties and the signaling agent to receptors on the same cell.

In some embodiments, a linker connects the two targeting moieties to each other and this linker has a short length and a linker connects a targeting moiety and a signaling agent this linker is longer than the linker connecting the two targeting moieties. For example, the difference in amino acid length between the linker connecting the two targeting moieties and the linker connecting a targeting moiety and a signaling agent may be about 100, about 95, about 90, about 85, about 80, about 75, about 70, about 65, about 60, about 55, about 50, about 45, about 40, about 35, about 30, about 25, about 20, about 19, about 18, about 17, about 16, about 15, about 14, about 13, about 12, about 11, about 10, about 9, about 8, about 7, about 6, about 5, about 4, about 3, or about 2 amino acids. In some embodiments, the linker is flexible. In another embodiment, the linker is rigid.

In various embodiments, the linker is substantially comprised of glycine and serine residues (e.g. about 30%, or about 40%, or about 50%, or about 60%, or about 70%, or about 80%, or about 90%, or about 95%, or about 97% glycines and serines). For example, in some embodiments, the linker is (Gly₄Ser)_n, where n is from about 1 to about 8, e.g. 1, 2, 3, 4, 5, 6, 7, or 8 (SEQ ID NOs: 1010-1017). In an embodiment, the linker sequence is

GGSGGGGGGGSGGGGS (SEQ ID NO: 1018). Additional illustrative linkers include, but are not limited to, linkers having the sequence LE, GGGGS (SEQ ID NO: 1010), (GGGGS)_n (n=1-4) (SEQ ID NOS: 1010-1013), (Gly)₈ (SEQ ID NO: 1019), (Gly)₆ (SEQ ID NO: 1020), (EAAAK)_n (n=1-3) (SEQ ID NOS: 1021-1023); A(EAAAK)_nA (n = 2-5) (SEQ ID NO: 1024-1027), AEA(AKEAAKA (SEQ ID NO: 1024), A(EAAAK)₄AE(AEA(AKEAAKA (SEQ ID NO: 1028), PAPAP (SEQ ID NO: 1029), KESGSVSSEQLAQFRSLD (SEQ ID NO: 1030), EGKSSGSGSESKST (SEQ ID NO: 1031), GSAGSAAGSGEF (SEQ ID NO: 1032), and (XP)_n, with X designating any amino acid, e.g., Ala, Lys, or Glu. In various embodiments, the linker is (GGGGS)_n (n=1-20) (SEQ ID NO: 1033 - SEQ ID NO: 1052). In some embodiments, the linker is G. In some embodiments, the linker is AAA. In some embodiments, the linker is (GGGGS)_n (n=9-20) (SEQ ID NOS: 1053-1064).

In some embodiments, the linker is one or more of GGGSE (SEQ ID NO: 1065), GSESG (SEQ ID NO: 1066), GSEGS (SEQ ID NO: 1067), GEGGSGEGSSGEGSSSEGGGSEGGGSEGGGSEGGG (SEQ ID NO: 1068), and a linker of randomly placed G, S, and E every 4 amino acid intervals.

In some embodiments, a Clec9A binding agent is linked to a modified signaling agent. In various exemplary embodiments, the Clec9A binding agent is linked to a modified IFN α 2. By way of example, in some embodiments, a Clec9A binding agent linked to a modified IFN α 2 is represented as R1CHCL50-linker-hIFN α 2_R149A or 3LEC89-linker- hIFN α 2_R149A, wherein the linker is any of the above disclosed linkers.

In some embodiments, the linker is a hinge region of an antibody (e.g., of IgG, IgA, IgD, and IgE, inclusive of subclasses (e.g. IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2)). In various embodiments, the linker is a hinge region of an antibody (e.g., of IgG, IgA, IgD, and IgE, inclusive of subclasses (e.g. IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2)). The hinge region, found in IgG, IgA, IgD, and IgE class antibodies, acts as a flexible spacer, allowing the Fab portion to move freely in space. In contrast to the constant regions, the hinge domains are structurally diverse, varying in both sequence and length among immunoglobulin classes and subclasses. For example, the length and flexibility of the hinge region varies among the IgG subclasses. The hinge region of IgG1 encompasses amino acids 216-231 and, because it is freely flexible, the Fab fragments can rotate about their axes of symmetry and move within a sphere centered at the first of two inter-heavy chain disulfide bridges. IgG2 has a shorter hinge than IgG1, with 12 amino acid residues and four disulfide bridges. The hinge region of IgG2 lacks a glycine residue, is relatively short, and contains a rigid poly-proline double helix, stabilized by extra inter-heavy chain disulfide bridges. These properties restrict the flexibility of the IgG2 molecule. IgG3 differs from the other subclasses by its unique extended hinge region (about four times as long as the IgG1 hinge), containing 62 amino acids (including 21 prolines and 11 cysteines), forming an inflexible poly-proline double helix. In IgG3, the Fab fragments are relatively far away from the Fc fragment, giving the molecule a greater flexibility. The elongated hinge in IgG3 is also responsible for its higher molecular weight compared to the other subclasses. The hinge region of IgG4 is shorter than that of IgG1 and its flexibility is intermediate between that of IgG1 and IgG2. The flexibility of the hinge regions reportedly decreases in the order IgG3>IgG1>IgG4>IgG2.

According to crystallographic studies, the immunoglobulin hinge region can be further subdivided functionally into three regions: the upper hinge region, the core region, and the lower hinge region. See Shin *et al.*, 1992 *Immunological Reviews* 130:87. The upper hinge region includes amino acids from the carboxyl end of C_{H1} to the first residue in the hinge that restricts motion, generally the first cysteine residue that forms an interchain disulfide bond between the two heavy chains. The length of the upper hinge region correlates with the segmental flexibility of the antibody. The core hinge region contains the inter-heavy chain disulfide bridges, and the lower hinge region joins the amino terminal end of the C_{H2} domain and includes residues in C_{H2}. *Id.* The core hinge region of wild-type human IgG1 contains the sequence Cys-Pro-Pro-Cys (SEQ ID NO: 1069), which, when dimerized by disulfide bond formation, results in a cyclic octapeptide believed to act as a pivot, thus conferring flexibility. In various embodiments, the present linker comprises, one, or two, or three of the upper hinge region, the core region, and the lower hinge region of any antibody (e.g., of IgG, IgA, IgD, and IgE, inclusive of subclasses (e.g. IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2)). The hinge region may also contain one or more glycosylation sites, which include a number of structurally distinct types of sites for carbohydrate attachment. For example, IgA1 contains five glycosylation sites within a 17-amino-acid segment of the hinge region, conferring resistance of the hinge region polypeptide to intestinal proteases, considered an advantageous property for a secretory immunoglobulin. In various embodiments, the linker of the present invention comprises one or more glycosylation sites. In various embodiments, the linker is a hinge-CH2-CH3 domain of a human IgG4 antibody.

If desired, the present Clec9A binding agent can be linked to an antibody Fc region, comprising one or both of C_{H2} and C_{H3} domains, and optionally a hinge region. For example, vectors encoding the present Clec9A binding agents linked as a single nucleotide sequence to an Fc region can be used to prepare such polypeptides.

In some embodiments, the linker is a synthetic linker such as PEG.

In various embodiments, the linker may be functional. For example, without limitation, the linker may function to improve the folding and/or stability, improve the expression, improve the pharmacokinetics, and/or improve the bioactivity of the present Clec9A binding agent. In another example, the linker may function to target the Clec9A binding agent to a particular cell type or location.

Modifications and Production of Clec9A binding agents

In various embodiments, the Clec9A binding agent comprises a targeting moiety that is a VHH. In various embodiments, the VHH is not limited to a specific biological source or to a specific method of preparation. For example, the VHH can generally be obtained: (1) by isolating the V_HH domain of a naturally occurring heavy chain antibody; (2) by expression of a nucleotide sequence encoding a naturally occurring V_HH domain; (3) by "humanization" of a naturally occurring V_HH domain or by expression of a nucleic acid encoding a such humanized V_HH domain; (4) by "camelization" of a naturally occurring VH domain from any animal species, such as from a mammalian species, such as from a human being, or by expression of a nucleic acid encoding such a camelized VH domain; (5) by "camelization" of a "domain antibody" or "Dab" as described in the art, or by expression of a nucleic acid encoding such a camelized VH domain; (6) by using synthetic or semi-synthetic techniques for

preparing proteins, polypeptides or other amino acid sequences known in the art; (7) by preparing a nucleic acid encoding a VHH using techniques for nucleic acid synthesis known in the art, followed by expression of the nucleic acid thus obtained; and/or (8) by any combination of one or more of the foregoing.

In an embodiment, the Clec9A binding agent comprises a VHH that corresponds to the V_HH domains of naturally occurring heavy chain antibodies directed against human Clec9A. In some embodiments, such V_HH sequences can generally be generated or obtained by suitably immunizing a species of Camelid with a Clec9A molecule, (*i.e.*, so as to raise an immune response and/or heavy chain antibodies directed against Clec9A), by obtaining a suitable biological sample from the Camelid (such as a blood sample, or any sample of B-cells), and by generating V_HH sequences directed against Clec9A, starting from the sample, using any suitable known techniques. In some embodiments, naturally occurring V_HH domains against Clec9A can be obtained from naive libraries of Camelid V_HH sequences, for example, by screening such a library using Clec9A or at least one part, fragment, antigenic determinant or epitope thereof using one or more screening techniques known in the art. Such libraries and techniques are, for example, described in WO9937681, WO0190190, WO03025020 and WO03035694, the entire contents of which are hereby incorporated by reference. In some embodiments, improved synthetic or semi-synthetic libraries derived from naive V_HH libraries may be used, such as V_HH libraries obtained from naive V_HH libraries by techniques such as random mutagenesis and/or CDR shuffling, as for example, described in WO0043507, the entire contents of which are hereby incorporated by reference. In some embodiments, another technique for obtaining V_HH sequences directed against a Clec9A involves suitably immunizing a transgenic mammal that is capable of expressing heavy chain antibodies (*i.e.*, so as to raise an immune response and/or heavy chain antibodies directed against Clec9A), obtaining a suitable biological sample from the transgenic mammal (such as a blood sample, or any sample of B-cells), and then generating V_HH sequences directed against Clec9A starting from the sample, using any suitable known techniques. For example, for this purpose, the heavy chain antibody-expressing mice and the further methods and techniques described in WO02085945 and in WO04049794 (the entire contents of which are hereby incorporated by reference) can be used.

In an embodiment, the Clec9A binding agent comprises a VHH that has been "humanized" *i.e.*, by replacing one or more amino acid residues in the amino acid sequence of the naturally occurring V_HH sequence (and in particular in the framework sequences) by one or more of the amino acid residues that occur at the corresponding position(s) in a VH domain from a conventional 4-chain antibody from a human being. This can be performed using humanization techniques known in the art. In some embodiments, possible humanizing substitutions or combinations of humanizing substitutions may be determined by methods known in the art, for example, by a comparison between the sequence of a VHH and the sequence of a naturally occurring human VH domain. In some embodiments, the humanizing substitutions are chosen such that the resulting humanized VHHs still retain advantageous functional properties. Generally, as a result of humanization, the VHHs of the invention may become more "human-like," while still retaining favorable properties such as a reduced immunogenicity, compared to the corresponding naturally occurring V_HH domains. In various embodiments, the humanized VHHs of the invention

can be obtained in any suitable manner known in the art and thus are not strictly limited to polypeptides that have been obtained using a polypeptide that comprises a naturally occurring V_HH domain as a starting material.

In an embodiment, the Clec9A binding agent comprises a VHH that has been "camelized," *i.e.*, by replacing one or more amino acid residues in the amino acid sequence of a naturally occurring VH domain from a conventional 4-chain antibody by one or more of the amino acid residues that occur at the corresponding position(s) in a V_HH domain of a heavy chain antibody of a camelid. In some embodiments, such "camelizing" substitutions are inserted at amino acid positions that form and/or are present at the VH-VL interface, and/or at the so-called Camelidae hallmark residues (see, for example, WO9404678, the entire contents of which are hereby incorporated by reference). In some embodiments, the VH sequence that is used as a starting material or starting point for generating or designing the camelized VHH is a VH sequence from a mammal, for example, the VH sequence of a human being, such as a VH3 sequence. In various embodiments, the camelized VHHs can be obtained in any suitable manner known in the art (*i.e.*, as indicated under points (1)-(8) above) and thus are not strictly limited to polypeptides that have been obtained using a polypeptide that comprises a naturally occurring VH domain as a starting material.

In various embodiments, both "humanization" and "camelization" can be performed by providing a nucleotide sequence that encodes a naturally occurring V_HH domain or VH domain, respectively, and then changing, in a manner known in the art, one or more codons in the nucleotide sequence in such a way that the new nucleotide sequence encodes a "humanized" or "camelized" VHH, respectively. This nucleic acid can then be expressed in a manner known in the art, so as to provide the desired VHH of the invention. Alternatively, based on the amino acid sequence of a naturally occurring V_HH domain or VH domain, respectively, the amino acid sequence of the desired humanized or camelized VHH of the invention, respectively, can be designed and then synthesized *de novo* using techniques for peptide synthesis known in the art. Also, based on the amino acid sequence or nucleotide sequence of a naturally occurring V_HH domain or VH domain, respectively, a nucleotide sequence encoding the desired humanized or camelized VHH, respectively, can be designed and then synthesized *de novo* using techniques for nucleic acid synthesis known in the art, after which the nucleic acid thus obtained can be expressed in a manner known in the art, so as to provide the desired VHH of the invention. Other suitable methods and techniques for obtaining the VHHs of the invention and/or nucleic acids encoding the same, starting from naturally occurring VH sequences or V_HH sequences, are known in the art, and may, for example, comprise combining one or more parts of one or more naturally occurring VH sequences (such as one or more FR sequences and/or CDR sequences), one or more parts of one or more naturally occurring V_HH sequences (such as one or more FR sequences or CDR sequences), and/or one or more synthetic or semi-synthetic sequences, in a suitable manner, so as to provide a VHH of the invention or a nucleotide sequence or nucleic acid encoding the same.

Methods for producing the Clec9A binding agents of the invention are described herein. For example, DNA sequences encoding the Clec9A binding agents of the invention can be chemically synthesized using methods known in the art. Synthetic DNA sequences can be ligated to other appropriate nucleotide sequences, including, *e.g.*, expression control sequences, to produce gene expression constructs encoding the desired Clec9A binding

agents. Accordingly, in various embodiments, the present invention provides for isolated nucleic acids comprising a nucleotide sequence encoding the Clec9A binding agent of the invention.

Nucleic acids encoding the Clec9A binding agent of the invention can be incorporated (ligated) into expression vectors, which can be introduced into host cells through transfection, transformation, or transduction techniques. For example, nucleic acids encoding the Clec9A binding agent of the invention can be introduced into host cells by retroviral transduction. Illustrative host cells are *E.coli* cells, Chinese hamster ovary (CHO) cells, human embryonic kidney 293 (HEK 293) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and myeloma cells. Transformed host cells can be grown under conditions that permit the host cells to express the genes that encode the Clec9A binding agent of the invention. Accordingly, in various embodiments, the present invention provides expression vectors comprising nucleic acids that encode the Clec9A binding agent of the invention. In various embodiments, the present invention additionally provides host cells comprising such expression vectors.

Specific expression and purification conditions will vary depending upon the expression system employed. For example, if a gene is to be expressed in *E. coli*, it is first cloned into an expression vector by positioning the engineered gene downstream from a suitable bacterial promoter, e.g., Trp or Tac, and a prokaryotic signal sequence. In another example, if the engineered gene is to be expressed in eukaryotic host cells, e.g., CHO cells, it is first inserted into an expression vector containing for example, a suitable eukaryotic promoter, a secretion signal, enhancers, and various introns. The gene construct can be introduced into the host cells using transfection, transformation, or transduction techniques.

The Clec9A binding agent of the invention can be produced by growing a host cell transfected with an expression vector encoding the Clec9A binding agent under conditions that permit expression of the protein. Following expression, the protein can be harvested and purified using techniques well known in the art, e.g., affinity tags such as glutathione-S-transferase (GST) and histidine (His) tags or by chromatography. In an embodiment, the Clec9A binding agent comprises a His tag. In an embodiment, the Clec9A binding agent comprises a His tag and a proteolytic site to allow cleavage of the His tag.

Accordingly, in various embodiments, the present invention provides for a nucleic acid encoding a Clec9A binding agent of the present invention. In various embodiments, the present invention provides for a host cell comprising a nucleic acid encoding a Clec9A binding agent of the present invention.

In various embodiments, the present Clec9A binding agent or chimeric protein comprising the same may be expressed *in vivo*, for instance, in a patient. For example, in various embodiments, the present Clec9A binding agent or chimeric protein comprising the same may be administered in the form of nucleic acid which encodes the present Clec9A binding agents or chimeric proteins comprising the same. In various embodiments, the nucleic acid is DNA or RNA. In some embodiments, present Clec9A binding agent or chimeric protein comprising the same is encoded by a modified mRNA, *i.e.* an mRNA comprising one or more modified nucleotides. In some embodiments, the modified mRNA comprises one or more modifications found in U.S. Patent No. 8,278,036, the entire contents of

which are hereby incorporated by reference. In some embodiments, the modified mRNA comprises one or more of m5C, m5U, m6A, s2U, Ψ, and 2'-O-methyl-U. In some embodiments, the present invention relates to administering a modified mRNA encoding one or more of the present chimeric proteins. In some embodiments, the present invention relates to gene therapy vectors comprising the same. In some embodiments, the present invention relates to gene therapy methods comprising the same. In various embodiments, the nucleic acid is in the form of an oncolytic virus, e.g. an adenovirus, reovirus, measles, herpes simplex, Newcastle disease virus or vaccinia.

Pharmaceutically Acceptable Salts and Excipients

The Clec9A binding agents (and/or any other therapeutic agents) described herein can possess a sufficiently basic functional group, which can react with an inorganic or organic acid, or a carboxyl group, which can react with an inorganic or organic base, to form a pharmaceutically acceptable salt. A pharmaceutically acceptable acid addition salt is formed from a pharmaceutically acceptable acid, as is well known in the art. Such salts include the pharmaceutically acceptable salts listed in, for example, *Journal of Pharmaceutical Science*, 66, 2-19 (1977) and *The Handbook of Pharmaceutical Salts; Properties, Selection, and Use*. P. H. Stahl and C. G. Wermuth (eds.), Verlag, Zurich (Switzerland) 2002, which are hereby incorporated by reference in their entirety.

Pharmaceutically acceptable salts include, by way of non-limiting example, sulfate, citrate, acetate, oxalate, chloride, bromide, iodide, nitrate, bisulfate, phosphate, acid phosphate, isonicotinate, lactate, salicylate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate, camphorsulfonate, pamoate, phenylacetate, trifluoroacetate, acrylate, chlorobenzoate, dinitrobenzoate, hydroxybenzoate, methoxybenzoate, methylbenzoate, o-acetoxybenzoate, naphthalene-2-benzoate, isobutyrate, phenylbutyrate, α-hydroxybutyrate, butyne-1,4-dicarboxylate, hexyne-1,4-dicarboxylate, caprate, caprylate, cinnamate, glycollate, heptanoate, hippurate, malate, hydroxymaleate, malonate, mandelate, mesylate, nicotinate, phthalate, teraphthalate, propiolate, propionate, phenylpropionate, sebacate, suberate, p-bromobenzenesulfonate, chlorobenzenesulfonate, ethylsulfonate, 2-hydroxyethylsulfonate, methylsulfonate, naphthalene-1-sulfonate, naphthalene-2-sulfonate, naphthalene-1,5-sulfonate, xylenesulfonate, and tartarate salts.

The term "pharmaceutically acceptable salt" also refers to a salt of the compositions of the present invention having an acidic functional group, such as a carboxylic acid functional group, and a base. Suitable bases include, but are not limited to, hydroxides of alkali metals such as sodium, potassium, and lithium; hydroxides of alkaline earth metal such as calcium and magnesium; hydroxides of other metals, such as aluminum and zinc; ammonia, and organic amines, such as unsubstituted or hydroxy-substituted mono-, di-, or tri-alkylamines, dicyclohexylamine; tributyl amine; pyridine; N-methyl, N-ethylamine; diethylamine; triethylamine; mono-, bis-, or tris-(2-OH-lower alkylamines), such as mono-, bis-, or tris-(2-hydroxyethyl)amine, 2-hydroxy-tert-butylamine, or tris-(hydroxymethyl)methylamine, N,N-di-lower alkyl-N-(hydroxyl-lower alkyl)-amines, such as N,N-dimethyl-N-(2-

hydroxyethyl)amine or tri-(2-hydroxyethyl)amine; N-methyl-D-glucamine; and amino acids such as arginine, lysine, and the like.

In some embodiments, the compositions described herein are in the form of a pharmaceutically acceptable salt.

Pharmaceutical Compositions and Formulations

In various embodiments, the present invention pertains to pharmaceutical compositions comprising the Clec9A binding agents (and/or any other therapeutic agents) described herein and a pharmaceutically acceptable carrier or excipient. In some embodiments, the present invention pertains to pharmaceutical compositions comprising the present Clec9A binding agents. In another embodiment, the present invention pertains to pharmaceutical compositions comprising any other therapeutic agents described herein. In a further embodiment, the present invention pertains to pharmaceutical compositions comprising a combination of the present Clec9A binding agents and any other therapeutic agents described herein. Any pharmaceutical compositions described herein can be administered to a subject as a component of a composition that comprises a pharmaceutically acceptable carrier or vehicle. Such compositions can optionally comprise a suitable amount of a pharmaceutically acceptable excipient so as to provide the form for proper administration.

In various embodiments, pharmaceutical excipients can be liquids, such as water and oils, including those of petroleum, animal, vegetable, or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. The pharmaceutical excipients can be, for example, saline, gum acacia, gelatin, starch paste, talc, keratin, colloidal silica, urea and the like. In addition, auxiliary, stabilizing, thickening, lubricating, and coloring agents can be used. In one embodiment, the pharmaceutically acceptable excipients are sterile when administered to a subject. Water is a useful excipient when any agent described herein is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid excipients, specifically for injectable solutions. Suitable pharmaceutical excipients also include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. Any agent described herein, if desired, can also comprise minor amounts of wetting or emulsifying agents, or pH buffering agents. Other examples of suitable pharmaceutical excipients are described in *Remington's Pharmaceutical Sciences* 1447-1676 (Alfonso R. Gennaro eds., 19th ed. 1995), incorporated herein by reference.

The present invention includes the described pharmaceutical compositions (and/or additional therapeutic agents) in various formulations. Any inventive pharmaceutical composition (and/or additional therapeutic agents) described herein can take the form of solutions, suspensions, emulsion, drops, tablets, pills, pellets, capsules, capsules containing liquids, gelatin capsules, powders, sustained-release formulations, suppositories, emulsions, aerosols, sprays, suspensions, lyophilized powder, frozen suspension, desiccated powder, or any other form suitable for use. In one embodiment, the composition is in the form of a capsule. In another embodiment, the composition is in the form of a tablet. In yet another embodiment, the pharmaceutical composition is formulated in the form of a

soft-gel capsule. In a further embodiment, the pharmaceutical composition is formulated in the form of a gelatin capsule. In yet another embodiment, the pharmaceutical composition is formulated as a liquid.

Where necessary, the inventive pharmaceutical compositions (and/or additional agents) can also include a solubilizing agent. Also, the agents can be delivered with a suitable vehicle or delivery device as known in the art. Combination therapies outlined herein can be co-delivered in a single delivery vehicle or delivery device.

The formulations comprising the inventive pharmaceutical compositions (and/or additional agents) of the present invention may conveniently be presented in unit dosage forms and may be prepared by any of the methods well known in the art of pharmacy. Such methods generally include the step of bringing the therapeutic agents into association with a carrier, which constitutes one or more accessory ingredients. Typically, the formulations are prepared by uniformly and intimately bringing the therapeutic agent into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product into dosage forms of the desired formulation (e.g., wet or dry granulation, powder blends, etc., followed by tableting using conventional methods known in the art).

In various embodiments, any pharmaceutical compositions (and/or additional agents) described herein is formulated in accordance with routine procedures as a composition adapted for a mode of administration described herein.

Routes of administration include, for example: oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, sublingual, intranasal, intracerebral, intravaginal, transdermal, rectally, by inhalation, or topically. Administration can be local or systemic. In some embodiments, the administering is effected orally. In another embodiment, the administration is by parenteral injection. The mode of administration can be left to the discretion of the practitioner, and depends in-part upon the site of the medical condition. In most instances, administration results in the release of any agent described herein into the bloodstream.

In one embodiment, the Clec9A binding agent described herein is formulated in accordance with routine procedures as a composition adapted for oral administration. Compositions for oral delivery can be in the form of tablets, lozenges, aqueous or oily suspensions, granules, powders, emulsions, capsules, syrups, or elixirs, for example. Orally administered compositions can comprise one or more agents, for example, sweetening agents such as fructose, aspartame or saccharin; flavoring agents such as peppermint, oil of wintergreen, or cherry; coloring agents; and preserving agents, to provide a pharmaceutically palatable preparation. Moreover, where in tablet or pill form, the compositions can be coated to delay disintegration and absorption in the gastrointestinal tract thereby providing a sustained action over an extended period of time. Selectively permeable membranes surrounding an osmotically active driving any Clec9A binding agents described herein are also suitable for orally administered compositions. In these latter platforms, fluid from the environment surrounding the capsule is imbibed by the driving compound, which swells to displace the agent or agent composition through an aperture. These delivery platforms can provide an essentially zero order delivery profile as opposed to the spiked profiles of immediate release formulations. A time-delay material such as glycerol monostearate or glycerol stearate can also

be useful. Oral compositions can include standard excipients such as mannitol, lactose, starch, magnesium stearate, sodium saccharin, cellulose, and magnesium carbonate. In one embodiment, the excipients are of pharmaceutical grade. Suspensions, in addition to the active compounds, may contain suspending agents such as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar, tragacanth, *etc.*, and mixtures thereof.

Dosage forms suitable for parenteral administration (*e.g.* intravenous, intramuscular, intraperitoneal, subcutaneous and intra-articular injection and infusion) include, for example, solutions, suspensions, dispersions, emulsions, and the like. They may also be manufactured in the form of sterile solid compositions (*e.g.* lyophilized composition), which can be dissolved or suspended in sterile injectable medium immediately before use. They may contain, for example, suspending or dispersing agents known in the art. Formulation components suitable for parenteral administration include a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl paraben; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as EDTA; buffers such as acetates, citrates or phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose.

For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor ELTM (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). The carrier should be stable under the conditions of manufacture and storage, and should be preserved against microorganisms. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol), and suitable mixtures thereof.

The compositions provided herein, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

Any inventive pharmaceutical compositions (and/or additional agents) described herein can be administered by controlled-release or sustained-release means or by delivery devices that are well known to those of ordinary skill in the art. Examples include, but are not limited to, those described in U.S. Patent Nos. 3,845,770; 3,916,899; 3,536,809; 3,598,123; 4,008,719; 5,674,533; 5,059,595; 5,591,767; 5,120,548; 5,073,543; 5,639,476; 5,354,556; and 5,733,556, each of which is incorporated herein by reference in its entirety. Such dosage forms can be useful for providing controlled- or sustained-release of one or more active ingredients using, for example, hydropropyl cellulose, hydropropylmethyl cellulose, polyvinylpyrrolidone, other polymer matrices, gels, permeable membranes, osmotic systems, multilayer coatings, microparticles, liposomes, microspheres, or a combination thereof to provide the desired release profile in varying proportions. Suitable controlled- or sustained-release formulations known to those skilled in the art, including those described herein, can be readily selected for use with the active ingredients of the agents described herein. The invention thus provides single unit dosage forms suitable for oral administration such as, but not limited to, tablets, capsules, gelcaps, and caplets that are adapted for controlled- or sustained-release.

Controlled- or sustained-release of an active ingredient can be stimulated by various conditions, including but not limited to, changes in pH, changes in temperature, stimulation by an appropriate wavelength of light, concentration or availability of enzymes, concentration or availability of water, or other physiological conditions or compounds.

In another embodiment, a controlled-release system can be placed in proximity of the target area to be treated, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)). Other controlled-release systems discussed in the review by Langer, 1990, *Science* 249:1527-1533) may be used.

Pharmaceutical formulations preferably are sterile. Sterilization can be accomplished, for example, by filtration through sterile filtration membranes. Where the composition is lyophilized, filter sterilization can be conducted prior to or following lyophilization and reconstitution.

Administration and Dosage

It will be appreciated that the actual dose of the Clec9A binding agent and/or any therapeutic agents described herein to be administered according to the present invention will vary according to the particular dosage form, and the mode of administration. Many factors that may modify the action of the Clec9A binding agent (e.g., body weight, gender, diet, time of administration, route of administration, rate of excretion, condition of the subject, drug combinations, genetic disposition and reaction sensitivities) can be taken into account by those skilled in the art. Administration can be carried out continuously or in one or more discrete doses within the maximum tolerated dose. Optimal administration rates for a given set of conditions can be ascertained by those skilled in the art using conventional dosage administration tests.

In some embodiments, a suitable dosage of the Clec9A binding agent and/or any therapeutic agents described herein is in a range of about 0.01 mg/kg to about 10 g/kg of body weight of the subject, about 0.01 mg/kg to about 1 g/kg of body weight of the subject, about 0.01 mg/kg to about 100 mg/kg of body weight of the subject, about 0.01 mg/kg to about 10 mg/kg of body weight of the subject, for example, about 0.01 mg/kg, about 0.02 mg/kg, about 0.03 mg/kg, about 0.04 mg/kg, about 0.05 mg/kg, about 0.06 mg/kg, about 0.07 mg/kg, about 0.08 mg/kg, about 0.09 mg/kg, about 0.1 mg/kg, about 0.2 mg/kg, about 0.3 mg/kg, about 0.4 mg/kg, about 0.5 mg/kg, about 0.6 mg/kg, about 0.7 mg/kg, about 0.8 mg/kg, about 0.9 mg/kg, about 1 mg/kg, about 1.1 mg/kg, about 1.2 mg/kg, about 1.3 mg/kg, about 1.4 mg/kg, about 1.5 mg/kg, about 1.6 mg/kg, about 1.7 mg/kg, about 1.8 mg/kg, 1.9 mg/kg, about 2 mg/kg, about 3 mg/kg, about 4 mg/kg, about 5 mg/kg, about 6 mg/kg, about 7 mg/kg, about 8 mg/kg, about 9 mg/kg, about 10 mg/kg body weight, about 100 mg/kg body weight, about 1 g/kg of body weight, about 10 g/kg of body weight, inclusive of all values and ranges therebetween.

Individual doses of the Clec9A binding agent and/or any therapeutic agents described herein can be administered in unit dosage forms containing, for example, from about 0.01 mg to about 100 g, from about 0.01 mg to about 75 g, from about 0.01 mg to about 50 g, from about 0.01 mg to about 25 g, about 0.01 mg to about 10 g, about 0.01 mg to about 7.5 g, about 0.01 mg to about 5 g, about 0.01 mg to about 2.5 g, about 0.01 mg to about 1 g, about

0.01 mg to about 100 mg, from about 0.1 mg to about 100 mg, from about 0.1 mg to about 90 mg, from about 0.1 mg to about 80 mg, from about 0.1 mg to about 70 mg, from about 0.1 mg to about 60 mg, from about 0.1 mg to about 50 mg, from about 0.1 mg to about 40 mg active ingredient, from about 0.1 mg to about 30 mg, from about 0.1 mg to about 20 mg, from about 0.1 mg to about 10 mg, from about 0.1 mg to about 5 mg, from about 0.1 mg to about 3 mg, from about 0.1 mg to about 1 mg per unit dosage form, or from about 5 mg to about 80 mg per unit dosage form. For example, a unit dosage form can be about 0.01 mg, about 0.02 mg, about 0.03 mg, about 0.04 mg, about 0.05 mg, about 0.06 mg, about 0.07 mg, about 0.08 mg, about 0.09 mg, about 0.1 mg, about 0.2 mg, about 0.3 mg, about 0.4 mg, about 0.5 mg, about 0.6 mg, about 0.7 mg, about 0.8 mg, about 0.9 mg, about 1 mg, about 2 mg, about 3 mg, about 4 mg, about 5 mg, about 6 mg, about 7 mg, about 8 mg, about 9 mg about 10 mg, about 15 mg, about 20 mg, about 25 mg, about 30 mg, about 35 mg, about 40 mg, about 45 mg, about 50 mg, about 55 mg, about 60 mg, about 65 mg, about 70 mg, about 75 mg, about 80 mg, about 85 mg, about 90 mg, about 95 mg, about 100 mg, about 200 mg, about 500 mg, about 1 g, about 2.5 g, about 5 g, about 10 g, about 25 g, about 50 g, about 75 g, about 100 g, inclusive of all values and ranges therebetween.

In one embodiment, the Clec9A binding agent and/or any therapeutic agents described herein are administered at an amount of from about 0.01 mg to about 100 g daily, from about 0.01 mg to about 75 g daily, from about 0.01 mg to about 50 g daily, from about 0.01 mg to about 25 g daily, from about 0.01 mg to about 10 g daily, from about 0.01 mg to about 7.5 g daily, from about 0.01 mg to about 5 g daily, from about 0.01 mg to about 2.5 g daily, from about 0.01 mg to about 1 g daily, from about 0.01 mg to about 100 mg daily, from about 0.1 mg to about 100 mg daily, from about 0.1 mg to about 95 mg daily, from about 0.1 mg to about 90 mg daily, from about 0.1 mg to about 85 mg daily, from about 0.1 mg to about 80 mg daily, from about 0.1 mg to about 75 mg daily, from about 0.1 mg to about 70 mg daily, from about 0.1 mg to about 65 mg daily, from about 0.1 mg to about 60 mg daily, from about 0.1 mg to about 55 mg daily, from about 0.1 mg to about 50 mg daily, from about 0.1 mg to about 45 mg daily, from about 0.1 mg to about 40 mg daily, from about 0.1 mg to about 35 mg daily, from about 0.1 mg to about 30 mg daily, from about 0.1 mg to about 25 mg daily, from about 0.1 mg to about 20 mg daily, from about 0.1 mg to about 15 mg daily, from about 0.1 mg to about 10 mg daily, from about 0.1 mg to about 5 mg daily, from about 0.1 mg to about 3 mg daily, from about 0.1 mg to about 1 mg daily, or from about 5 mg to about 80 mg daily. In various embodiments, the Clec9A binding agent is administered at a daily dose of about 0.01 mg, about 0.02 mg, about 0.03 mg, about 0.04 mg, about 0.05 mg, about 0.06 mg, about 0.07 mg, about 0.08 mg, about 0.09 mg, about 0.1 mg, about 0.2 mg, about 0.3 mg, about 0.4 mg, about 0.5 mg, about 0.6 mg, about 0.7 mg, about 0.8 mg, about 0.9 mg, about 1 mg, about 2 mg, about 3 mg, about 4 mg, about 5 mg, about 6 mg, about 7 mg, about 8 mg, about 9 mg about 10 mg, about 15 mg, about 20 mg, about 25 mg, about 30 mg, about 35 mg, about 40 mg, about 45 mg, about 50 mg, about 55 mg, about 60 mg, about 65 mg, about 70 mg, about 75 mg, about 80 mg, about 85 mg, about 90 mg, about 95 mg, about 100 mg, about 200 mg, about 500 mg, about 1 g, about 2.5 g, about 5 g, about 7.5 g, about 10 g, about 25 g, about 50 g, about 75 g, about 100 g, inclusive of all values and ranges therebetween.

In accordance with certain embodiments of the invention, the pharmaceutical composition comprising the Clec9A binding agent and/or any therapeutic agents described herein may be administered, for example, more than once

daily (e.g., about two times, about three times, about four times, about five times, about six times, about seven times, about eight times, about nine times, or about ten times daily), about once per day, about every other day, about every third day, about once a week, about once every two weeks, about once every month, about once every two months, about once every three months, about once every six months, or about once every year.

Combination Therapy and Additional Therapeutic Agents

In various embodiments, the pharmaceutical composition of the present invention is co-administered in conjunction with additional therapeutic agent(s). Co-administration can be simultaneous or sequential.

In one embodiment, the additional therapeutic agent and the Clec9A binding agent of the present invention are administered to a subject simultaneously. The term "simultaneously" as used herein, means that the additional therapeutic agent and the Clec9A binding agent are administered with a time separation of no more than about 60 minutes, such as no more than about 30 minutes, no more than about 20 minutes, no more than about 10 minutes, no more than about 5 minutes, or no more than about 1 minute. Administration of the additional therapeutic agent and the Clec9A binding agent can be by simultaneous administration of a single formulation (e.g., a formulation comprising the additional therapeutic agent and the Clec9A binding agent) or of separate formulations (e.g., a first formulation including the additional therapeutic agent and a second formulation including the Clec9A binding agent).

Co-administration does not require the therapeutic agents to be administered simultaneously, if the timing of their administration is such that the pharmacological activities of the additional therapeutic agent and the Clec9A binding agent overlap in time, thereby exerting a combined therapeutic effect. For example, the additional therapeutic agent and the Clec9A binding agent can be administered sequentially. The term "sequentially" as used herein means that the additional therapeutic agent and the Clec9A binding agent are administered with a time separation of more than about 60 minutes. For example, the time between the sequential administration of the additional therapeutic agent and the Clec9A binding agent can be more than about 60 minutes, more than about 2 hours, more than about 5 hours, more than about 10 hours, more than about 1 day, more than about 2 days, more than about 3 days, more than about 1 week, or more than about 2 weeks, or more than about one month apart. The optimal administration times will depend on the rates of metabolism, excretion, and/or the pharmacodynamic activity of the additional therapeutic agent and the Clec9A binding agent being administered. Either the additional therapeutic agent or the Clec9A binding agent cell may be administered first.

Co-administration also does not require the therapeutic agents to be administered to the subject by the same route of administration. Rather, each therapeutic agent can be administered by any appropriate route, for example, parenterally or non-parenterally.

In some embodiments, the Clec9A binding agent described herein acts synergistically when co-administered with another therapeutic agent. In such embodiments, the Clec9A binding agent and the additional therapeutic agent may be administered at doses that are lower than the doses employed when the agents are used in the context of monotherapy.

In some embodiments, the present invention pertains to chemotherapeutic agents as additional therapeutic agents. For example, without limitation, such combination of the present Clec9A binding agents and chemotherapeutic agent find use in the treatment of cancers, as described elsewhere herein. Examples of chemotherapeutic agents include, but are not limited to, alkylating agents such as thiotepa and CYTOXAN cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramidate, triethylenethiophosphoramidate and trimethylolomelamine; acetogenins (e.g., bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatins; cally statin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (e.g., cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB 1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimustine; antibiotics such as the enediyne antibiotics (e.g., calicheamicin, especially calicheamicin gammall and calicheamicin omegall (see, e.g., Agnew, Chem. Intl. Ed. Engl., 33: 183-186 (1994))); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabycin, caminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN doxorubicin (including morpholino- doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxy doxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as minogluthethimide, mitotane, trilostane; folic acid replenisher such as frolic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestabucil; bisantrene; edatraxate; demecolcine; diaziquone; elformithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguanzone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK polysaccharide complex (JHS Natural Products, Eugene, Oreg.); razoxane; rhizoxin; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (e.g., T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g., TAXOL paclitaxel (Bristol-Myers Squibb Oncology, Princeton, N.J.), ABRAXANE Cremophor-free, albumin-engineered nanoparticle

formulation of paclitaxel (American Pharmaceutical Partners, Schaumburg, 111.), and TAXOTERE doxetaxel (Rhône-Poulenc Rorer, Antony, France); chloranbucil; GEMZAR gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin, oxaliplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; NAVELBINE. vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; irinotecan (Camptosar, CPT-11) (including the treatment regimen of irinotecan with 5-FU and leucovorin); topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine; combretastatin; leucovorin (LV); oxaliplatin, including the oxaliplatin treatment regimen (FOLFOX); lapatinib (Tykerb); inhibitors of PKC- α , Raf, H-Ras, EGFR (e.g., erlotinib (Tarceva)) and VEGF-A that reduce cell proliferation and pharmaceutically acceptable salts, acids or derivatives of any of the above. In addition, the methods of treatment can further include the use of radiation. In addition, the methods of treatment can further include the use of photodynamic therapy.

Accordingly, in some embodiments, the present invention relates to combination therapies using the Clec9A binding agent and a chemotherapeutic agent. In some embodiments, the present invention relates to administration of the Clec9A binding agent to a patient undergoing treatment with a chemotherapeutic agent. In some embodiments, the chemotherapeutic agent is a DNA-intercalating agent such as, without limitation, doxorubicin, cisplatin, daunorubicin, and epirubicin. In an embodiment, the DNA-intercalating agent is doxorubicin.

In illustrative embodiments, the Clec9A binding agent acts synergistically when co-administered with doxorubicin. In an illustrative embodiment, the Clec9A binding agent acts synergistically when co-administered with doxorubicin for use in treating tumor or cancer. For example, co-administration of the Clec9A binding agent and doxorubicin may act synergistically to reduce or eliminate the tumor or cancer, or slow the growth and/or progression and/or metastasis of the tumor or cancer. In illustrative embodiments, the combination of the Clec9A binding agent and doxorubicin may exhibit improved safety profiles when compared to the agents used alone in the context of monotherapy. In illustrative embodiments, the Clec9A binding agent and doxorubicin may be administered at doses that are lower than the doses employed when the agents are used in the context of monotherapy. In some embodiments, the Clec9A binding agent comprises a mutated interferon such as a mutated IFN α . In illustrative embodiments, the mutated IFN α comprises one or more mutations at positions 148, 149, and 153 with reference to SEQ ID NO: 337 or SEQ ID NO: 338, such as the substitutions M148A, R149A, and L153A.

In some embodiments, the present invention relates to combination therapy with one or more immune-modulating agents, for example, without limitation, agents that modulate immune checkpoint. In various embodiments, the immune-modulating agent targets one or more of PD-1, PD-L1, and PD-L2. In various embodiments, the immune-modulating agent is PD-1 inhibitor. In various embodiments, the immune-modulating agent is an antibody specific for one or more of PD-1, PD-L1, and PD-L2. For instance, in some embodiments, the immune-modulating agent is an antibody such as, by way of non-limitation, nivolumab, (ONO-4538/BMS-936558, MDX1106, OPDIVO, BRISTOL MYERS SQUIBB), pembrolizumab (KEYTRUDA, MERCK), pidilizumab (CT-011, CURE TECH), MK-3475 (MERCK), BMS 936559 (BRISTOL MYERS SQUIBB), MPDL3280A (ROCHE). In some embodiments, the immune-modulating agent targets one or more of CD137 or CD137L. In various embodiments, the immune-

modulating agent is an antibody specific for one or more of CD137 or CD137L. For instance, in some embodiments, the immune-modulating agent is an antibody such as, by way of non-limitation, urelumab (also known as BMS-663513 and anti-4-1BB antibody). In some embodiments, the present chimeric protein is combined with urelumab (optionally with one or more of nivolumab, lirilumab, and urelumab) for the treatment of solid tumors and/or B-cell non-Hodgkins lymphoma and/or head and neck cancer and/or multiple myeloma. In some embodiments, the immune-modulating agent is an agent that targets one or more of CTLA-4, AP2M1, CD80, CD86, SHP-2, and PPP2R5A. In various embodiments, the immune-modulating agent is an antibody specific for one or more of CTLA-4, AP2M1, CD80, CD86, SHP-2, and PPP2R5A. For instance, in some embodiments, the immune-modulating agent is an antibody such as, by way of non-limitation, ipilimumab (MDX-010, MDX-101, Yervoy, BMS) and/or tremelimumab (Pfizer). In some embodiments, the present chimeric protein is combined with ipilimumab (optionally with bavituximab) for the treatment of one or more of melanoma, prostate cancer, and lung cancer. In various embodiments, the immune-modulating agent targets CD20. In various embodiments, the immune-modulating agent is an antibody specific CD20. For instance, in some embodiments, the immune-modulating agent is an antibody such as, by way of non-limitation, Ofatumumab (GENMAB), obinutuzumab (GAZYVA), AME-133v (APPLIED MOLECULAR EVOLUTION), Ocrelizumab (GENENTECH), TRU-015 (TRUBION/EMERGENT), veltuzumab (IMMU-106).

In some embodiments, the present invention relates to combination therapy using the Clec9A binding agent and a checkpoint inhibitor. In some embodiments, the present invention relates to administration of the Clec9A binding agent to a patient undergoing treatment with a checkpoint inhibitor. In some embodiments, the checkpoint inhibitor is an agent that targets one or more of PD-1, PD-L1, PD-L2, and CTLA-4 (including any of the anti-PD-1, anti-PD-L1, anti-PD-L2, and anti-CTLA-4 agents described herein). In some embodiment, the checkpoint inhibitor is one or more of nivolumab, (ONO-4538/BMS-936558, MDX1106, OPDIVO, BRISTOL MYERS SQUIBB), pembrolizumab (KEYTRUDA, MERCK), pidilizumab (CT-011, CURE TECH), MK-3475 (MERCK), BMS 936559 (BRISTOL MYERS SQUIBB), MPDL3280A (ROCHE), ipilimumab (MDX-010, MDX-101, Yervoy, BMS) and tremelimumab (Pfizer). In an embodiment, the checkpoint inhibitor is an antibody against PD-L1.

In illustrative embodiments, the Clec9A binding agent acts synergistically when co-administered with the anti-PD-L1 antibody. In an illustrative embodiment, the Clec9A binding agent acts synergistically when co-administered with the anti-PD-L1 antibody for use in treating tumor or cancer. For example, co-administration of the Clec9A binding agent and the anti-PD-L1 antibody may act synergistically to reduce or eliminate the tumor or cancer, or slow the growth and/or progression and/or metastasis of the tumor or cancer. In some embodiments, the combination of the Clec9A binding agent and the anti-PD-L1 antibody may exhibit improved safety profiles when compared to the agents used alone in the context of monotherapy. In some embodiments, the Clec9A binding agent and the anti-PD-L1 antibody may be administered at doses that are lower than the doses employed when the agents are used in the context of monotherapy. In some embodiments, the Clec9A binding agent comprises a mutated interferon such as a mutated IFN α . In illustrative embodiments, the mutated IFN α comprises one or more

mutations at positions 148, 149, and 153 with reference to SEQ ID NO: 337 or SEQ ID NO: 338, such as the substitutions M148A, R149A, and L153A.

In some embodiments, the present invention relates to combination therapies using the Clec9A binding agent and an immunosuppressive agent. In some embodiments, the present invention relates to administration of the Clec9A binding agent to a patient undergoing treatment with an immunosuppressive agent. In an embodiment, the immunosuppressive agent is TNF.

In illustrative embodiments, the Clec9A binding agent acts synergistically when co-administered with TNF. In an illustrative embodiment, the Clec9A binding agent acts synergistically when co-administered with TNF for use in treating tumor or cancer. For example, co-administration of the Clec9A binding agent and TNF may act synergistically to reduce or eliminate the tumor or cancer, or slow the growth and/or progression and/or metastasis of the tumor or cancer. In some embodiments, the combination of the Clec9A binding agent and TNF may exhibit improved safety profiles when compared to the agents used alone in the context of monotherapy. In some embodiments, the Clec9A binding agent and TNF may be administered at doses that are lower than the doses employed when the agents are used in the context of monotherapy. In some embodiments, the Clec9A binding agent comprises a mutated interferon such as a mutated IFN α . In illustrative embodiments, the mutated IFN α comprises one or more mutations at positions 148, 149, and 153 with reference to SEQ ID NO: 337 or SEQ ID NO: 338, such as the substitutions M148A, R149A, and L153A.

In some embodiments, the Clec9A binding agent acts synergistically when used in combination with Chimeric Antigen Receptor (CAR) T-cell therapy. In an illustrative embodiment, the Clec9A binding agent acts synergistically when used in combination with CAR T-cell therapy in treating tumor or cancer. In an embodiment, the Clec9A binding agent acts synergistically when used in combination with CAR T-cell therapy in treating blood-based tumors. In an embodiment, the Clec9A binding agent acts synergistically when used in combination with CAR T-cell therapy in treating solid tumors. For example, use of the Clec9A binding agent and CAR T-cells may act synergistically to reduce or eliminate the tumor or cancer, or slow the growth and/or progression and/or metastasis of the tumor or cancer. In various embodiments, the Clec9A binding agent of the invention induces CAR T-cell division. In various embodiments, the Clec9A binding agent of the invention induces CAR T-cell proliferation. In various embodiments, the Clec9A binding agent of the invention prevents anergy of the CAR T cells.

In various embodiments, the CAR T-cell therapy comprises CAR T cells that target antigens (*e.g.*, tumor antigens) such as, but not limited to, carbonic anhydrase IX (CAIX), 5T4, CD19, CD20, CD22, CD30, CD33, CD38, CD47, CS1, CD138, Lewis-Y, L1-CAM, MUC16, ROR-1, IL13R α 2, gp100, prostate stem cell antigen (PSCA), prostate-specific membrane antigen (PSMA), B-cell maturation antigen (BCMA), human papillomavirus type 16 E6 (HPV-16 E6), CD171, folate receptor alpha (FR- α), GD2, human epidermal growth factor receptor 2 (HER2), mesothelin, EGFRvIII, fibroblast activation protein (FAP), carcinoembryonic antigen (CEA), and vascular endothelial growth factor receptor 2 (VEGF-R2), as well as other tumor antigens well known in the art. Additional illustrative tumor antigens include, but are not limited to MART-1/Melan-A, gp100, Dipeptidyl peptidase IV (DPPIV), adenosine

deaminase-binding protein (ADAbp), cyclophilin b, Colorectal associated antigen (CRC)-0017-1A/GA733, Carcinoembryonic Antigen (CEA) and its immunogenic epitopes CAP-1 and CAP-2, etv6, aml1, Prostate Specific Antigen (PSA) and its immunogenic epitopes PSA-1, PSA-2, and PSA-3, T-cell receptor/CD3-zeta chain, MAGE-family of tumor antigens (e.g., MAGE-A1, MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A7, MAGE-A8, MAGE-A9, MAGE-A10, MAGE-A11, MAGE-A12, MAGE-Xp2 (MAGE-B2), MAGE-Xp3 (MAGE-B3), MAGE-Xp4 (MAGE-B4), MAGE-C1, MAGE-C2, MAGE-C3, MAGE-C4, MAGE-C5), GAGE-family of tumor antigens (e.g., GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, GAGE-7, GAGE-8, GAGE-9), BAGE, RAGE, LAGE-1, NAG, GnT-V, MUM-1, CDK4, tyrosinase, p53, MUC family, HER2/neu, p21ras, RCAS1, α -fetoprotein, E-cadherin, α -catenin, β -catenin and γ -catenin, p120ctn, gp100 Pmel117, PRAME, NY-ESO-1, cdc27, adenomatous polyposis coli protein (APC), fodrin, Connexin 37, Ig-idiotypic, p15, gp75, GM2 and GD2 gangliosides, viral products such as human papilloma virus proteins, Smad family of tumor antigens, Imp-1, NA, EBV-encoded nuclear antigen (EBNA)-1, brain glycogen phosphorylase, SSX-1, SSX-2 (HOM-MEL-40), SSX-1, SSX-4, SSX-5, SCP-1 CT-7, c-erbB-2, CD19, CD37, CD56, CD70, CD74, CD138, AGS16, MUC1, GPNMB, Ep-CAM, PD-L1, and PD-L2.

Exemplary CAR T-cell therapy include, but are not limited to, JCAR014 (Juno Therapeutics), JCAR015 (Juno Therapeutics), JCAR017 (Juno Therapeutics), JCAR018 (Juno Therapeutics), JCAR020 (Juno Therapeutics), JCAR023 (Juno Therapeutics), JCAR024 (Juno Therapeutics), CTL019 (Novartis), KTE-C19 (Kite Pharma), BPX-401 (Bellicum Pharmaceuticals), BPX-501 (Bellicum Pharmaceuticals), BPX-601 (Bellicum Pharmaceuticals), bb2121 (Bluebird Bio), CD-19 Sleeping Beauty cells (Ziopharm Oncology), UCART19 (Cellestis), UCART123 (Cellestis), UCART38 (Cellestis), UCARTCS1 (Cellestis), OXB-302 (Oxford BioMedica), MB-101 (Mustang Bio) and CAR T-cells developed by Innovative Cellular Therapeutics.

In some embodiments, the Clec9A binding agent is used in a method of treating multiple sclerosis (MS) in combination with one or more MS therapeutics including, but not limited to, 3-interferons, L acetate, T-interferon, IFN- β -2 (U. S. Patent Publication No. 2002/0025304), spirogermaniums (e.g., N-(3-dimethylaminopropyl)-2-aza-8,8-dimethyl-8-germaspiro [4:5] decane, N-(3-dimethylaminopropyl)-2-aza-8,8-diethyl-8-germaspiro [4:5] decane, N-(3-dimethylaminopropyl)-2-aza-8,8-dipropyl-8-germaspiro [4:5] decane, and N-(3-dimethylaminopropyl)-2-aza-8,8-dibutyl-8-germaspiro [4:5] decane), vitamin D analogs (e.g., 1,25 (OH) 2D3, (see, e.g., U.S. Patent No. 5,716,946)), prostaglandins (e.g., latanoprost, brimonidine, PGE1, PGE2 and PGE3, see, e.g., U. S. Patent Publication No. 2002/0004525), tetracycline and derivatives (e.g., minocycline and doxycycline, see, e.g., U.S. Patent Publication No. 20020022608), a VLA-4 binding antibody (see, e.g., U.S. Patent Publication No. 2009/0202527), adrenocorticotrophic hormone, corticosteroid, prednisone, methylprednisone, 2-chlorodeoxyadenosine, mitoxantrone, sulphasalazine, methotrexate, azathioprine, cyclophosphamide, cyclosporin, fumarate, anti-CD20 antibody (e.g., rituximab), and tizanidine hydrochloride.

In some embodiments, the Clec9A binding agent is used in combination with one or more therapeutic agents that treat one or more symptoms or side effects of MS. Such agents include, but are not limited to, amantadine, baclofen, papaverine, meclizine, hydroxyzine, sulfamethoxazole, ciprofloxacin, docusate, pemoline, dantrolene,

desmopressin, dexamethasone, tolterodine, phenylloin, oxybutynin, bisacodyl, venlafaxine, amitriptyline, methenamine, clonazepam, isoniazid, vardenafil, nitrofurantoin, psyllium hydrophilic mucilloid, alprostadil, gabapentin, nortriptyline, paroxetine, propantheline bromide, modafinil, fluoxetine, phenazopyridine, methylprednisolone, carbamazepine, imipramine, diazepam, sildenafil, bupropion, and sertraline.

In some embodiments, the Clec9A binding agent is used in a method of treating multiple sclerosis in combination with one or more of the disease modifying therapies (DMTs) described herein (e.g. the agents of Table A). In some embodiments, the present invention provides an improved therapeutic effect as compared to use of one or more of the DMTs described herein (e.g. the agents listed in the Table A below) without the one or more disclosed binding agent. In an embodiment, the combination of the Clec9A binding agent and the one or more DMTs produces synergistic therapeutic effects.

Table A: Illustrative Disease Modifying Therapies

Generic Name	Branded Name/Company	Frequency/Route of Delivery/Usual Dose
teriflunomide	AUBAGIO (GENZYME)	Every day; pill taken orally; 7 mg or 14 mg.
interferon beta-1a	AVONEX (BIOGEN IDEC)	Once a week; intramuscular (into the muscle) injection; 30 mcg
interferon beta-1b	BETASERON (BAYER HEALTHCARE PHARMACEUTICALS, INC.)	Every other day; subcutaneous (under the skin) injection; 250 mcg.
glatiramer acetate	COPAXONE (TEVA NEUROSCIENCE)	Every day; subcutaneous (under the skin) injection; 20 mg (20,000 mcg) OR Three times a week; subcutaneous (under the skin) injection; 40 mg (40,000 mcg)
interferon beta-1b	EXTAVIA (NOVARTIS PHARMACEUTICALS CORP.)	Every other day; subcutaneous (under the skin) injection; 250 mcg.
fingolimod	GILENYA (NOVARTIS PHARMACEUTICALS CORP.)	Every day; capsule taken orally; 0.5 mg.
Alemtuzumab (anti-CD52 monoclonal antibody)	LEMTRADA (GENZYME)	Intravenous infusion on five consecutive days, followed by intravenous infusion on three consecutive days one year later (12 mg)
mitoxantrone	NOVANTRONE (EMD SERONO)	Four times a year by IV infusion in a medical facility. Lifetime cumulative dose limit of approximately 8–12 doses over 2–3 years (140 mg/m ²).
pegylated interferon beta-1a	PLEGRIDY (BIOGEN IDEC)	Every 14 days; subcutaneous (under the skin) injection; 125 mcg
interferon beta-1a	REBIF (EMD SERONO, INC.)	Three times a week; subcutaneous (under the skin) injection; 44 mcg
dimethyl fumarate (BG-12)	TECFIDERA (BIOGEN IDEC)	Twice a day; capsule taken orally; 120 mg for one week and 240 mg thereafter
Natalizumab (humanized monoclonal antibody VLA-4 antagonist)	TYSABRI (BIOGEN IDEC)	Every four weeks by IV infusion in a registered infusion facility; 300 mg
DMTs in Development		
Amiloride (targets Acid-sensing ion channel-1)	PAR PHARMACEUTICAL, PERRIGO COMPANY ,	Oral

Generic Name	Branded Name/Company	Frequency/Route of Delivery/Usual Dose
Epithelial sodium channel Na ⁺ /H ⁺ exchanger)	SIGMAPHARM LABORATORIES	
ATX-MS-1467 (targets Major histocompatibility complex class II T cell responses to myelin basic protein)	APITOPE / MERCK SERONO	Intradermal Subcutaneous
BAF312 (targets Sphingosine 1-phosphate (S1P) receptor subtypes S1P1 and S1P5 B cell distribution T cell distribution)	NOVARTIS PHARMA	Oral
BGC20-0134 (targets Proinflammatory and anti-inflammatory cytokines)	BTG PLC	Oral
BIIB033 (targets LINGO-1 ("leucine-rich repeat and immunoglobulin-like domain-containing, Nogo receptor-interacting protein"))	BIOGEN	Intravenous infusion used in Phase I and Phase II trials Subcutaneous injection used in Phase I trial
Cladribine (targets CD4+ T cells DNA synthesis and repair E-selectin Intracellular adhesion molecule-1 Pro-inflammatory cytokines interleukin 2 and interleukin 2R Pro-inflammatory cytokines interleukin 8 and RANTES Cytokine secretion Monocyte and lymphocyte migration)	MERCK SERONO	Oral
Cyclophosphamide (targets T cells, particularly CD4+ helper T cells B cells)	BAXTER HEALTHCARE CORPORATION	Oral, monthly intravenous pulses
Daclizumab (humanized monoclonal antibody targeting CD25 Immune modulator of T cells)	BIOGEN IDEC/ABBVIE BIOTHERAPEUTICS	Projected to be IM injection once monthly
Dalfampridine (targets Voltage-gated potassium channels Degenerin/epithelial sodium channels L-type calcium channels that contain subunit Cavbeta3)	ACORDA THERAPEUTICS / BIOGEN IDEC	One tablet every 12 hours (extended release), 10 mg twice a day
Dronabinol (targets Cannabinoid receptor CB1 Cannabinoid receptor CB2)	ABBVIE INC.	Oral
Firategrast (targets Alpha4beta1 integrin)	GLAXOSMITHKLINE	Oral
GNbAC1MSRV-Env (targets envelope protein of the MS-associated retrovirus)	GENEURO SA / SERVIER	Intravenous infusion

Generic Name	Branded Name/Company	Frequency/Route of Delivery/Usual Dose
Idebenone (targets Reactive oxygen species)	SANTHERA PHARMACEUTICALS	Oral Dose in clinical trial for PPMS is 2250 mg per day (750 mg dose, 3 times per day)
Imilecleucel-T (targets Myelin-specific, autoreactive T cells)	OPEXA THERAPEUTICS / MERCK SERONO	Subcutaneous Given 5 times per year, according to information from the manufacturer
Laquinimod	TEVA	Projected to be 0.6 mg or 1.2 mg oral tablet taken daily
Masitinib (targets KIT (a stem cell factor, also called c-KIT) receptor as well as select other tyrosine kinases Mast cells)	AB SCIENCE	Oral
MEDI-551 (targets CD19, a B cell-specific antigen that is part of the B cell receptor complex and that functions in determining the threshold for B cell activation B cells Plasmablasts, B cells that express CD19 (but not CD20) and that secrete large quantities of antibodies; depletion of plasmablasts may be useful in autoimmune diseases involving pathogenic autoantibodies)	MEDIMMUNE	Intravenous Subcutaneous
Minocycline (targets T cells Microglia Leukocyte migration Matrix metalloproteinases)	VARIOUS	Oral Available as pellet-filled capsules and an oral suspension
MIS416 (targets Innate immune system Pathogen-associated molecular pattern recognition receptors of the innate immune system Myeloid cells of the innate immune system, which might be able to remodel the deregulated immune system activity that occurs in SPMS)	INNATE IMMUNOTHERAPEUTICS	Intravenous
Mycophenolate mofetil (targets Purine synthesis)	MANUFACTURED BY GENENTECH	Oral
Naltrexone (targets Opioid receptors Toll-like receptor 4)	VARIOUS	Given at low doses (3 to 4.5 mg per day) in oral form as "Low-dose naltrexone" (or "LDN")
Ocrelizumab and Ofatumumab (humanized monoclonal antibodies targeting CD20 B cell suppression)	ROCHE / GSK	Projected to be IV infusion

Generic Name	Branded Name/Company	Frequency/Route of Delivery/Usual Dose
ONO-4641 (targets Sphingosine 1-phosphate receptor)	ONO PHARMACEUTICAL CO.	Oral
Phenytoin (targets Sodium channels)	PFIZER	Intravenous Intramuscular (less favored option) Oral
Ponesimod	ACTELION	To be determined
Raltegravir (targets Retroviral integrase Herpesvirus DNA packaging terminase)	MERCK	Oral 400 mg tablet twice daily, according to information from the manufacturer
RHB-104	REDHILL BIOPHARMA LIMITED	95 mg clarithromycin, 45 mg rifabutin, and 10 mg clofazimine
Riluzole (targets Glutamatergic neurotransmission Glutamate uptake and release Voltage-gated sodium channels Protein kinase C)	COVIS PHARMA / SANOFI	Oral

MS disease progression may be most intensive, and most damaging, at the earliest stages of disease progression. Accordingly, counter to many reimbursement policies and physician practice in light of, for example, costs and side effect mitigation, it may be most beneficial for a patient's long term disease status to begin treatment with the most intensive DMTs, for instance so-called second-line therapies. In some embodiments, a patient is treated with a regimen of the Clec9A binding agent in combination with a second-line therapy. Such a combination is used to reduce the side effect profile of one or more second-line therapies. In some embodiments, the combination is used to reduce dose of frequency of administration of one or more second-line therapies. For example, the doses of agents listed in Table A provided above may be reduced by about 50%, or about 40%, or about 30%, or about 25% in the context of the combination and the/or the frequency of dosing may be decreased to be half as often, or a third as often or may be reduced from, for example, daily to every other day or weekly, every other day to weekly or bi-weekly, weekly to bi-weekly or monthly, *etc.* Accordingly, in some embodiments, the Clec9A binding agent increase patient adherence by allowing for more convenient treatment regimens. Further, some DMTs have a suggested lifetime dose limitation *e.g.* for mitoxantrone, the lifetime cumulative dose should be strictly limited to 140 mg/m², or 2 to 3 years of therapy. In some embodiments, supplementation with the Clec9A binding agent preserves patient's access to mitoxantrone by allowing for lower or less frequent dosing with this DMT.

In some embodiments, the patient is a naive patient, who has not received treatment with one or more DMTs, and the Clec9A binding agent is used to buffer the side effects of a second-line therapy. Accordingly, the naive patient is able to benefit from the long-term benefits of a second-line therapy at disease outset. In some embodiments, the Clec9A binding agent is used as an entry therapy that precedes the use of a second-line therapy. For example, the Clec9A binding agent may be administered for an initial treatment period of about 3 months to stabilize disease and then the patient may be transitioned to a maintenance therapy of a second line agent.

It is generally believed that naive patients are more likely to respond to therapy as compared to patients that have received, and perhaps failed one or more DMT. In some embodiments, the Clec9a binding agent finds use in patients that have received, and perhaps failed one or more DMT. For example, in some embodiments, the Clec9A binding agent increases the therapeutic effect in patients that have received, and perhaps failed one or more DMT and may allow these patients to respond like naive patients.

In some embodiments, the patient has received or is receiving treatment with one or more DMTs and is not responding well. For example, the patient may be refractory or poorly responsive to one or more DMTs. In some embodiments, the patient is refractory, or poorly responsive to one or more of teriflunomide (AUBAGIO (GENZYME)); interferon beta-1a (AVONEX (BIOGEN IDEC)); interferon beta-1b (BETASERON (BAYER HEALTHCARE PHARMACEUTICALS, INC.)); glatiramer acetate (COPAXONE (TEVA NEUROSCIENCE)); interferon beta-1b (EXTAVIA (NOVARTIS PHARMACEUTICALS CORP.)); fingolimod (GILENYA (NOVARTIS PHARMACEUTICALS CORP.)); alemtuzumab (LEMTRADA (GENZYME)); mitoxantrone (NOVANTRONE (EMD SERONO)); pegylated interferon beta-1a (PLEGRIDY (BIOGEN IDEC)); interferon beta-1a (REBIF (EMD SERONO, INC.)); dimethyl fumarate (BG-12) (TECFIDERA (BIOGEN IDEC)); and natalizumab (TYSABRI (BIOGEN IDEC)). In some embodiments, the one or more disclosed binding agent results in a therapeutic benefit of one or more DMTs in the patient and therefore reduces or eliminates the non-responsiveness to the DMT. For instance, this may spare the patient therapy with one or more DMTs at a higher dosing or frequency.

In patients with more aggressive disease, one approach is an induction treatment model, where a therapy with strong efficacy but strong safety concerns would be given first, followed by a maintenance therapy. An example of such a model might include initial treatment with alemtuzumab, followed by IFN- β , GA, or BG-12. In some embodiments, the one or more disclosed binding agent is used to prevent the need to switch therapies for maintenance. In some embodiments, the one or more disclosed binding agent is used to as maintenance therapy to one or more DMTs, including second line therapies. In some embodiments, the one or more disclosed binding agent is used to as first therapy in an induction, followed by another DMT as a maintenance therapy- such as, for example, a first line therapy.

In some embodiments, the one or more disclosed binding agent may be administered for an initial treatment period of about 3 months to stabilize disease and then the patient may be transitioned to a maintenance therapy of a first line agent.

In various embodiments, the one or more disclosed binding agent is used to reduce one or more side effects of a DMT, including without limitation any agent disclosed herein. For example, the one or more disclosed binding agent may be used in a regimen that allows dose sparing for one or more DMTs and therefore results in fewer side effects. For example, in some embodiments, the one or more disclosed binding agent may reduce one or more side effects of AUBAGIO or related agents, which may include hair thinning, diarrhea, flu, nausea, abnormal liver tests and unusual numbness or tingling in the hands or feet (paresthesias), levels of white blood cells, which can increase the risk of infections; increase in blood pressure; and severe liver damage. In some embodiments, the

one or more disclosed binding agent may reduce one or more side effects of AVONEX or related agents which include flu-like symptoms following injection, depression, mild anemia, liver abnormalities, allergic reactions, and heart problems. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of BETASERON or related agents which include flu-like symptoms following injection, injection site reactions, allergic reactions, depression, liver abnormalities, and low white blood cell counts. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of COPAXONE or related agents which include injection site reactions, vasodilation (dilation of blood vessels); chest pain; a reaction immediately after injection, which includes anxiety, chest pain, palpitations, shortness of breath, and flushing. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of EXTAVIA or related agents which include flu-like symptoms following injection, injection site reactions, allergic reactions, depression, liver abnormalities, and low white blood cell counts. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of GILENYA or related agents which include headache, flu, diarrhea, back pain, liver enzyme elevations, cough, slowed heart rate following first dose, infections, and swelling in the eye. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of LEMTRADA or related agents which include rash, headache, fever, nasal congestion, nausea, urinary tract infection, fatigue, insomnia, upper respiratory tract infection, hives, itching, thyroid gland disorders, fungal infection, pain in joints, extremities and back, diarrhea, vomiting, flushing, and infusion reactions (including nausea, hives, itching, insomnia, chills, flushing, fatigue, shortness of breath, changes in the sense of taste, indigestion, dizziness, pain). In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of NOVANTRONE or related agents which include blue-green urine 24 hours after administration; infections, bone marrow suppression (fatigue, bruising, low blood cell counts), nausea, hair thinning, bladder infections, mouth sores, and serious liver and heart damage. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of PLEGRIDY or related agents which include flu-like symptoms following injection, injection site reactions, depression, mild anemia, liver abnormalities, allergic reactions, and heart problems. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of REBIF or related agents which include flu-like symptoms following injection, injection site reactions, liver abnormalities, depression, allergic reactions, and low red or white blood cell counts. In some embodiments, one or more disclosed binding agent may reduce one or more side effects of TECFIDERA or related agents which include flushing (sensation of heat or itching and a blush on the skin), gastrointestinal issues (nausea, diarrhea, abdominal pain), rash, protein in the urine, elevated liver enzymes; and reduction in blood lymphocyte (white blood cell) counts. In some embodiments, the one or more disclosed binding agent may reduce one or more side effects of TYSABRI or related agents which include headache, fatigue, urinary tract infections, depression, respiratory tract infections, joint pain, upset stomach, abdominal discomfort, diarrhea, vaginitis, pain in the arms or legs, rash, allergic or hypersensitivity reactions within two hours of infusion (dizziness, fever, rash, itching, nausea, flushing, low blood pressure, difficulty breathing, chest pain).

In some embodiments, the present invention relates to combination therapy with one or more chimeric agents described in WO 2013/10779, WO 2015/007536, WO 2015/007520, WO 2015/007542, and WO 2015/007903, the entire contents of which are hereby incorporated by reference in their entireties.

In some embodiments, inclusive of, without limitation, infectious disease applications, the present invention pertains to anti-infectives as additional therapeutic agents. In some embodiments, the anti-infective is an anti-viral agent including, but not limited to, Abacavir, Acyclovir, Adefovir, Amprenavir, Atazanavir, Cidofovir, Darunavir, Delavirdine, Didanosine, Docosanol, Efavirenz, Elvitegravir, Emtricitabine, Enfuvirtide, Etravirine, Famciclovir, and Foscarnet. In some embodiments, the anti-infective is an anti-bacterial agent including, but not limited to, cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and ceftobiprole); fluoroquinolone antibiotics (cipro, Levaquin, floxin, tequin, avelox, and norflox); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); monobactam antibiotics (aztreonam); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem). In some embodiments, the anti-infectives include anti-malarial agents (e.g., chloroquine, quinine, mefloquine, primaquine, doxycycline, artemether/lumefantrine, atovaquone/proguanil and sulfadoxine/pyrimethamine), metronidazole, tinidazole, ivermectin, pyrantel pamoate, and albendazole.

In some embodiments, inclusive, without limitation, of autoimmune applications, the additional therapeutic agent is an immunosuppressive agent. In some embodiments, the immunosuppressive agent is an anti-inflammatory agent such as a steroidal anti-inflammatory agent or a non-steroidal anti-inflammatory agent (NSAID). Steroids, particularly the adrenal corticosteroids and their synthetic analogues, are well known in the art. Examples of corticosteroids useful in the present invention include, without limitation, hydroxyltriamcinolone, alpha-methyl dexamethasone, beta-methyl betamethasone, beclomethasone dipropionate, betamethasone benzoate, betamethasone dipropionate, betamethasone valerate, clobetasol valerate, desonide, desoxymethasone, dexamethasone, diflorasone diacetate, diflucortolone valerate, fludrenolone, flucorolone acetonide, flumethasone pivalate, fluosinolone acetonide, fluocinonide, flucortine butylester, fluocortolone, fluprednidene (fluprednylidene) acetate, flurandrenolone, halcinonide, hydrocortisone acetate, hydrocortisone butyrate, methylprednisolone, triamcinolone acetonide, cortisone, cortodoxone, flucetonide, fludrocortisone, difluorosone diacetate, fluradrenolone acetonide, medrysone, amcinafel, amcinafide, betamethasone and the balance of its esters, chloroprednisone, clocortelone, clescinolone, dichlorisone, difluprednate, flucorlonide, flunisolid, fluoromethalone, fluperolone, fluprednisolone, hydrocortisone, meprednisone, paramethasone, prednisolone, prednisone, beclomethasone dipropionate. (NSAIDS) that may be used in the present invention, include but are not limited to, salicylic acid, acetyl salicylic acid, methyl salicylate, glycol salicylate, salicylides, benzyl-2,5-diacetoxybenzoic acid, ibuprofen, fulindac, naproxen, ketoprofen, etofenamate, phenylbutazone, and indomethacin. In some embodiments, the immunosuppressive agent may be cytostatics such as alkylating agents, antimetabolites (e.g., azathioprine, methotrexate), cytotoxic antibiotics, antibodies (e.g., basiliximab, daclizumab, and muromonab), anti-immunophilins (e.g., cyclosporine, tacrolimus, sirolimus), interferons, opioids, TNF binding

proteins, mycophenolates, and small biological agents (e.g., fingolimod, myriocin). Additional anti-inflammatory agents are described, for example, in U.S. Patent No. 4,537,776, the entire contents of which is incorporated by reference herein.

In some embodiments, the Clec9A binding agent described herein, include derivatives that are modified, *i.e.*, by the covalent attachment of any type of molecule to the composition such that covalent attachment does not prevent the activity of the composition. For example, but not by way of limitation, derivatives include composition that have been modified by, *inter alia*, glycosylation, lipidation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, *etc.* Any of numerous chemical modifications can be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, *etc.*

In still other embodiments, the Clec9A binding agent described herein further comprise a cytotoxic agent, comprising, in illustrative embodiments, a toxin, a chemotherapeutic agent, a radioisotope, and an agent that causes apoptosis or cell death. Such agents may be conjugated to a composition described herein.

The Clec9A binding agent described herein may thus be modified post-translationally to add effector moieties such as chemical linkers, detectable moieties such as for example fluorescent dyes, enzymes, substrates, bioluminescent materials, radioactive materials, and chemiluminescent moieties, or functional moieties such as for example streptavidin, avidin, biotin, a cytotoxin, a cytotoxic agent, and radioactive materials.

Illustrative cytotoxic agents include, but are not limited to, methotrexate, aminopterin, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine; alkylating agents such as mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU), mitomycin C, lomustine (CCNU), 1-methylnitrosourea, cyclophosphamide, mechlorethamine, busulfan, dibromomannitol, streptozotocin, mitomycin C, cis-dichlorodiamine platinum (II) (DDP) cisplatin and carboplatin (paraplatin); anthracyclines include daunorubicin (formerly daunomycin), doxorubicin (adriamycin), detorubicin, carminomycin, idarubicin, epirubicin, mitoxantrone and bisantrene; antibiotics include dactinomycin (actinomycin D), bleomycin, calicheamicin, mithramycin, and anthramycin (AMC); and antimetabolic agents such as the vinca alkaloids, vincristine and vinblastine. Other cytotoxic agents include paclitaxel (taxol), ricin, pseudomonas exotoxin, gemcitabine, cytochalasin B, gramicidin D, ethidium bromide, emetine, etoposide, tenoposide, colchicin, dihydroxy anthracin dione, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, puromycin, procarbazine, hydroxyurea, asparaginase, corticosteroids, mytotane (O,P'-(DDD)), interferons, and mixtures of these cytotoxic agents.

Further cytotoxic agents include, but are not limited to, chemotherapeutic agents such as carboplatin, cisplatin, paclitaxel, gemcitabine, calicheamicin, doxorubicin, 5-fluorouracil, mitomycin C, actinomycin D, cyclophosphamide, vincristine, bleomycin, VEGF antagonists, EGFR antagonists, platins, taxols, irinotecan, 5-fluorouracil, gemcytabine, leucovorine, steroids, cyclophosphamide, melphalan, vinca alkaloids (e.g., vinblastine, vincristine, vindesine and vinorelbine), mustines, tyrosine kinase inhibitors, radiotherapy, sex hormone antagonists, selective androgen receptor modulators, selective estrogen receptor modulators, PDGF antagonists,

TNF antagonists, IL-1 antagonists, interleukins (e.g. IL-12 or IL-2), IL-12R antagonists, Toxin conjugated monoclonal antibodies, tumor antigen specific monoclonal antibodies, Erbitux, Avastin, Pertuzumab, anti-CD20 antibodies, Rituxan, ocrelizumab, ofatumumab, DXL625, HERCEPTIN®, or any combination thereof. Toxic enzymes from plants and bacteria such as ricin, diphtheria toxin and Pseudomonas toxin may be conjugated to the therapeutic agents (e.g. antibodies) to generate cell-type-specific-killing reagents (Youle, *et al.*, Proc. Nat'l Acad. Sci. USA 77:5483 (1980); Gilliland, *et al.*, Proc. Nat'l Acad. Sci. USA 77:4539 (1980); Krolick, *et al.*, Proc. Nat'l Acad. Sci. USA 77:5419 (1980)).

Other cytotoxic agents include cytotoxic ribonucleases as described by Goldenberg in U.S. Pat. No. 6,653,104. Embodiments of the invention also relate to radioimmunoconjugates where a radionuclide that emits alpha or beta particles is stably coupled to the Clec9A binding agent, with or without the use of a complex-forming agent. Such radionuclides include beta-emitters such as Phosphorus-32, Scandium-47, Copper-67, Gallium-67, Yttrium-88, Yttrium-90, Iodine-125, Iodine-131, Samarium-153, Lutetium-177, Rhenium-186 or Rhenium-188, and alpha-emitters such as Astatine-211, Lead-212, Bismuth-212, Bismuth-213 or Actinium-225.

Illustrative detectable moieties further include, but are not limited to, horseradish peroxidase, acetylcholinesterase, alkaline phosphatase, beta-galactosidase and luciferase. Further illustrative fluorescent materials include, but are not limited to, rhodamine, fluorescein, fluorescein isothiocyanate, umbelliferone, dichlorotriazinylamine, phycoerythrin and dansyl chloride. Further illustrative chemiluminescent moieties include, but are not limited to, luminol. Further illustrative bioluminescent materials include, but are not limited to, luciferin and aequorin. Further illustrative radioactive materials include, but are not limited to, Iodine-125, Carbon-14, Sulfur-35, Tritium and Phosphorus-32.

Methods of Treatment

Methods and compositions described herein have application to treating various diseases and disorders, including, but not limited to cancer, infections, immune disorders, and inflammatory diseases or conditions.

Further, any of the present agents may be for use in the treating, or the manufacture of a medicament for treating, various diseases and disorders, including, but not limited to cancer, infections, immune disorders, inflammatory diseases or conditions, and autoimmune diseases.

In some embodiments, the present invention relates to the treatment of, or a patient having cancer. As used herein, cancer refers to any uncontrolled growth of cells that may interfere with the normal functioning of the bodily organs and systems, and includes both primary and metastatic tumors. Primary tumors or cancers that migrate from their original location and seed vital organs can eventually lead to the death of the subject through the functional deterioration of the affected organs. A metastasis is a cancer cell or group of cancer cells, distinct from the primary tumor location, resulting from the dissemination of cancer cells from the primary tumor to other parts of the body. Metastases may eventually result in death of a subject. For example, cancers can include benign and malignant cancers, polyps, hyperplasia, as well as dormant tumors or micrometastases.

Illustrative cancers that may be treated include, but are not limited to, basal cell carcinoma, biliary tract cancer; bladder cancer; bone cancer; brain and central nervous system cancer; breast cancer; cancer of the peritoneum; cervical cancer; choriocarcinoma; colon and rectum cancer; connective tissue cancer; cancer of the digestive system; endometrial cancer; esophageal cancer; eye cancer; cancer of the head and neck; gastric cancer (including gastrointestinal cancer); glioblastoma; hepatic carcinoma; hepatoma; intra-epithelial neoplasm; kidney or renal cancer; larynx cancer; leukemia; liver cancer; lung cancer (*e.g.*, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung); melanoma; myeloma; neuroblastoma; oral cavity cancer (lip, tongue, mouth, and pharynx); ovarian cancer; pancreatic cancer; prostate cancer; retinoblastoma; rhabdomyosarcoma; rectal cancer; cancer of the respiratory system; salivary gland carcinoma; sarcoma; skin cancer; squamous cell cancer; stomach cancer; testicular cancer; thyroid cancer; uterine or endometrial cancer; cancer of the urinary system; vulval cancer; lymphoma including Hodgkin's and non-Hodgkin's lymphoma, as well as B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia; chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); acute myeloid leukemia (AML); Hairy cell leukemia; chronic myeloblastic leukemia; as well as other carcinomas and sarcomas; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (*e.g.* that associated with brain tumors), and Meigs' syndrome.

In various embodiments, the present invention provides Clec9A binding agents which are part of a chimera that further comprises modified signaling agents for the treatment of cancer. In some embodiments, the Clec9A binding agents of the invention significantly reduce and/or eliminate tumors. In some embodiments, the present Clec9A binding agents significantly reduce and/or eliminate tumors when administered to a subject in combination with other anti-cancer agents such as chemotherapeutic agents, checkpoint inhibitors, and immunosuppressive agents. In various embodiments, the combination of Clec9A binding agents and other anti-cancer agents synergistically reduced tumor size and/or eliminated tumor cells.

In various embodiments, the present invention relates to cancer combination therapies with a Clec9A binding agent that is part of a chimera comprising one or more targeting moieties and one or more modified signaling agents. Accordingly, the present invention provides for chimeric or fusion proteins that include, for example, a targeting moiety against Clec9A and one or more signaling agents and uses thereof in combination with anti-cancer agents.

For instance, in various embodiments, the present invention pertains to combination therapies for cancer involving chimeras of a Clec9A binding agent described herein and a modified signaling agent, including, without limitation a mutated human interferon, such as IFN alpha, including human interferon alpha 2.

In other embodiments, the present Clec9A binding agent is part of a chimera that comprises multiple targeting moieties and therefore be present in bispecific or trispecific formats. For instance, in various embodiments, the

present invention pertains to combination therapies for cancer involving chimeras of a Clec9A binding agent and a checkpoint inhibitor binding agent (e.g. anti-PD-L1, anti-PD-1, anti-PD-L2, or anti-CTLA) described herein and a modified signaling agent, including, without limitation a mutated human interferon, such as IFN alpha, including human interferon alpha 2.

In various embodiments, the signaling agent is modified to have reduced affinity or activity for one or more of its receptors, which allows for attenuation of activity (inclusive of agonism or antagonism) and/or prevents non-specific signaling or undesirable sequestration of the chimeric protein. In some embodiments, the reduced affinity or activity at the receptor is restorable by attachment with one or more of the targeting moieties described herein.

In some embodiments, the present invention relates to the treatment of, or a patient having a microbial infection and/or chronic infection. Illustrative infections include, but are not limited to, HIV/AIDS, tuberculosis, osteomyelitis, hepatitis B, hepatitis C, Epstein-Barr virus or parvovirus, T cell leukemia virus, bacterial overgrowth syndrome, fungal or parasitic infections.

In various embodiments, the present compositions are used to treat or prevent one or more inflammatory diseases or conditions, such as inflammation, acute inflammation, chronic inflammation, respiratory disease, atherosclerosis, restenosis, asthma, allergic rhinitis, atopic dermatitis, septic shock, rheumatoid arthritis, inflammatory bowel disease, inflammatory pelvic disease, pain, ocular inflammatory disease, celiac disease, Leigh Syndrome, Glycerol Kinase Deficiency, Familial eosinophilia (FE), autosomal recessive spastic ataxia, laryngeal inflammatory disease; Tuberculosis, Chronic cholecystitis, Bronchiectasis, Silicosis and other pneumoconioses.

In various embodiments, the present invention has application to treating autoimmune and/or neurodegenerative diseases.

In various embodiments, the present compositions are used to treat or prevent one or more conditions characterized by undesirable CTL activity, and/or a conditions characterized by high levels of cell death. For instance, in various embodiments, the present compositions are used to treat or prevent one or more conditions associated with uncontrolled or overactive immune response.

In various embodiments, the present compositions are used to treat or prevent one or more autoimmune and/or neurodegenerative diseases or conditions, such as MS, diabetes mellitus, lupus, celiac disease, Crohn's disease, ulcerative colitis, Guillain-Barre syndrome, scleroderms, Goodpasture's syndrome, Wegener's granulomatosis, autoimmune epilepsy, Rasmussen's encephalitis, Primary biliary sclerosis, Sclerosing cholangitis, Autoimmune hepatitis, Addison's disease, Hashimoto's thyroiditis, Fibromyalgia, Menier's syndrome; transplantation rejection (e.g., prevention of allograft rejection) pernicious anemia, rheumatoid arthritis, systemic lupus erythematosus, dermatomyositis, Sjogren's syndrome, lupus erythematosus, myasthenia gravis, Reiter's syndrome, Grave's disease, and other autoimmune diseases.

In various embodiments, the present invention is used to treat or prevent various autoimmune and/or neurodegenerative diseases. In some embodiments, the autoimmune and/or neurodegenerative diseases selected

from MS (including without limitation the subtypes described herein), Alzheimer's disease (including, without limitation, Early-onset Alzheimer's, Late-onset Alzheimer's, and Familial Alzheimer's disease (FAD), Parkinson's disease and parkinsonism (including, without limitation, Idiopathic Parkinson's disease, Vascular parkinsonism, Drug-induced parkinsonism, Dementia with Lewy bodies, Inherited Parkinson's, Juvenile Parkinson's), Huntington's disease, Amyotrophic lateral sclerosis (ALS, including, without limitation, Sporadic ALS, Familial ALS, Western Pacific ALS, Juvenile ALS, Hiramaya Disease).

In various embodiments, the present invention is used to treat or prevent MS. In various embodiments, the Clec9a binding agents as described herein are used to eliminate and reduce multiple MS symptoms. Illustrative symptoms associated with multiple sclerosis, which can be prevented or treated with the compositions and methods described herein, include: optic neuritis, diplopia, nystagmus, ocular dysmetria, internuclear ophthalmoplegia, movement and sound phosphenes, afferent pupillary defect, paresis, monoparesis, paraparesis, hemiparesis, quadraparesis, plegia, paraplegia, hemiplegia, tetraplegia, quadraplegia, spasticity, dysarthria, muscle atrophy, spasms, cramps, hypotonia, clonus, myoclonus, myokymia, restless leg syndrome, footdrop, dysfunctional reflexes, paraesthesia, anaesthesia, neuralgia, neuropathic and neurogenic pain, l'hermitte's sign, proprioceptive dysfunction, trigeminal neuralgia, ataxia, intention tremor, dysmetria, vestibular ataxia, vertigo, speech ataxia, dystonia, dysdiadochokinesia, frequent micturation, bladder spasticity, flaccid bladder, detrusor-sphincter dyssynergia, erectile dysfunction, anorgasm, frigidity, constipation, fecal urgency, fecal incontinence, depression, cognitive dysfunction, dementia, mood swings, emotional lability, euphoria, bipolar syndrome, anxiety, aphasia, dysphasia, fatigue, Uhthoff's symptom, gastroesophageal reflux, and sleeping disorders. Mitigation or amelioration or one more of these symptoms in a subject can be achieved by the one or more agent as described herein.

In various embodiments, the Clec9A binding agents as described herein is used to treat or prevent clinically isolated syndrome (CIS). A clinically isolated syndrome (CIS) is a single monosymptomatic attack compatible with MS, such as optic neuritis, brain stem symptoms, and partial myelitis. Patients with CIS that experience a second clinical attack are generally considered to have clinically definite multiple sclerosis (CDMS). Over 80 percent of patients with CIS and MRI lesions go on to develop MS, while approximately 20 percent have a self-limited process. Patients who experience a single clinical attack consistent with MS may have at least one lesion consistent with multiple sclerosis prior to the development of clinically definite multiple sclerosis. In various embodiments, the presently described Clec9a binding agents is used to treat CIS so it does not develop into MS, including, for example RRMS.

In various embodiments, the Clec9A binding agents as described herein are used to treat or prevent radiologically isolated syndrome (RIS). In RIS, incidental imaging findings suggest inflammatory demyelination in the absence of clinical signs or symptoms. In various embodiments, the Clec9A binding agent is used to treat RIS so it does not develop into MS, including, for example RRMS.

In various embodiments, the Clec9A binding agents as described herein are used to treat one or more of benign multiple sclerosis; relapsing-remitting multiple sclerosis (RRMS); secondary progressive multiple sclerosis (SPMS); progressive relapsing multiple sclerosis (PRMS); and primary progressive multiple sclerosis (PPMS).

Benign multiple sclerosis is a retrospective diagnosis which is characterized by 1-2 exacerbations with complete recovery, no lasting disability and no disease progression for 10-15 years after the initial onset. Benign multiple sclerosis may, however, progress into other forms of multiple sclerosis. In various embodiments, the Clec9a binding agent is used to treat benign multiple sclerosis so it does not develop into MS.

Patients suffering from RRMS experience sporadic exacerbations or relapses, as well as periods of remission. Lesions and evidence of axonal loss may or may not be visible on MRI for patients with RRMS. In various embodiments, the Clec9a binding agents as described herein are used to treat RRMS. In some embodiments, RRMS includes patients with RRMS; patients with SPMS and superimposed relapses; and patients with CIS who show lesion dissemination on subsequent MRI scans according to McDonald's criteria. A clinical relapse, which may also be used herein as "relapse," "confirmed relapse," or "clinically defined relapse," is the appearance of one or more new neurological abnormalities or the reappearance of one or more previously observed neurological abnormalities. This change in clinical state must last at least 48 hours and be immediately preceded by a relatively stable or improving neurological state of at least 30 days. In some embodiments, an event is counted as a relapse when the subject's symptoms are accompanied by observed objective neurological changes, consistent with an increase of at least 1.00 in the Expanded Disability Status Scale (EDSS) score or one grade in the score of two or more of the seven FS or two grades in the score of one of FS as compared to the previous evaluation.

SPMS may evolve from RRMS. Patients afflicted with SPMS have relapses, a diminishing degree of recovery during remissions, less frequent remissions and more pronounced neurological deficits than RRMS patients. Enlarged ventricles, which are markers for atrophy of the corpus callosum, midline center and spinal cord, are visible on MRI of patients with SPMS. In various embodiments, the Clec9a binding agents as described herein is used to treat RRMS so it does not develop into SPMS.

PPMS is characterized by a steady progression of increasing neurological deficits without distinct attacks or remissions. Cerebral lesions, diffuse spinal cord damage and evidence of axonal loss are evident on the MRI of patients with PPMS. PPMS has periods of acute exacerbations while proceeding along a course of increasing neurological deficits without remissions. Lesions are evident on MRI of patients suffering from PPMS. In various embodiments, the Clec9A binding agent as described herein is used to treat RRMS and/or SPMS so it does not develop into PPMS.

In some embodiments, the Clec9A binding agents as described herein are used in a method of treatment of relapsing forms of MS. In some embodiments, the Clec9A binding agent is used in a method of treatment of relapsing forms of MS to slow the accumulation of physical disability and/or reduce the frequency of clinical exacerbations, and, optionally, for patients who have experienced a first clinical episode and have MRI features consistent with MS. In some embodiments, the Clec9a binding agents as described herein are used in a method of treatment of worsening relapsing-remitting MS, progressive-relapsing MS or secondary-progressive MS to reduce neurologic disability and/or the frequency of clinical exacerbations. In some embodiments, the Clec9A binding agents reduce the frequency and/or severity of relapses.

In some embodiments, the Clec9A binding agents are used in a method of treatment of relapsing forms of MS in patients who have had an inadequate response to (or are refractory to) one, or two, or three, or four, or five, or six, or seven, or eight, or nine, or ten or more disease modifying therapies (DMTs).

In various embodiments, the subject's symptoms may be assessed quantitatively, such as by EDSS, or decrease in the frequency of relapses, or increase in the time to sustained progression, or improvement in the magnetic resonance imaging (MRI) behavior in frequent, serial MRI studies and compare the patient's status measurement before and after treatment. In a successful treatment, the patient status will have improved (e.g., the EDSS measurement number or frequency of relapses will have decreased, or the time to sustained progression will have increased, or the MRI scans will show less pathology).

In some embodiments, the patient can be evaluated, e.g., before, during or after receiving the Clec9a binding agents e.g., for indicia of responsiveness. Various clinical or other indicia of effectiveness of treatment, e.g., EDSS score; MRI scan; relapse number, rate, or severity; multiple sclerosis functional composite (MSFC); multiple sclerosis quality of life inventory (MSQLI); Paced Serial Addition Test (PASAT); symbol digit modalities test (SDMT); 25-foot walk test; 9-hole peg test; low contrast visual acuity; Modified Fatigue Impact Scale; expanded disability status score (EDSS); multiple sclerosis functional composite (MSFC); Beck Depression Inventory; and 7/24 Spatial Recall Test can be used. In various embodiments, the Clec9A binding agents cause an improvement in one or more of these measures. Further, the patient can be monitored at various times during a regimen. In some embodiments, the Clec9a binding agents cause a disease improvement as assessed by MacDonald dissemination in space and time. For example, for dissemination in space, lesion imaging, such as, by way of illustration, Barkhof-Tintore MR imaging criteria, may be used, including at least one gadolinium-enhancing lesion or 9 T2 hyperintense lesions; at least one infratentorial lesion; at least one juxtacortical lesion; at least about three periventricular lesions; and a spinal cord lesion. For dissemination in time, MRI can also be used; for example, if an MRI scan of the brain performed at ≥ 3 months after an initial clinical event demonstrates a new gadolinium-enhancing lesion, this may indicate a new CNS inflammatory event, because the duration of gadolinium enhancement in MS is usually less than 6 weeks. If there are no gadolinium-enhancing lesions but a new T2 lesion (presuming an MRI at the time of the initial event), a repeat MR imaging scan after another 3 months may be needed with demonstration of a new T2 lesion or gadolinium-enhancing lesion.

In some embodiments, disease effects are assessed using any of the measures described in Lavery, *et al.* Multiple Sclerosis International, Vol 2014 (2014), Article ID 262350, the entire contents of which are hereby incorporated by reference.

In some embodiments, the Clec9A binding agent results in one or more of: (a) prevention of worsening in disability defined as deterioration by 1.0 point on EDSS, (b) increase in time to relapse, (c) reduction or stabilization of number and/or volume of gadolinium enhancing lesions, (d) decreased annualized relapse rate, (e) increased relapse duration and severity by NRS score, (f) decrease in disease activity as measured by MRI (annual rate of new or enlarging lesions), (g) lower average number of relapses at 1 year, or 2 years, (h) sustained disease

progression as measured by the EDSS at 3 months, (i) prevention of conversion to CDMS, (j) no or few new or enhancing T2 lesions, (k) minimal change in hyperintense T2 lesion volume, (l) increased time to McDonald defined MS, (m) prevention of progression of disability as measured by sustained worsening of EDSS at 12 weeks, (n) reduction in time to relapse at 96 weeks, and (o) reduction or stabilization of brain atrophy (e.g. percentage change from baseline).

In one embodiment, the Clec9A binding agents are administered and is effective to result in a decreased rate of relapse (e.g., at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or greater reduction in rate of relapse) compared to the rate of relapse before administration (e.g., compared to the rate of relapse following administration for 12 months or for less than 12 months, e.g., about 10, or about 8, or about 4, or about 2 or less months) of treatment, or before commencement of treatment, when measured between 3-24 months (e.g., between 6-18 months, e.g., 12 months) after a previous relapse.

In one embodiment, the Clec9A binding agents are administered and are effective to result in a prevention of an increase in EDSS score from a pre-treatment state. The Kurtzke Expanded Disability Status Scale (EDSS) is a method of quantifying disability in multiple sclerosis. The EDSS replaced the previous Disability Status Scales which used to bunch people with MS in the lower brackets. The EDSS quantifies disability in eight Functional Systems (FS) and allows neurologists to assign a Functional System Score (FSS) in each of these. The Functional Systems are: pyramidal, cerebellar, brainstem, sensory, bowel and bladder, visual and cerebral.

In one embodiment, the Clec9A binding agents are administered and is effective to result in a decreased EDSS score (e.g., a decrease of 1, 1.5, 2, 2.5, 3 points or more, e.g., over at least three months, six months, one year, or longer) compared to the EDSS score following administration of the Clec9a binding agents (e.g. for 12 months or for less than 12 months, e.g., less than 10, 8, 4 or less months, or before the commencement of treatment).

In one embodiment, the Clec9A binding agents are administered and is effective to result in a decreased number of new lesions overall or of any one type (e.g., at least 10%, 20%, 30%, 40% decrease), compared to the number of new lesions following administration of the Clec9A binding agents for 12 months or for less than 12 months, e.g., less than 10, 8, 4 or less months, or before commencement of treatment;

In one embodiment, the Clec9A binding agents are administered and is effective to result in a decreased number of lesions overall or of any one type (e.g., at least 10%, 20%, 30%, 40% decrease), compared to the number of lesions following administration of the Clec9a binding agents for 12 months or for less than 12 months, e.g., less than 10, 8, 4 or less months, or before commencement of treatment;

In one embodiment, the Clec9A binding agents are administered and is effective to result in a reduced rate of appearance of new lesions overall or of any one type (e.g., at least 10%, 20%, 30%, 40% reduced rate), compared to the rate of appearance of new lesions following administration for 12 months or for less than 12 months, e.g., less than 10, 8, 4 or less months, or before commencement of treatment;

In one embodiment, the Clec9A binding agents are administered and is effective to result in a reduced increase in lesion area overall or of any one type (e.g., at least 10%, 20%, 30%, 40% decreased increase), compared to an increase in lesion area following administration for 12 months or less than 12 months, e.g., less than 10, 8, 4 or less months, or before commencement of treatment.

In one embodiment, the Clec9A binding agents are administered and is effective to result in a reduced incidence or symptom of optic neuritis (e.g., improved vision), compared to the incidence or symptom of optic neuritis following administration for 12 months or for less than 12 months, e.g., less than 10, 8, 4 or less months, or before commencement of treatment.

In various embodiments, methods of the invention are useful in treatment a human subject. In some embodiments, the human is a pediatric human. In other embodiments, the human is an adult human. In other embodiments, the human is a geriatric human. In other embodiments, the human may be referred to as a patient. In some embodiments, the human is a female. In some embodiments, the human is a male.

In certain embodiments, the human has an age in a range of from about 1 to about 18 months old, from about 18 to about 36 months old, from about 1 to about 5 years old, from about 5 to about 10 years old, from about 10 to about 15 years old, from about 15 to about 20 years old, from about 20 to about 25 years old, from about 25 to about 30 years old, from about 30 to about 35 years old, from about 35 to about 40 years old, from about 40 to about 45 years old, from about 45 to about 50 years old, from about 50 to about 55 years old, from about 55 to about 60 years old, from about 60 to about 65 years old, from about 65 to about 70 years old, from about 70 to about 75 years old, from about 75 to about 80 years old, from about 80 to about 85 years old, from about 85 to about 90 years old, from about 90 to about 95 years old or from about 95 to about 100 years old. In various embodiments, the human has an age of more than 30 years old.

Immune Modulation

In various embodiments, the present compositions are capable of, or find use in methods of, immune modulation. For instance, in various embodiments, the present methods of treatment may involve the immune modulation described herein. In some embodiments, the immune modulation involves IFN signaling, including modified IFN signaling, in the context of a dendritic cell (DC).

In various embodiments, a multi-specific Clec9a binding agent is provided. In some embodiments, such multi-specific Clec9a binding agent of the invention recognizes and binds to Clec9A and one or more antigens found on one or more immune cells, which can include, without limitation, megakaryocytes, thrombocytes, erythrocytes, mast cells, basophils, neutrophils, eosinophils, monocytes, macrophages, natural killer cells, T lymphocytes (e.g., cytotoxic T lymphocytes, T helper cells, natural killer T cells), B lymphocytes, plasma cells, dendritic cells, or subsets thereof. In some embodiments, the Clec9A binding agent specifically binds to an antigen of interest and effectively directly or indirectly recruits one or more immune cells.

In some embodiments, the Clec9a binding agent specifically binds to an antigen of interest and effectively directly or indirectly recruits one of more immune cells to cause an immunosuppressive effect, e.g. the Clec9a binding agent directly or indirectly recruits an immunosuppressive immune cell. In some embodiments, the immunosuppressive immune cell is a regulatory T cell (or "Tregs" which, as used herein, refers to a subpopulation of T cells which modulate the immune system, abrogate autoimmune disease, maintain tolerance to self-antigens and thwart anti-tumor immune responses). Other immunosuppressive immune cells include myeloid suppressor cells (or "MSC," which, as used herein, refers to a heterogeneous population of cells, defined by their myeloid origin, immature state, and ability to potently suppress T cell responses); tumor associated neutrophils (or "TANs" which, as used herein, refers to a subset of neutrophils that are capable of suppressing immune responses); tumor associated macrophages (or "TAMs" which, as used herein, refers to a subset of macrophages that may reduce an immune response), M2 macrophages, and/or tumor-inducing mast cells (which as used herein, refers to a subset of bone marrow-derived, long-lived, heterogeneous cellular population). Also, immunosuppressive immune cells include Th2 cells and Th17 cells. Additionally, immunosuppressive immune cells include immune cells, e.g., CD4+ and/or CD8+ T cells, expressing one or more checkpoint inhibitory receptors (e.g. receptors, including CTLA-4, B7-H3, B7-H4, TIM-3, expressed on immune cells that prevent or inhibit uncontrolled immune responses). See Stagg, J. *et. al.*, Immunotherapeutic approach in triple-negative breast cancer. *Ther Adv Med Oncol.* (2013) 5(3):169-181).

In some embodiments, the Clec9a binding agent stimulates regulatory T cell (Treg) proliferation. Treg cells are characterized by the expression of the Foxp3 (Forkhead box p3) transcription factor. Most Treg cells are CD4+ and CD25+, and can be regarded as a subset of helper T cells, although a small population may be CD8+. Thus the immune response which is to be modulated by a method of the invention may comprise inducing proliferation of Treg cells, optionally in response to an antigen. Thus the method may comprise administering to the subject a composition comprising the antigen, wherein the antigen is associated with a binding agent having affinity for Clec9A. The antigen may be administered with an adjuvant which promotes proliferation of Treg cells.

Insofar as this method involves stimulating proliferation and differentiation of Treg cells in response to a specific antigen, it can be considered to be a method of stimulating an immune response. However, given that Treg cells may be capable of modulating the response of other cells of the immune system against an antigen in other ways, e.g. inhibiting or suppressing their activity, the effect on the immune system as a whole may be to modulate (e.g. suppress or inhibit) the response against that antigen. Thus the methods of this aspect of the invention can equally be referred to as methods of modulating (e.g. inhibiting or suppressing) an immune response against an antigen.

In some embodiments, the methods therapeutically or prophylactically inhibit or suppress an undesirable immune response against a particular antigen, even in a subject with pre-existing immunity or an on-going immune response to that antigen. This may be particularly useful, for example, in the treatment of autoimmune disease.

Under certain conditions, it may also be possible to tolerize a subject against a particular antigen by targeting the antigen to an antigen presenting cell expressing Clec9A. The invention thus provides a method for inducing

tolerance in a subject towards an antigen, comprising administering to the subject a composition comprising the antigen, wherein the antigen is associated with a binding agent having affinity for Clec9A and wherein the antigen is administered in the absence of an adjuvant. Tolerance in this context typically involves depletion of immune cells which would otherwise be capable of responding to that antigen, or inducing a lasting reduction in responsiveness to an antigen in such immune cells.

It may be particularly desirable to raise a Treg response against an antigen to which the subject exhibits, or is at risk of developing, an undesirable immune response. For example, it may be a self-antigen against which an immune response occurs in an autoimmune disease. Examples of autoimmune diseases in which specific antigens have been identified as potentially pathogenically significant include multiple sclerosis (myelin basic protein), insulin-dependent diabetes mellitus (glutamic acid decarboxylase), insulin-resistant diabetes mellitus (insulin receptor), celiac disease (gliadin), bullous pemphigoid (collagen type XVII), auto-immune haemolytic anaemia (Rh protein), auto-immune thrombocytopenia (GpIIb/IIIa), myasthenia gravis (acetylcholine receptor), Graves' disease (thyroid-stimulating hormone receptor), glomerulonephritis, such as Goodpasture's disease (alpha3(IV)NC1 collagen), and pernicious anaemia (intrinsic factor). Alternatively the target antigen may be an exogenous antigen which stimulates a response which also causes damage to host tissues. For example, acute rheumatic fever is caused by an antibody response to a Streptococcal antigen which cross-reacts with a cardiac muscle cell antigen. Thus these antigens, or particular fragments or epitopes thereof, may be suitable antigens for use in the present invention.

In some embodiments, the present agents, or methods using these agents, disrupt Clec9A signaling (e.g. via neutralization of Clec9A), e.g. by reducing or inhibiting Clec9A binding to its ligand. Some autoimmune diseases are characterized by unusually high levels of cell death and it is believed that immune responses against self antigens associated with these cells may contribute to the pathogenesis of these conditions. Clec9A antagonists may therefore be used to prevent Clec9A from binding to the ligand exposed in dead and dying cells (e.g. those undergoing immunogenic cell death) and may thus inhibit or prevent stimulation of immune responses against these antigens.

In various embodiments, the present agents, or methods using these agents, reduce or suppress autoreactive T cells. In some embodiments, the multi-specific Clec9a binding agent, optionally through an interferon signaling in the context of a chimera, causes this immunosuppression. In some embodiments, the multi-specific Clec9a binding agent stimulates PD-L1 or PD-L2 signaling and/or expression which may suppress autoreactive T cells. In some embodiments, the Clec9A binding agent, optionally through an interferon signaling in the context of a chimera, causes this immunosuppression. In some embodiments, the Clec9A binding agent stimulates PD-L1 or PD-L2 signaling and/or expression which may suppress autoreactive T cells.

In various embodiments, the present methods comprise modulating the ratio of regulatory T cells to effector T cells in favor of immunosuppression, for instance, to treat autoimmune diseases. For instance, the present methods, in some embodiments, reduce and/or suppress one or more of cytotoxic T cells; effector memory T cells; central

memory T cells; CD8⁺ stem cell memory effector cells; TH1 effector T-cells; TH2 effector T cells; TH9 effector T cells; TH17 effector T cells. For instance, the present methods, in some embodiments, increase and/or stimulate one or more of CD4⁺CD25⁺FOXP3⁺ regulatory T cells, CD4⁺CD25⁺ regulatory T cells, CD4⁺CD25⁻ regulatory T cells, CD4⁺CD25^{high} regulatory T cells, TIM-3⁺PD-1⁺ regulatory T cells, lymphocyte activation gene-3 (LAG-3)⁺ regulatory T cells, CTLA-4/CD152⁺ regulatory T cells, neuropilin-1 (Nrp-1)⁺ regulatory T cells, CCR4⁺CCR8⁺ regulatory T cells, CD62L (L-selectin)⁺ regulatory T cells, CD45RBlow regulatory T cells, CD127^{low} regulatory T cells, LRRC32/GARP⁺ regulatory T cells, CD39⁺ regulatory T cells, GITR⁺ regulatory T cells, LAP⁺ regulatory T cells, 1B11⁺ regulatory T cells, BTLA⁺ regulatory T cells, type 1 regulatory T cells (Tr1 cells), T helper type 3 (Th3) cells, regulatory cell of natural killer T cell phenotype (NKTregs), CD8⁺ regulatory T cells, CD8⁺CD28⁻ regulatory T cells and/or regulatory T-cells secreting IL-10, IL-35, TGF- β , TNF- α , Galectin-1, IFN- γ and/or MCP1.

In some embodiments, the present methods favor immune inhibitory signals over immune stimulatory signals. In some embodiments, the present methods allow for reversing or suppressing immune activating or co-stimulatory signals. In some embodiments, the present methods allow for providing immune inhibitory signals. For instance, in some embodiments, the present agents and methods reduce the effects of an immune stimulatory signal, which, without limitation, is one or more of 4-1BB, OX-40, HVEM, GITR, CD27, CD28, CD30, CD40, ICOS ligand; OX-40 ligand, LIGHT (CD258), GITR ligand, CD70, B7-1, B7-2, CD30 ligand, CD40 ligand, ICOS, ICOS ligand, CD137 ligand and TL1A. Further, in some embodiments, the present agents and methods increase the effects of an immune inhibitory signal, which, without limitation, is one or more of CTLA-4, PD-L1, PD-L2, PD-1, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160 (also referred to as BY55), CGEN-15049, CHK 1 and CHK2 kinases, A2aR, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), and various B-7 family ligands (including, but are not limited to, B7-1, B7-2, B7-DC, B7-H1, B7-H2, B7-H3, B7-H4, B7-H5, B7-H6 and B7-H7. Kits

The present invention also provides kits for the administration of any Clec9A binding agent described herein (e.g. with or without additional therapeutic agents). The kit is an assemblage of materials or components, including at least one of the inventive pharmaceutical compositions described herein. Thus, in some embodiments, the kit contains at least one of the pharmaceutical compositions described herein.

The exact nature of the components configured in the kit depends on its intended purpose. In one embodiment, the kit is configured for the purpose of treating human subjects.

Instructions for use may be included in the kit. Instructions for use typically include a tangible expression describing the technique to be employed in using the components of the kit to effect a desired therapeutic outcome, such as to treat cancer. Optionally, the kit also contains other useful components, such as, diluents, buffers, pharmaceutically acceptable carriers, syringes, catheters, applicators, pipetting or measuring tools, bandaging materials or other useful paraphernalia as will be readily recognized by those of skill in the art.

The materials and components assembled in the kit can be provided to the practitioner stored in any convenience and suitable ways that preserve their operability and utility. For example, the components can be provided at room, refrigerated or frozen temperatures. The components are typically contained in suitable packaging materials. In

various embodiments, the packaging material is constructed by well-known methods, preferably to provide a sterile, contaminant-free environment. The packaging material may have an external label which indicates the contents and/or purpose of the kit and/or its components.

Definitions

As used herein, “a,” “an,” or “the” can mean one or more than one.

Further, the term “about” when used in connection with a referenced numeric indication means the referenced numeric indication plus or minus up to 10% of that referenced numeric indication. For example, the language “about 50” covers the range of 45 to 55.

An “effective amount,” when used in connection with medical uses is an amount that is effective for providing a measurable treatment, prevention, or reduction in the rate of pathogenesis of a disease of interest.

As used herein, something is “decreased” if a read-out of activity and/or effect is reduced by a significant amount, such as by at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 97%, at least about 98%, or more, up to and including at least about 100%, in the presence of an agent or stimulus relative to the absence of such modulation. As will be understood by one of ordinary skill in the art, in some embodiments, activity is decreased and some downstream read-outs will decrease but others can increase.

Conversely, activity is “increased” if a read-out of activity and/or effect is increased by a significant amount, for example by at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 97%, at least about 98%, or more, up to and including at least about 100% or more, at least about 2-fold, at least about 3-fold, at least about 4-fold, at least about 5-fold, at least about 6-fold, at least about 7-fold, at least about 8-fold, at least about 9-fold, at least about 10-fold, at least about 50-fold, at least about 100-fold, in the presence of an agent or stimulus, relative to the absence of such agent or stimulus.

As referred to herein, all compositional percentages are by weight of the total composition, unless otherwise specified. As used herein, the word “include,” and its variants, is intended to be non-limiting, such that recitation of items in a list is not to the exclusion of other like items that may also be useful in the compositions and methods of this technology. Similarly, the terms “can” and “may” and their variants are intended to be non-limiting, such that recitation that an embodiment can or may comprise certain elements or features does not exclude other embodiments of the present technology that do not contain those elements or features.

Although the open-ended term “comprising,” as a synonym of terms such as including, containing, or having, is used herein to describe and claim the invention, the present invention, or embodiments thereof, may alternatively be described using alternative terms such as “consisting of” or “consisting essentially of.”

As used herein, the words “preferred” and “preferably” refer to embodiments of the technology that afford certain benefits, under certain circumstances. However, other embodiments may also be preferred, under the same or

other circumstances. Furthermore, the recitation of one or more preferred embodiments does not imply that other embodiments are not useful, and is not intended to exclude other embodiments from the scope of the technology.

The amount of compositions described herein needed for achieving a therapeutic effect may be determined empirically in accordance with conventional procedures for the particular purpose. Generally, for administering therapeutic agents for therapeutic purposes, the therapeutic agents are given at a pharmacologically effective dose. A “pharmacologically effective amount,” “pharmacologically effective dose,” “therapeutically effective amount,” or “effective amount” refers to an amount sufficient to produce the desired physiological effect or amount capable of achieving the desired result, particularly for treating the disorder or disease. An effective amount as used herein would include an amount sufficient to, for example, delay the development of a symptom of the disorder or disease, alter the course of a symptom of the disorder or disease (e.g., slow the progression of a symptom of the disease), reduce or eliminate one or more symptoms or manifestations of the disorder or disease, and reverse a symptom of a disorder or disease. Therapeutic benefit also includes halting or slowing the progression of the underlying disease or disorder, regardless of whether improvement is realized.

Effective amounts, toxicity, and therapeutic efficacy can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to about 50% of the population) and the ED₅₀ (the dose therapeutically effective in about 50% of the population). The dosage can vary depending upon the dosage form employed and the route of administration utilized. The dose ratio between toxic and therapeutic effects is the therapeutic index and can be expressed as the ratio LD₅₀/ED₅₀. In some embodiments, compositions and methods that exhibit large therapeutic indices are preferred. A therapeutically effective dose can be estimated initially from in vitro assays, including, for example, cell culture assays. Also, a dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ as determined in cell culture, or in an appropriate animal model. Levels of the described compositions in plasma can be measured, for example, by high performance liquid chromatography. The effects of any particular dosage can be monitored by a suitable bioassay. The dosage can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment.

In certain embodiments, the effect will result in a quantifiable change of at least about 10%, at least about 20%, at least about 30%, at least about 50%, at least about 70%, or at least about 90%. In some embodiments, the effect will result in a quantifiable change of about 10%, about 20%, about 30%, about 50%, about 70%, or even about 90% or more. Therapeutic benefit also includes halting or slowing the progression of the underlying disease or disorder, regardless of whether improvement is realized.

As used herein, “methods of treatment” are equally applicable to use of a composition for treating the diseases or disorders described herein and/or compositions for use and/or uses in the manufacture of a medicaments for treating the diseases or disorders described herein.

EXAMPLES

Example 1. Construction and Evaluation of VHHs Specific for Human Clec9A

Isolation of Antigen-specific VHHs

A VHH library was constructed from an immunized llama. Three consecutive rounds of panning of a VHH library were performed in solution using stably transfected CHO-K1 cells expressing human Clec9A. The enrichment for antigen-specific phages was assessed after each round of panning by comparing the number of phagemid particles eluted from transfected cells (output) with the number of phagemid particles used for panning (input). The phage output increased about 10-fold in the 2nd round and about 10³-fold in the 3rd round, as compared to the output from the 1st round. The input phage was always about 10¹¹ and the output from first round was about 10⁸ phage particles. 285 randomly selected colonies from the 1st, 2nd and 3rd panning rounds (95 from each round) were sequenced and then grouped based on CDR3 sequences. Using crude periplasmic extracts including VHHs, 95 unique sequences were analyzed by flow cytometry for specificity to human Clec9A using CHO-K1 cells stably transfected with human Clec9A. The parental non-transfected CHO-K1 cells served as negative control cell. An irrelevant VHH was used as negative nanobody control. Flow cytometry experiments revealed that 66 different VHHs, belonging to 25 different groups (see Figure 3), were specific for human Clec9A. Table B below provides a description of 66 clones representing the 66 different anti-human Clec9A VHH genes. *E. coli* TG1 harboring recombinant phagemid pMECS containing anti-human Clec9A VHH sequences was generated and stored at -80°C. The vector pMECS codes for ampicillin resistance.

Table B		
E. coli strain + Vector	Nanobody (Nb)	NSF Reference No. (Glycerol stock)
TG1, pMECS	1LEC 7	4826
TG1, pMECS	1LEC 9	4827
TG1, pMECS	1LEC 26	4828
TG1, pMECS	1LEC 27	4829
TG1, pMECS	1LEC 28	4830
TG1, pMECS	1LEC 30	4831
TG1, pMECS	1LEC 38	4832
TG1, pMECS	1LEC 42	4833
TG1, pMECS	1LEC 51	4834
TG1, pMECS	1LEC 61	4835
TG1, pMECS	1LEC 62	4836
TG1, pMECS	1LEC 63	4837
TG1, pMECS	1LEC 64	4838
TG1, pMECS	1LEC 70	4839
TG1, pMECS	1LEC 84	4840
TG1, pMECS	1LEC 88	4841
TG1, pMECS	1LEC 91	4842
TG1, pMECS	1LEC 92	4843
TG1, pMECS	1LEC 94	4844
TG1, pMECS	2LEC 6	4845
TG1, pMECS	2LEC 13	4846
TG1, pMECS	2LEC 16	4847
TG1, pMECS	2LEC 20	4848
TG1, pMECS	2LEC 23	4849
TG1, pMECS	2LEC 24	4850
TG1, pMECS	2LEC 26	4851
TG1, pMECS	2LEC 38	4852

TG1, pMECS	2LEC 48	4853
TG1, pMECS	2LEC 53	4854
TG1, pMECS	2LEC 54	4855
TG1, pMECS	2LEC 55	4856
TG1, pMECS	2LEC 59	4857
TG1, pMECS	2LEC 60	4858
TG1, pMECS	2LEC 61	4859
TG1, pMECS	2LEC 62	4860
TG1, pMECS	2LEC 63	4861
TG1, pMECS	2LEC67	4862
TG1, pMECS	2LEC 68	4863
TG1, pMECS	2LEC 76	4864
TG1, pMECS	2LEC 83	4865
TG1, pMECS	2LEC 88	4866
TG1, pMECS	2LEC 89	4867
TG1, pMECS	2LEC 90	4868
TG1, pMECS	2LEC 93	4869
TG1, pMECS	2LEC 95	4870
TG1, pMECS	3LEC 4	4871
TG1, pMECS	3LEC 6	4872
TG1, pMECS	3LEC 9	4873
TG1, pMECS	3LEC 11	4874
TG1, pMECS	3LEC 13	4875
TG1, pMECS	3LEC 15	4876
TG1, pMECS	3LEC 22	4877
TG1, pMECS	3LEC 23	4878
TG1, pMECS	3LEC 27	4879
TG1, pMECS	3LEC 30	4880
TG1, pMECS	3LEC 36	4881
TG1, pMECS	3LEC 55	4882
TG1, pMECS	3LEC 57	4883
TG1, pMECS	3LEC 61	4884
TG1, pMECS	3LEC 62	4885
TG1, pMECS	3LEC 66	4886
TG1, pMECS	3LEC 69	4887
TG1, pMECS	3LEC 76	4888
TG1, pMECS	3LEC 82	3889
TG1, pMECS	3LEC 89	4890
TG1, pMECS	3LEC 94	4891

Transformation of non-suppressor strain (e.g. WK6) with recombinant pMECS

The VHH gene cloned in pMECS vector contained PelB signal sequence at the N-terminus and HA tag and His₆ tag at the C-terminus (PelB leader-VHH-HA-His₆). The PelB leader sequence directed the VHH to the periplasmic space of the *E. coli*, and the HA and His₆ tags was used for the purification and detection of VHH (e.g. in ELISA, Western Blot, etc.).

In pMECS vector, the His₆ tag was followed by an amber stop codon (TAG) and this amber stop codon was followed by gene III of M13 phage. In suppressor *E. coli* strains (e.g. TG1), the amber stop codon was read as glutamine and therefore the VHH was expressed as fusion protein with protein III of the phage which allowed the display of

the VHH on the phage coat for panning. In TG1 suppressor strains, the efficiency of suppression is not 100% and therefore the expression of VHHs in suppressor strains led to two different types of VHH molecules, fused to protein III and without protein III). In non-suppressor *E. coli* strains (e. g., WK6), the amber stop codon was read as stop codon and therefore the resulting VHH was not fused to protein III.

In order to express and purify VHHs cloned in pMECS vector, pMECS was prepared containing the gene of the VHH of interest, and the plasmid was transformed into a non-suppressor strain (e.g., WK6). The VHH of the resulting clone was sequenced using the MP057 primer (5'-TTATGCTTCCGGCTCGTATG-3') (SEQ ID NO: 1070) to verify the identity of the clone. Antigen binding capacity was retested by ELISA or any other appropriate assay. The non-suppressor strain (e.g., WK6) containing the recombinant pMECS vector with the VHH gene was used for the expression and purification of the VHH.

In pMECS vector, the His₆ tag was cleaved off upon storage of the VHH. Accordingly, the VHH gene was recloned from pMECS into pHEN6c vector, if the His₆ tag was to be used for detection, etc. Specifically, the VHH gene was amplified by PCR using recombinant pMECS harboring the VHH gene as template and primers A6E and PMCF. Primers A6E and PMCF were framework1 and framework4 primers, respectively. The primer sequences were as follows:

- Primer A6E (5' GAT GTG CAG CTG CAG GAG TCT GGR* GGA GG 3') (SEQ ID NO: 1071).
- Primer PMCF (5' CTA GTG CGG CCG CTG AGG AGA CGG TGA CCT GGG T 3') (SEQ ID NO: 1072).
- Universal reverse primer (5' TCA CAC AGG AAA CAG CTA TGA C 3') (SEQ ID NO: 1073).
- Universal forward primer (5' CGC CAG GGT TTT CCC AGT CAC GAC 3') (SEQ ID NO: 1074).

*R stands for A or G. PstI, NotI and BstEII (Eco91I) recognition sequences are shown in bold, italic and underline, respectively.

The amplification protocol included about 30 cycles of PCR, each cycle included 30 seconds at 94°C, 30 seconds at 55°C and 45 seconds at 72°C, followed by 10 minutes extension at 72°C at the end of PCR. A fragment of about 400 bp was amplified.

The PCR product was purified (e.g. by Qiaquick PCR purification kit from Qiagen) and digested overnight with PstI. The purified PCR product was digested with BstEII overnight (or with Eco91I from Fermentas). The temperature used for digestion varied. For example, digestion with BstEII was done at 50°C or 60°C depending on the supplier of the enzyme.

For ligation, the PCR product was purified. The pHEN6c vector was digested with PstI for 3 hours, purified as described above, and then digested with BstEII for 2 to 3 hours. Alternatively, digestion was carried out using Eco91I from Fermentas. The digested vector was ran on 1% agarose gel, with the vector band excised out of the gel and purified (e.g. by Qiaquick gel extraction kit from Qiagen). The PCR fragment was subsequently ligated to the vector.

Electrocompetent WK6 cells were transformed with the ligation reaction, and transformants were selected using LB/agar/ampicillin (100 µg/ml)/glucose (1-2%) plates. Positive clones were screened by PCR using universal reverse and universal forward primers. A fragment of about 550 bp was amplified, if the insert was present. To verify the identity of the clones, at least 2 clones per each VHH were sequenced using universal reverse primers. Antigen binding capacity was retested by ELISA or any other appropriate assay.

Following the above protocol, the VHH gene cloned in pHEN6c vector was generated which contained PelB signal sequence at the N-terminus and His₆-tail at the C-terminus. The PelB leader sequence directed the VHH to the periplasmic space of the *E. coli*, and the His-tag was used for the purification and detection of VHH (e.g. in ELISA, Western Blot, etc.).

Expression and purification of VHHs

Expression and purification of VHHs were carried out. Specifically, on day 1, 10-20 ml of LB + ampicillin (100 µg/ml) + glucose (1%) were inoculated with a freshly transformed WK6 colony. This pre-culture was incubated at 37°C overnight with shaking at 200-250 rpm. On day 2, a TB medium was used for expressing the VHHs. The TB medium included, per liter: 2.3 g KH₂PO₄, 16.4 g K₂HPO₄·3H₂O, 12 g Tryptone (Duchefa Biochemie), 24 g Yeast (Duchefa Biochemie), and 4 ml 100% glycerol (Duchefa Biochemie)

A baffled shaker flask of 1 liter was filled with 330 ml TB and autoclaved. KH₂PO₄ and K₂HPO₄·3H₂O were not autoclaved. Instead, KH₂PO₄ and K₂HPO₄·3H₂O were prepared, filter sterilized, and then added to the rest of the medium that was already autoclaved. About 1 ml of the pre-culture was added to 330 ml of TB supplemented with 100 µg/ml Ampicillin, 2 mM MgCl₂ and 0.1% glucose and subsequently grew at 37°C with shaking (200-250 rpm) until an OD₆₀₀ of 0.6-0.9 was reached. IPTG (final concentration of 1 mM) was added to induce VHH expression. The culture was incubated at 28°C with shaking overnight (about 16-18 hours). The OD₆₀₀ after overnight induction was usually between 25 and 30. At least 1 liter of culture (3 bottles) per clone was prepared with an average yield of between 1 and 15 mg/l.

Extraction of the VHHs from the periplasm of *E. coli* was carried out on day 3. The solutions used included: TES: 0.2 M Tris pH 8.0, 0.5 mM EDTA, 0.5 M sucrose, TES/4: TES diluted 4 times in water.

The overnight induced cultures were centrifuged for 8 minutes at 8000 rpm. The cell pellets from 1 liter culture were resuspended in 12 ml TES by pipetting up and down and shaken for 1 hour on ice. Per each 12 ml TES used, about 18 ml TES/4 were added and incubated on ice for an additional hour with shaking followed by centrifuge for 30 minutes at 8000 rpm at 4°C. The supernatant which contained proteins extracted from the periplasmic space was transferred to fresh falcon tubes.

The VHHs were subsequently purified by IMAC which utilized the following solution: HIS-select (SIGMA), PBS, and 50 mM NaAcetate pH 4.6.

His-select was equilibrated with PBS. Specifically, per periplasmic extract derived from 1 liter culture, 1 ml of Resin (about 2 ml His-select solution) was added to a 50 ml falcon tube. PBS was also added to final volume of 50 ml

and mixed. Centrifugation was carried out at 2000 rpm for 2 minutes, and the supernatant was discarded. The resin was washed with PBS twice as described above. The periplasmic extract was added to the resin, incubated for 30 minutes to 1 hour at room temperature with gentle shaking. The samples were loaded on PD-10 columns with a filter at the bottom (GE healthcare, cat. No. 17-0435-01) and washed with 50 to 100 ml PBS (50-100 ml PBS per 1 ml resin used). Elution was carried out for 3 times, each time with 1 ml PBS/0.5 M imidazole per 1 ml resin used (for efficient elution, resuspend the beads and leave overnight at 4°C with the bottom of the column closed). Dialysis was performed overnight at 4°C against PBS (cutoff 3500 daltons) to remove imidazole. For efficient dialysis, the dialysis buffer (PBS) was changed 2-3 times. Alternatively, instead of elution with imidazole, the bound VHHs could be eluted with 10 ml 50 mM Na-acetate pH 4.6. If 50 mM Na-acetate pH 4.6 was used to elute VHHs, the eluted VHHs was immediately neutralized with 1M Tris pH 8.0, and no dialysis was required.

The amount of protein was estimated by OD₂₈₀ measurement of eluted sample. Extinction coefficient of each clone was determined by protParam tool under primary structure analysis at the Expasy proteomics server. Further purification of VHHs could be achieved by different methods. For example, the samples could be concentrated (Vivaspin 5000 MW cutoff, Vivascience) by centrifuging at 2000 rpm at 4°C until an appropriate volume for loading on a Superdex 75 16/60 was obtained (max. 4 ml). The concentrated sample was loaded on a Superdex 75 16/60 column equilibrated with PBS. Peak fractions were pooled, and OD₂₈₀ measurements were performed for quantification. In general, VHHs eluted after 85-95 minutes when run at 1 ml/min. Aliquots of concentrated VHH samples were stored at -20°C at a concentration of about 1 mg/ml.

Example 2. Functional Characterization of Human Clec9A Binding VHHs

The binding characteristics of various VHHs (as described in Example 1) were tested by flow cytometry. HEK293-T cells were transfected with a human Clec9A expression plasmid and stained with the His-tagged VHHs at 2 µg/ml, followed by staining with an anti-His Fitc conjugated antibody. Binding was measured by detecting cellular fluorescence via flow cytometry. Results as shown in Figure 4 show that the VHHs bound to Clec9A.

Example 3. Dendritic Cell Signaling Induced by Anti-human Clec9A VHH Chimeras

The term "AcTaferon" is used herein to reference an interferon-based chimera. In the following example, unless noted, mutations to IFN are relative to human IFN-α2 - SEQ ID NO:2.

A dendritic cell pSTAT signaling assay was undertaken. Chimeras studied were anti-human Clec9A VHH/ human IFN R149A fusions. Two doses of the agents were studied: 100 ng/ml and 500 ng/ml.

The anti-human Clec9A VHHs used in this Example were 2LEC13, 2LEC20, 2LEC38, 3LEC6, and 3LEC30.

Briefly, human PBMCs were isolated from blood obtained from healthy donors. Approximately 120 ml of blood was collected from each donor using heparin coated tubes (12 tubes). The blood was kept at room temperature and processed immediately. Briefly, blood was diluted 1:1 with DPBS and 25 ml was gently layered onto 15 ml of Lympholyte H. After centrifugation, the mononuclear cell rings were collected and cells were washed three times with DPBS (PBS Dulbecco's Phosphate Buffered Saline, Wisent, catalog #311-425-LL) and counted. Dendritic

cells were enriched from the PBMC population using "DC- enrichment kit" containing a combination of lineage specific monoclonal antibodies in PBS and a suspension of magnetic particles (STEMCELL Technologies Catalogue number 19251), according to manufacturer's instructions.

Dendritic cells (DC) were stimulated for 15 minutes in the presence or absence of test items and controls (PBS) and the level of phosphorylated-STAT1 (pSTAT1, specifically pY701-STAT1) was determined in isolated DC cell populations (Lin-(CD14/CD16/CD20/CD56/CD3)/HLA-DR+) by flow cytometry. Post stimulation, cells were fixed (BD Cytofix fixation buffer, BD Bioscience, catalog #554655), then permeabilized with Perm buffer II (BD PhosFlow Perm Buffer, BD Bioscience, catalog #558052). Cells were then stained for phosphoSTAT1 and for DC surface markers (Lin-/HLA-DR+) (see Table C below). Both intra-cellular and surface staining were performed at the same time. Flow cytometry and data acquisition was performed after cell washing with DPBS.

Table C: List of antibodies for flow cytometry staining

Marker / Product Name	Fluorochrome	Clone	Purpose	Supplier-Catalog Number
pSTAT1	AlexaFluor647	4a	phospho-STAT1	BD-562870
Anti-human CD3	PE	UCHT1	T cells marker Lineage depletion	BD-561809
Anti-human CD14	PE	M5E2	Monocytes markers Lineage depletion	BD-555398
anti-human CD16	PE	B73.1	NK, Neutrophils, Monocytes marker Lineage depletion	BD-561313
anti-human CD19	PE	H1B19	B cells marker Lineage depletion	BD-555413
anti-human CD56	PE	B159	NK cells marker Lineage depletion	BD-555516
Anti-human HLA-DR	FITC	TU36	MHC II marker DC discrimination	BD-555560
Anti-human CD11c	BV421	B-Ly6	DC discrimination	BD-562561
LIVE/DEAD Fixable Aqua Dead Cell Stain	Aqua	N/Ap	Viability dye	ThermoFisher- L34957
Normal mouse IgG	N/Ap	N/Ap	Fc receptor blocker Blocking agent	ThermoFisher- 10400C

Figure 5 shows the data, expressed as a fold change of the percentage of pSTAT⁺ dendritic cells.

This study clearly shows that a human CLEC9A antigen-targeting construct comprising an IFN signaling agent whose activity is recoverable upon cell targeting (IFN R149A) promotes IFN signaling in human dendritic cells (as determined by pSTAT1 induction). Thus, targeting IFN to human dendritic cells using a targeting moiety directed at human CLEC9A antigen results in triggering of a pronounced IFN signal transduction.

Example 4. Construction and Evaluation of VHHs Specific for Human Clec9A

Variants of human Clec9A VHH R1CHCL50 and 3LEC89 were produced and analyzed. The typical VHH framework hallmark residues at positions 37, 44, 45, 47 and 84 (US2008/0107601; Kabat numbering schedule) were not humanized, while the N-terminal Q in both sequences was mutated to D to avoid pyroglutamate formation. Four variant sequences of R1CHCL50 and 3LEC89 were generated and tested.

R1CHCL50 (wild type):

QVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 327);

R1CHCL50_opt1 (E1D-A74S-K83R-Q108L):

DVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 328);

R1CHCL50_opt2 (E1D-A74S-K83R-Q108L-H13Q):

DVQLVESGGGLVQPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVTGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 329);

R1CHCL50_opt3 (E1D-A74S-K83R-Q108L-T64K):

DVQLVESGGGLVHPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVKGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 330);

R1CHCL50_opt4 (E1D-A74S-K83R-Q108L-H13Q-T64K):

DVQLVESGGGLVQPGGSLRLSCAASGSFSSINVMGWYRQAPGKERELVARITNLGLPNYADSVKGRFTISRDN
KNTVYLQMNSLRPEDTAVYYCYLVALKAIEYWGQGTQVTVSS (SEQ ID NO: 331);

3LEC_89 (wild type):

QVQLQESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
AGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 332);

3LEC_89_opt1 (E1D-Q5V-Q108L):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
AGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 333);

3LEC_89_opt2 (E1D-Q5V-Q108L-A74S):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
SGNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 334);

3LEC_89_opt3 (E1D-Q5V-Q108L-G75K):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
AKNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 335); and

3LEC_89_opt4 (E1D-Q5V-Q108L-A74S-G75K):

DVQLVESGGGLVQPGGSLRLSCAASGRIFSVNAMGWYRQAPGKQRELVAITNQGAPTYADSVKGRFTISRDN
SKNTVYLQMNSLRPEDTAVYYCKAFTRGDDYWGQGTQVTVSS (SEQ ID NO: 336).

Production and purification

Wild type and variants (opt1 through opt4) were synthesized by GeneArt (ThermoFisher) and cloned in the pHEN6C vector for bacterial periplasmic expression with a C-terminal his6 tag. Resulting constructs were transformed in WK6 cells. VHH expression was induced overnight with 1 mM IPTG, cells pelleted, and periplasmic extracts prepared using TES (0.2 M Tris pH 8.0, 0.5 mM EDTA, 0.5 M sucrose) and TES/4 buffers. Proteins were purified from extracts using the TALON Metal affinity resin according to the manufacturer's guidelines and imidazole was removed from the samples using PD10 columns (GE Healthcare). Average yields ranged from 0.8 to 5 mg per liter culture (see Figure 6 and Table D).

Table D: Yield (mg per liter)	
R1CHCL50	2.69
R1CHCL50_opt1 (E1D-A74S-K83R-Q108L)	0.86
R1CHCL50_opt2 (E1D-A74S-K83R-Q108L-H13Q)	1.15
R1CHCL50_opt3 (E1D-A74S-K83R-Q108L-T64K)	1.30
R1CHCL50_opt4 (E1D-A74S-K83R-Q108L-H13Q-T64K)	1.53
3LEC89	4.31
3LEC_89_opt1 (E1D-Q5V-Q108L)	1.65
3LEC_89_opt2 (E1D-Q5V-Q108L-A74S)	2.45
3LEC_89_opt3 (E1D-Q5V-Q108L-G75K)	2.33
3LEC_89_opt4 (E1D-Q5V-Q108L-A74S-G75K)	1.39

Thermostability and Affinity

Thermostabilities of the resulting VHH's were determined using SYPRO orange (Sigma-Aldrich) on a LightCycler 480 system (Roche) according to the manufacturers guidelines. Melting temperatures, calculated with the Protein Melting Analysis software (Roche), ranged from 75 to 83°C and are summarized in Table E.

Table E: Melting temperature (°C)	
R1CHCL50	77.51
R1CHCL50_opt1 (E1D-A74S-K83R-Q108L)	78.51
R1CHCL50_opt2 (E1D-A74S-K83R-Q108L-H13Q)	79.38
R1CHCL50_opt3 (E1D-A74S-K83R-Q108L-T64K)	82.60
R1CHCL50_opt4 (E1D-A74S-K83R-Q108L-H13Q-T64K)	82.07
3LEC89	75.08
3LEC_89_opt1 (E1D-Q5V-Q108L)	73.14
3LEC_89_opt2 (E1D-Q5V-Q108L-A74S)	77.46
3LEC_89_opt3 (E1D-Q5V-Q108L-G75K)	77.35
3LEC_89_opt4 (E1D-Q5V-Q108L-A74S-G75K)	77.47

Affinity

Affinities of the AFN's for Clec9A were determined using the bio-layer interferometry technology on an Octet system (ForteBio). For this purpose, biotinylated human CLEC9A was captured on a streptavidin sensor and affinity determined for 3 concentrations of VHH (50, 100 and 200 nM). Results from a global analysis of the 3 concentrations tested are summarized in Table F.

Table F: Affinities of VHH's for human Clec9A			
VHH	KD (M)	Kon (1/Ms)	Kdis (1/s)
R1CHCL50	1.719E-09	4.10E+05	7.05E-04
R1CHCL50_opt1 (E1D-A74S-K83R-Q108L)	1.291E-09	4.92E+05	6.35E-04
R1CHCL50_opt2 (E1D-A74S-K83R-Q108L-H13Q)	1.147E-09	6.30E+05	7.23E-04
R1CHCL50_opt3 (E1D-A74S-K83R-Q108L-T64K)	1.786E-09	5.59E+05	9.98E-04
R1CHCL50_opt4 (E1D-A74S-K83R-Q108L-H13Q-T64K)	2.697E-09	4.38E+05	1.18E-03
3LEC89	1.74E-09	4.16E+05	7.25E-04
3LEC_89_opt1 (E1D-Q5V-Q108L)	2.204E-09	3.91E+05	8.61E-04
3LEC_89_opt2 (E1D-Q5V-Q108L-A74S)	2.413E-09	3.38E+05	8.17E-04
3LEC_89_opt3 (E1D-Q5V-Q108L-G75K)	2.556E-09	4.38E+05	1.12E-03
3LEC_89_opt4 (E1D-Q5V-Q108L-A74S-G75K)	2.352E-09	4.17E+05	9.82E-04

Example 5. Construction and Evaluation of Chimeric Proteins Targeting Human Clec9A

Chimeric proteins comprising a human Clec9A targeting moiety and a mutated human IFN α 2 signalling moiety (R149A) were constructed and analyzed.

Construction, Production and Purification of Chimeric Proteins

Human Clec9A VHH's R1CHCL50 and 3LEC89 were genetically fused to human IFN α 2 R149A via a (GGG)₃linker. Constructs were synthesized by GeneArt (ThermoFisher) and cloned in the pHEN6C vector for bacterial periplasmic expression. After transformation in WK6 cells, AFN expression was induced overnight with 1 mM IPTG, cells were pelleted, and periplasmic extracts prepared using TES (0.2 M Tris pH 8.0, 0.5 mM EDTA, 0.5 M sucrose) and TES/4 buffers. Proteins were purified from extracts using the TALON Metal affinity resin according to the manufacturer's guidelines and imidazole was removed from the samples using PD10 columns (GE Healthcare).

Affinity

Affinities of the chimeric proteins for Clec9A were determined using the bio-layer interferometry technology on an Octet system (ForteBio). For this purpose, biotinylated human CLEC9A was captured on a streptavidin sensor and affinity was determined for 3 concentrations (12.5, 25 and 50 nM) of each chimeric protein. Results from a global analysis of the 3 concentrations tested are summarized in Table G.

Table G: Affinities of Chimeric Proteins Targeting Human Clec9A			
Chimeric Protein	KD (M)	Kon (1/Ms)	Kdis (1/s)
R1CHCL50-(GGG) ₃ -hIFN α 2_R149A	1.95E-09	1.34E+05	2.60E-04
3LEC89-(GGG) ₃ -hIFN α 2_R149A	1.76E-09	2.45E+05	4.32E-04

Biological Activity

The HL116 clone is derived from the human HT1080 cell line (ATCC CCL-121). It contains the firefly luciferase gene controlled by the IFN-inducible 6-16 promoter. Parental HL116 cells were transfected with an expression-vector encoding the human Clec9A sequence. Stable transfected clones were selected in G418-containing medium. Parental HL116 and HL116-hClec9A cells were seeded overnight at 20,000 cells per 96-well, and

stimulated with a serial dilution of chimeric protein for 6 hours. Luciferase activity was measured in cell lysates. Representative graphs are shown in Figures 7A-B. As shown in Figures 7A-B, the chimeric proteins had nearly no activity on Clec9A negative H116 cells. But the activity of the chimeric proteins was recovered in H116 cells expressing Clec9A.

Example 6. *In Vivo* efficacy of human CLEC9A AcTaferons

The CLEC9A VHHs 2LEC 16, 3LEC 22, 1LEC 28, 3LEC 30, and 3LEC 89, which belong to 4 different sequence groups, were selected to be evaluated for their *in vivo* antitumor efficacy in human CLEC9A VHH targeted AcTaferon (AFN) compositions (e.g., 2LEC16-hIFNa2_R149A, 3LEC22-hIFNa2_R149A, 1LEC28-hIFNa2_R149A, 3LEC30-hIFNa2_R149A, or 3LEC89-hIFNa2_R149A).

Human RL follicular lymphoma cell line (RL) tumor model in mice with humanized immune system: Mice with a humanized immune system were generated according to the following protocol. Mononuclear cells were collected following density gradient centrifugation using Lymphoprep from HLA-A2+ human cord blood samples. Human CD34+ hematopoietic stem cells (HSC) were isolated by MACS technology and examined for CD34+ purity and CD3+ contamination using FACS. HSC's with a CD34 purity of >80% were intrahepatically injected in 2-3 day old NSG mice that underwent myeloablative irradiation treatment at 100 cGy. At 8-12 weeks post HSC injection, human cell engraftment was analyzed with panleukocyte human and mouse CD45 markers using FACS and mice with >5% human CD45 cells, of total viable blood lymphocytes, were selected for tumor implantation. Twelve weeks post HSC injection, mice were subcutaneously injected with 2×10^6 RL tumor cells. Five days later, mice were treated with Flt3L injected peritoneally on a daily basis until day 18. Treatment with PBS (control) or 30 μ g human CLEC9A targeted AFNs was initiated by daily perilesional administration as of day 11 (when tumors had reached sizes of about 10 mm²) post tumor injection.

As shown in Figure 8, the CLEC9A VHH targeted AFNs had *in vivo* anti-tumor activity.

EQUIVALENTS

While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth and as follows in the scope of the appended claims.

Those skilled in the art will recognize, or be able to ascertain, using no more than routine experimentation, numerous equivalents to the specific embodiments described specifically herein. Such equivalents are intended to be encompassed in the scope of the following claims.

INCORPORATION BY REFERENCE

All patents and publications referenced herein are hereby incorporated by reference in their entireties.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

As used herein, all headings are simply for organization and are not intended to limit the disclosure in any manner. The content of any individual section may be equally applicable to all sections.

REFERENCES

The following are hereby incorporated by reference in their entireties:

Hart DN (1997) Dendritic cells: unique leukocyte populations which control the primary immune response. *Blood* 90: 3245-3287

Banchereau J and Steinman RM (1998) Dendritic cells and the control of immunity. *Nature* 392: 245-252

Bell D, Young JW and Banchereau J (1999) Dendritic cells. *Advances in Immunology* 72: 255-324

Shortman K and Liu YJ (2002) Mouse and human dendritic cell subtypes. *Nature Reviews Immunology* 2: 151-161

Poulin LF, Salio M, Griessinger E, Anjos-Afonso F, Craciun L, Chen JL, Keller AM, Joffre O, Zelenay S, Nye E, Le Moine A, Faure F, Donckier V, Sancho D, Cerundolo V, Bonnet D and Reis e Sousa C (2010) Characterization of human DNGR-1+ BDCA3+ leukocytes as putative equivalents of mouse CD8alpha+ dendritic cells. *The Journal of Experimental Medicine* 207: 1261-1271

Shortman K and Heath WR (2010) The CD8+ dendritic cell subset. *Immunological Reviews* 234: 18-31

Den Haan JM, Lehar SM and Bevan MJ (2000) CD8(+) but not CD8(-) dendritic cells cross-prime cytotoxic T cells in vivo. *Journal of Experimental Medicine* 192: 1685-1696

Heath WR, Belz GT, Behrens GM, Smith CM, Forehan SP, Parish IA, Davey GM, Wilson NS, Carbone FR and Villadangos JA (2004) Cross-presentation, dendritic cell subsets, and the generation of immunity to cellular antigens. *Immunological Reviews* 199: 9-26

Dallal RM and Lotze MT (2000) The dendritic cell and human cancer vaccines. *Current Opinion in Immunology* 12: 583-588

Steinman RM and Dhodapkar M (2001) Active immunization against cancer with dendritic cells: the near future. *International Journal of Cancer* 94: 459-473

Hsu FJ, Benike C, Fagnoni F, Liles TM, Czerwinski D, Taidi B, Engleman EG and Levy R (1996) Vaccination of patients with B-cell lymphoma using autologous antigen-pulsed dendritic cells. *Nature Medicine* 2: 52-58

Radford KJ and Caminschi I (2013) New generation of dendritic cell vaccines. *Human Vaccines & Immunotherapeutics* 9: 259-264

Bozzacco L, Trumpfheller C, Siegal FP, Mehndru S, Markowitz M, Carrington M, Nussenzweig MC, Piperno AG and Steinman RM (2007) DEC-205 receptor on dendritic cells mediates presentation of HIV gag protein to CD8+

T cells in a spectrum of human MHC I haplotypes. *Proceedings of the National Academy of Sciences of the United States of America* 104: 1289-1294

Birkholz K, Schwenkert M, Kellner C, Gross S, Fey G, Schuler-Thurner B, Schuler G, Schaft N and Dorrie J (2010) Targeting of DEC-205 on human dendritic cells results in efficient MHC class II-restricted antigen presentation. *Blood* 116: 2277-2285

Flynn BJ, Kastenmuller K, Wille-Reece U, Tomaras GD, Alam M, Lindsay RW, Salazar AM, Perdiguero B, Gomez CE, Wagner R, Esteban M, Park CG, Trumpheller C, Keler T, Pantaleo G, Steinman RM and Seder R (2011) Immunization with HIV Gag targeted to dendritic cells followed by recombinant New York vaccinia virus induces robust T-cell immunity in nonhuman primates. *Proceedings of the National Academy of Sciences of the United States of America* 108: 7131-7136

Idoyaga J, Lubkin A, Fiorese C, Lahoud MH, Caminschi I, Huang Y, Rodriguez A, Clausen BE, Park CG, Trumpheller C and Steinman RM (2011) Comparable T helper 1 (Th1) and CD8 T-cell immunity by targeting HIV gag p24 to CD8 dendritic cells within antibodies to Langerin, DEC205, and Clec9A. *Proceedings of the National Academy of Sciences of the United States of America* 108: 2384-2389

Sancho D, Joffre OP, Keller AM, Rogers NC, Martinez D, Hernanz-Falcon P, Rosewell I and Reis e Sousa C (2009) Identification of a dendritic cell receptor that couples sensing of necrosis to immunity. *Nature* 458: 899-903

Caminschi I, Proietto AI, Ahmet F, Kitsoulis S, Shin Teh J, Lo JC, Rizzitelli A, Wu L, Vremec D, van Dommelen SL, Campbell IK, Maraskovsky E, Braley H, Davey GM, Mottram P, van de Velde N, Jensen K, Lew AM, Wright MD, Heath WR, Shortman K and Lahoud MH (2008) The dendritic cell subtype-restricted C-type lectin Clec9A is a target for vaccine enhancement. *Blood* 112: 3264-3273

Sancho D, Mourao-Sa D, Joffre OP, Schulz O, Rogers NC, Pennington DJ, Carlyle JR and Reis e Sousa C (2008) Tumor therapy in mice via antigen targeting to a novel, DC-restricted C-type lectin. *Journal of Clinical Investigation* 118: 2098-2110

Lahoud MH, Ahmet F, Kitsoulis S, Wan SS, Vremec D, Lee CN, Phipson B, Shi W, Smyth GK, Lew AM, Kato Y, Mueller SN, Davey GM, Heath WR, Shortman K and Caminschi I (2011) Targeting antigen to mouse dendritic cells via Clec9A induces potent CD4 T cell responses biased toward a follicular helper phenotype. *Journal of Immunology* 187: 842-850

Schreibelt G, Klinkenberg LJ, Cruz LJ, Tacke P, Tel J, Kreutz M, Adema GJ, Brown GD, Figdor CG and de Vries IJ (2012) The C-type lectin receptor CLEC9A mediates antigen uptake and (cross-)presentation by human blood BDCA3+ myeloid dendritic cells. *Blood* 119: 2284-2292

Wesolowski J, Alzogaray V, Reyelt J, Unger M, Juarez K, Urrutia M, Cauerhff A, Danquah W, Rissiek B, Scheuplein F, Schwarz N, Adriouch S, Boyer O, Seman M, Licea A, Serreze DV, Goldbaum FA, Haag F and Koch-Nolte F (2009) Single domain antibodies: promising experimental and therapeutic tools in infection and immunity. *Medical Microbiology and Immunology* 198: 157-174

- Harmesen MM and De Haard HJ (2007) Properties, production, and applications of camelid single-domain antibody fragments. *Applied Microbiology and Biotechnology* 77: 13-22
- Dolk E, van Vliet C, Perez JM, Vriend G, Darbon H, Ferrat G, Cambillau C, Frenken LG and Verrips T (2005) Induced refolding of a temperature denatured llama heavy-chain antibody fragment by its antigen. *Proteins* 59: 555-564
- Muyldermans S (2013) Nanobodies: natural single-domain antibodies. *Annual Review of Biochemistry* 82: 775-797
- Lesterhuis WJ, Aarntzen EH, De Vries IJ, Schuurhuis DH, Figdor CG, Adema GJ and Punt CJ (2008) Dendritic cell vaccines in melanoma: from promise to proof? *Critical Reviews in Oncology/Hematology* 66: 118-134
- Vulink A, Radford KJ, Melief C and Hart DN (2008) Dendritic cells in cancer immunotherapy. *Advances in Cancer Research* 99: 363-407
- Luft T, Pang KC, Thomas E, Hertzog P, Hart DN, Trapani J and Cebon J (1998) Type I IFNs enhance the terminal differentiation of dendritic cells. *Journal of Immunology* 161: 1947-1953
- Paquette RL, Hsu NC, Kiercher SM, Park AN, Tran L, Roth MD and Glaspy JA (1998) Interferon-alpha and granulocyte-macrophage colony-stimulating factor differentiate peripheral blood monocytes into potent antigen-presenting cells. *Journal of Leukocyte Biology* 64: 358-367
- Radvanyi LG, Banerjee A, Weir M and Messner H (1999) Low levels of interferon-alpha induce CD86 (B7.2) expression and accelerates dendritic cell maturation from human peripheral blood mononuclear cells. *Scandinavian Journal of Immunology* 50: 499-509

The claims defining the invention are as follows:

1. A Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising an amino acid sequence having at least 98% identity with one of SEQ ID NOs: 332-336 and wherein the Clec9A binding agent comprises three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:
 - (a) CDR1 comprises an amino acid sequence of SEQ ID NO: 56;
 - (b) CDR2 comprises an amino acid sequence of SEQ ID NO: 191; and
 - (c) CDR3 comprises an amino acid sequence of SEQ ID NO: 202.
2. A Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:
 - (a) CDR1 comprises an amino acid sequence of SEQ ID NO: 53;
 - (b) CDR2 comprises an amino acid sequence of SEQ ID NO: 138; and
 - (c) CDR3 comprises an amino acid sequence of SEQ ID NO: 256.
3. The Clec9A binding agent of claim 2, comprising an amino acid sequence having at least 98% identity with SEQ ID NO: 330 or SEQ ID NO: 331.
4. A Clec9A binding agent comprising a recombinant heavy-chain-only antibody (VHH) comprising three complementarity determining regions (CDR1, CDR2, and CDR3), wherein:
 - (a) CDR1 comprises an amino acid sequence of SEQ ID NO: 53;
 - (b) CDR2 comprises an amino acid sequence of SEQ ID NO: 137; and
 - (c) CDR3 comprises an amino acid sequence of SEQ ID NO: 256, and
 wherein the Clec9A binding agent comprises an amino acid sequence having at least 98% identity with SEQ ID NO: 328 or SEQ ID NO: 329.
5. The Clec9A binding agent of any one of claims 1 to 4, wherein the Clec9A binding agent further comprises one or more signaling agents, optionally wherein the signaling agent is selected from one or more of an interferon, an interleukin, and a tumor necrosis factor, any of which are optionally modified.

6. The Clec9A binding agent of any one of claims 1 to 5, wherein the Clec9A binding agent further comprises one or more additional targeting moieties, optionally wherein the one or more additional targeting moieties recognize and optionally functionally modulate a tumor antigen, optionally wherein the one or more additional targeting moieties recognize and optionally functionally modulate an antigen on an immune cell, optionally wherein the immune cell is selected from a T cell, a B cell, a dendritic cell, a macrophage, neutrophil, and a NK cell.

7. The Clec9A binding agent of any one of claims 1 to 6, wherein the Clec9A binding agent recruits cytotoxic T cells to tumor cells or to the tumor environment, optionally wherein the Clec9A binding agent recognizes and binds Clec9A without substantially functionally modulating its activity.

8. A recombinant nucleic acid composition encoding the Clec9A binding agent of any one of claims 1 to 7.

9. A host cell comprising a nucleic acid of claim 8.

10. A chimeric protein comprising:

(a) a Clec9A binding agent of any one of claims 1-7; and

(b) a modified human IFN- α 2, said modified human IFN- α 2 having one or more mutations that confer improved safety as compared to a wild type IFN- α 2; and

wherein the targeting moiety and the modified signaling agent are optionally connected with one or more linkers, optionally wherein the modified human IFN- α 2 comprises one or more mutations at positions R149, R120, M148, and L153, optionally wherein the modified human IFN- α 2 comprises one or more mutations selected from R149A, R120E, and L153A.

11. The chimeric protein of claim 10, wherein the modified human IFN- α 2 comprises a R120E mutation and either a R149A or a L153A mutation.

12. A chimeric protein comprising:

(a) a Clec9A binding agent of any one of claims 1-7; and

(b) a modified human IFN- β , said modified human IFN- β having one or more mutations that confer improved safety as compared to a wild type IFN- β ; and

wherein the targeting moiety and the modified signaling agent are optionally connected with one or more linkers, optionally wherein the modified human IFN- β comprises one or more mutations at positions W22, R27, L32, R35, V148, L151, R152, and Y155, optionally wherein the modified human IFN- β comprises one or more mutations selected from W22G, R27G, L32A, L32G, R35A, R35G, V148G, L151G, R152A, R152G.

13. Use of a chimeric protein comprising a Clec9A binding agent of any one of claims 1-7 and a signaling agent that is a human interferon alpha 2 in the manufacture of a medicament for treating or preventing cancer.

[illegible]

[illegible]

[illegible]

[illegible]

Figure 1 (Continued)

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SEQ ID NO: 1129 31EC34 1 TTATACAGCTAGCTGCTGCTACCTAG--GGACAGGGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 434
SEQ ID NO: 1130 21EC35 1 TTATACGCTGCTAGCTGCTGCTACCCG--GGACAGGGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 434
SEQ ID NO: 1131 21EC36 1 ---TATGACTATGCT---ACTGG--GGACAGGGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 413
SEQ ID NO: 1132 11EC62 1 TTGATTCAGGACACACATCTGG--GGTACAGGGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 401
SEQ ID NO: 1133 31EC15 1 -----GGCTAGGATGACTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 401
SEQ ID NO: 1134 31EC9 1 TTAGTGGAACTGTTGACTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 416
SEQ ID NO: 1135 31EC61 1 TTAGTGGAACTGTTGACTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 416
SEQ ID NO: 1136 31EC38 1 TTAGTGGAACTGTTGACTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 416
SEQ ID NO: 1137 11EC31 1 GACGGTAGTAGTACTCCGCTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 404
SEQ ID NO: 1138 31EC27 1 GACGGTAGTAGTACTCCGCTACTGG--GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 404
SEQ ID NO: 1139 31EC6 1 GACGGTAGTAGTACTCCGCTACTGG-----GGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 404
SEQ ID NO: 1140 11EC31 1 TTGCGGAGGACTACAA-----AGGCTAGGAGGACCCAGGTCACCGTCTCTCTTAAGGGCCGCGCATACCGGTACGACGCTTCGGGACTACGGTTCGGACCTACGCTACCA : 423

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SEQ ID NO: 1075 21EC16 1 CTAG : 423
SEQ ID NO: 1076 31EC66 1 CTAG : 423
SEQ ID NO: 1077 21EC59 1 CTAG : 423
SEQ ID NO: 1078 11EC38 1 CTAG : 423
SEQ ID NO: 1079 21EC20 1 CTAG : 423
SEQ ID NO: 1080 21EC38 1 CTAG : 423
SEQ ID NO: 1081 31EC4 1 CTAG : 399
SEQ ID NO: 1082 21EC13 1 CTAG : 405
SEQ ID NO: 1083 21EC39 1 CTAG : 405
SEQ ID NO: 1084 11EC70 1 CTAG : 423
SEQ ID NO: 1085 21EC60 1 CTAG : 423
SEQ ID NO: 1086 31EC13 1 CTAG : 423
SEQ ID NO: 1087 31EC69 1 CTAG : 408
SEQ ID NO: 1088 21EC33 1 CTAG : 405
SEQ ID NO: 1089 11EC92 1 CTAG : 408
SEQ ID NO: 1090 31EC11 1 CTAG : 408
SEQ ID NO: 1091 11EC84 1 CTAG : 405
SEQ ID NO: 1092 31EC75 1 CTAG : 402
SEQ ID NO: 1093 21EC61 1 CTAG : 411
SEQ ID NO: 1094 11EC7 1 CTAG : 405
SEQ ID NO: 1095 21EC68 1 CTAG : 405
SEQ ID NO: 1096 31EC57 1 CTAG : 405
SEQ ID NO: 1097 11EC42 1 CTAG : 405
SEQ ID NO: 1098 31EC39 1 CTAG : 405
SEQ ID NO: 1099 21EC38 1 CTAG : 405
SEQ ID NO: 1100 31EC36 1 CTAG : 405
SEQ ID NO: 1101 31EC62 1 CTAG : 408
SEQ ID NO: 1102 11EC61 1 CTAG : 405
SEQ ID NO: 1103 21EC30 1 CTAG : 408

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Figure 1 (Continued)

SEQ ID NO: 1104 31EC55 : CTAG : 403
SEQ ID NO: 1105 21EC26 : CTAG : 403
SEQ ID NO: 1106 11EC94 : CTAG : 403
SEQ ID NO: 1107 11EC26 : CTAG : 403
SEQ ID NO: 1108 31EC23 : CTAG : 403
SEQ ID NO: 1109 31EC30 : CTAG : 403
SEQ ID NO: 1110 21EC55 : CTAG : 411
SEQ ID NO: 1111 11EC38 : CTAG : 403
SEQ ID NO: 1112 11EC64 : CTAG : 405
SEQ ID NO: 1113 21EC93 : CTAG : 405
SEQ ID NO: 1114 21EC53 : CTAG : 405
SEQ ID NO: 1115 21EC63 : CTAG : 405
SEQ ID NO: 1116 11EC63 : CTAG : 405
SEQ ID NO: 1117 11EC30 : CTAG : 405
SEQ ID NO: 1118 11EC27 : CTAG : 403
SEQ ID NO: 1119 11EC9 : CTAG : 405
SEQ ID NO: 1120 21EC76 : CTAG : 405
SEQ ID NO: 1121 21EC62 : CTAG : 426
SEQ ID NO: 1122 21EC23 : CTAG : 403
SEQ ID NO: 1123 21EC48 : CTAG : 403
SEQ ID NO: 1124 21EC54 : CTAG : 405
SEQ ID NO: 1125 11EC88 : CTAG : 414
SEQ ID NO: 1126 21EC6 : CTAG : 411
SEQ ID NO: 1127 31EC22 : CTAG : 411
SEQ ID NO: 1128 21EC24 : CTAG : 438
SEQ ID NO: 1129 31EC94 : CTAG : 438
SEQ ID NO: 1130 21EC95 : CTAG : 438
SEQ ID NO: 1131 21EC67 : CTAG : 417
SEQ ID NO: 1132 11EC62 : CTAG : 405
SEQ ID NO: 1133 31EC15 : CTAG : 405
SEQ ID NO: 1134 31EC9 : CTAG : 420
SEQ ID NO: 1135 31EC61 : CTAG : 420
SEQ ID NO: 1136 31EC92 : CTAG : 420
SEQ ID NO: 1137 11EC51 : CTAG : 403
SEQ ID NO: 1138 31EC27 : CTAG : 403
SEQ ID NO: 1139 31EC6 : CTAG : 403
SEQ ID NO: 1140 11EC91 : CTAG : 432

[illegible]

Figure 2 (Continued)

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SEQ ID NO: 1183 21E263 : QVQLQESGGELVQAGSSRLSCA-ASGSIINSMXNYRTPAGKQRELVAAI--TSQG--RTTVESVSGKFTIISRDNAK--TVFLQMSLKPEDIAVYFC--KA--FTRE : 101
SEQ ID NO: 1184 21E255 : QVQLQESGGELVTEZSLSCA-ASGSIINSMXNYRTPAGKQRELVAAI--TVQG--RLAYADSAKRAFTIISKESAKN--TVFLHSSLKPEDIAVNYCTINW--RKG- : 103
SEQ ID NO: 1185 21E215 : QVQLQESGGELVQAGSSRLSCA-ASGVSVFISINSMXNYRTPAGKQRELVAAI--ITQG--RTTVESVSGKFTIISRDNAK--TVFLQMSLKPEDIAVYFC--AK-- : 101
SEQ ID NO: 1186 21E238 : QVQLQESGGELVTEGSSRLSCA-ASVSISISINSMXNYRTPAGKQRELVAAI--TVGG--RLAYADSAKRAFTIISRDNAK--TVFLQMSLKPEDIAVNYCTINW--RDR- : 102
SEQ ID NO: 1187 21E23 : QVQLQESGGELVQAGSSRLSCA-ASGSITSINSMXNYRTPAGKQRELVAAI--TSQG--RLSYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--A--FQSS : 101
SEQ ID NO: 1188 21E276 : QVQLQESGGELVQAGSSRLSCV-VSGTIFISINSMXNYRTPAGKQRELVAAI--INQG--RLSYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--A--FQSS : 101
SEQ ID NO: 1189 21E262 : QVQLQESGGELVQAGSSRLSCA-AGSISIFISINSMXNYRTPAGKQRELVAGI--TIQG--RTTVESVSGKFTIISRDNAK--TVFLQMSLKPEDIAVYFC--VKTG : 103
SEQ ID NO: 1190 21E266 : QVQLQESGGELVQAGSSRLSCA-AGSISIVISINSMXNYRTPAGKQRELVAAI--INQETK--YSTSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--VKTG : 99
SEQ ID NO: 1191 21E224 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--SWSG--GSTIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1192 21E234 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--SWSG--GSTIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1193 21E235 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--SWSG--GSTIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1194 21E23 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQG--STIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1195 21E248 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQG--STIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 104
SEQ ID NO: 1196 21E267 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--SWSG--GSTIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 104
SEQ ID NO: 1197 21E222 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--SWSG--GSTIYADSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 103
SEQ ID NO: 1198 21E231 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 103
SEQ ID NO: 1199 21E254 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1200 21E262 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 103
SEQ ID NO: 1201 21E251 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 103
SEQ ID NO: 1202 21E227 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAAI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 104
SEQ ID NO: 1203 21E25 : QVQLQESGGELVQAGSSRLSCV-ASVNIISINSMXNYRTPAGKQRELVAGI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 104
SEQ ID NO: 1204 21E29 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1205 21E261 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106
SEQ ID NO: 1206 21E262 : QVQLQESGGELVQAGSSRLSCA-ASGRTFTIYAMNFRQAPKQRELVAGI--TSQGI--TNYANSVKGFRTIISRDNAK--TVFLQMSLKPEDIAVYFC--AEVSGERE : 106

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Figure 2 (Continued)

SEQ ID NO: 1158 21EC33.1 -GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1159 21EC16.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1160 21EC66.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1161 21EC59.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1162 21EC29.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1163 21EC20.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1164 21EC90.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1165 21EC90.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1166 21EC55.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1167 21EC46.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1168 21EC34.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1169 21EC30.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1170 21EC60.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1171 21EC13.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 141
 SEQ ID NO: 1172 21EC62.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1173 21EC26.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1174 21EC33.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1175 21EC27.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1176 21EC88.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1177 21EC34.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1178 21EC64.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1179 21EC23.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1180 21EC30.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1181 21EC63.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1182 21EC53.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1183 21EC63.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1184 21EC55.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 137
 SEQ ID NO: 1185 21EC15.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1186 21EC38.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1187 21EC9.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1188 21EC78.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1189 21EC62.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 142
 SEQ ID NO: 1190 21EC6.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 137
 SEQ ID NO: 1191 21EC24.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 146
 SEQ ID NO: 1192 21EC94.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 146
 SEQ ID NO: 1193 21EC35.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 146
 SEQ ID NO: 1194 21EC13.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1195 21EC43.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136
 SEQ ID NO: 1196 21EC67.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 139
 SEQ ID NO: 1197 21EC24.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 137
 SEQ ID NO: 1198 21EC91.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 144
 SEQ ID NO: 1199 21EC54.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1200 21EC62.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 135
 SEQ ID NO: 1201 21EC51.1 GGTVDGTA--GGTGTGTTSSAAAATPDPVDFGSHHHHHX : 136

Figure 2 (Continued)

SEQ ID NO: 1202	31EC27 : -----YW--GGGTIVSSAAAYFDVFDGSHHHHH : 136
SEQ ID NO: 1203	31EC6 : -----YW--GGGTIVSSAAAYFDVFDGSHHHHH : 136
SEQ ID NO: 1204	31EC9 : V----DYW--GGGTIVSSAAAYFDVFDGSHHHHH : 140
SEQ ID NO: 1205	31EC61 : V----DYW--GGGTIVSSAAAYFDVFDGSHHHHH : 140
SEQ ID NO: 1206	31EC81 : A----DYW--GGGTIVSSAAAYFDVFDGSHHHHH : 140

Figure 3

Group	Member(s)
1	1LEC42, 3LEC89, 2LEC38, 1LEC7, 3LEC57, 2LEC68, 1LEC61, 3LEC36, 2LEC61, 1LEC64, 2LEC93, 1LEC30, 1LEC63, 2LEC53, 2LEC63
2	3LEC62, 2LEC90, 3LEC55, 2LEC26, 1LEC94, 3LEC30, 1LEC26, 3LEC23, 1LEC27, 2LEC55, 1LEC38
3	1LEC92, 3LEC11
4	1LEC70
5	3LEC4
6	2LEC13, 2LEC89, 2LEC83
7	3LEC76
8	2LEC16, 3LEC66, 2LEC59, 1LEC28, 2LEC20, 2LEC88
9	2LEC60, 3LEC13
10	3LEC69
11	1LEC88
12	1LEC84
13	3LEC15
14	1LEC9, 2LEC76
15	2LEC62
16	2LEC6
17	2LEC24, 3LEC94, 2LEC95
18	2LEC23, 2LEC48
19	2LEC67
20	3LEC22
21	1LEC91
22	2LEC54
23	1LEC62
24	1LEC51, 3LEC27, 3LEC6
25	3LEC9, 3LEC61, 3LEC82

Figure 4

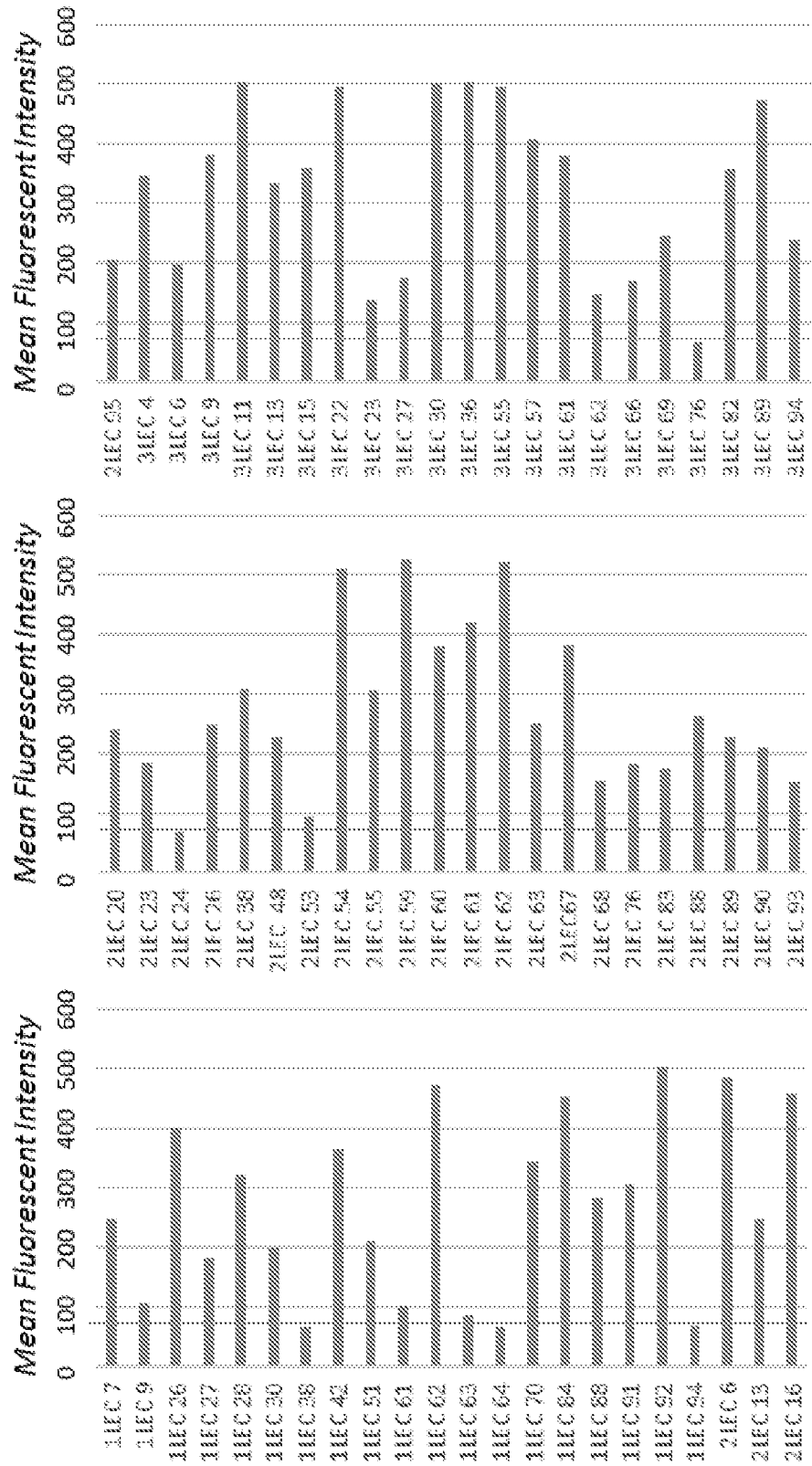


Figure 5

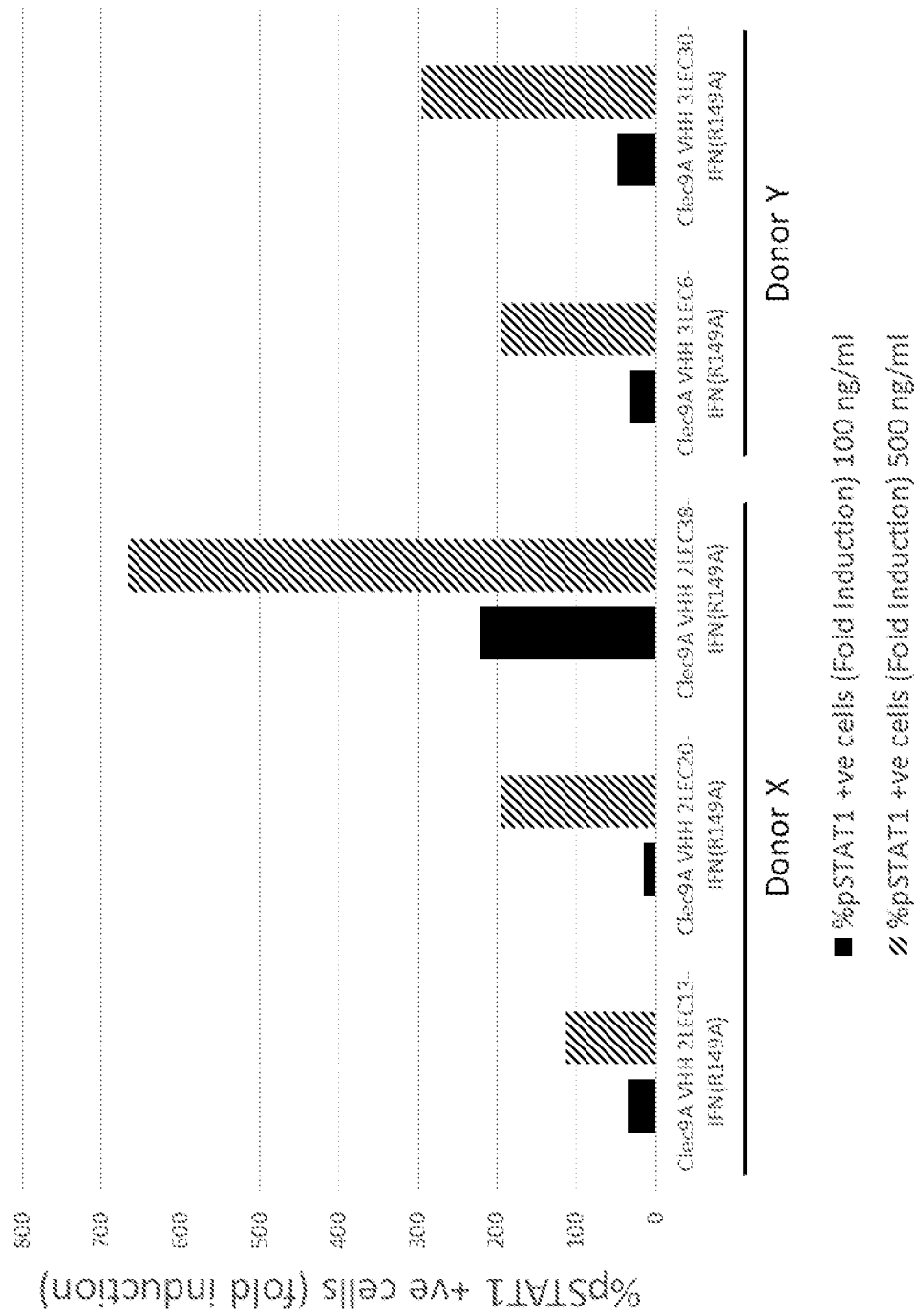


Figure 6

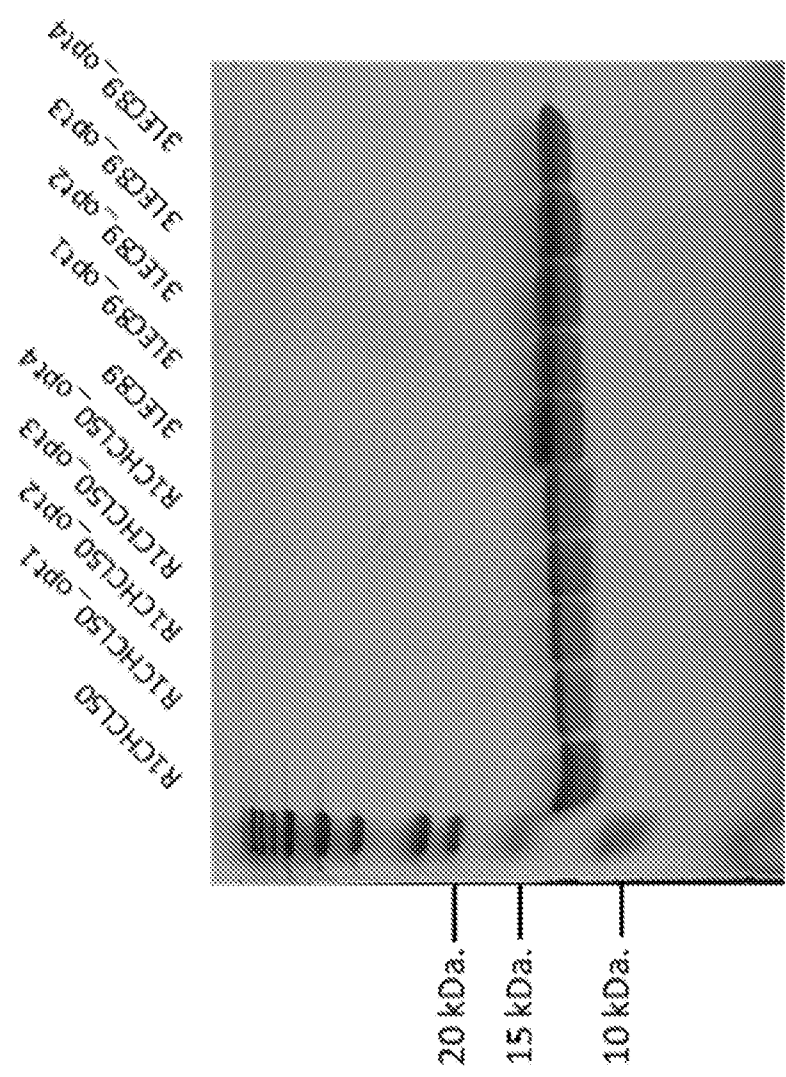


Figure 7A

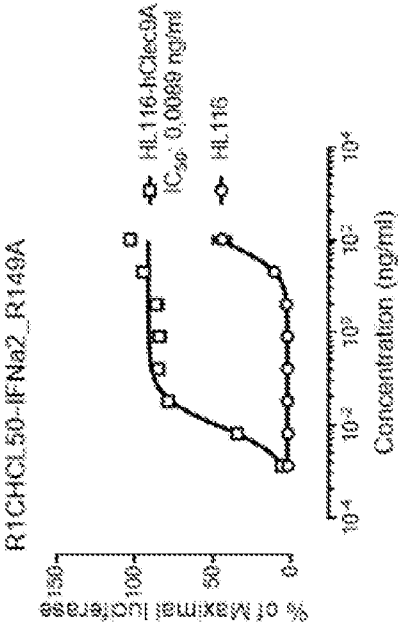
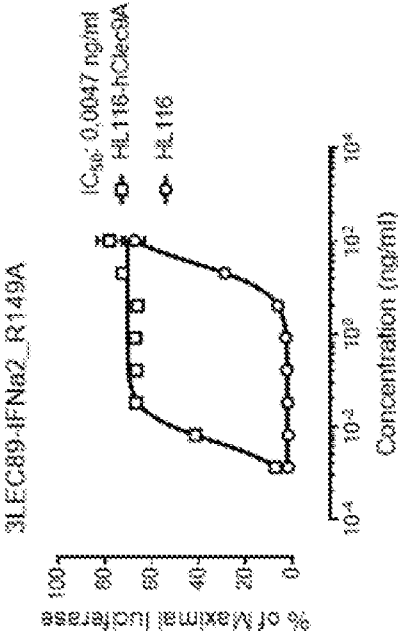


Figure 7B



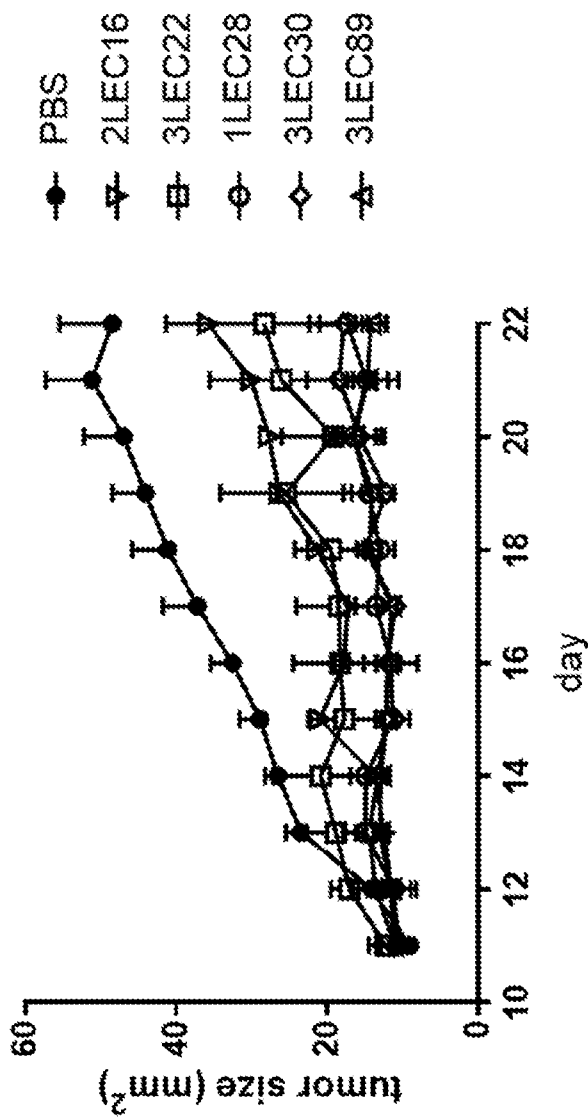


Figure 8

ORN-033PC_ST25.txt
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<120> CLEC9A BINDING AGENTS AND USE THEREOF
<130> ORN-033PC
<150> US 62/542,944
<151> 2017-08-09
<160> 1206
<170> PatentIn version 3.5
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Pro Asp Thr Tyr Gln Lys Cys Leu Ser Ser Asn Lys Cys Ser Gly Ala
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Cys Cys Leu Val Met Val Ile Ser Cys Val Phe Cys Met Gly Leu Leu
35 40 45

Thr Ala Ser Ile Phe Leu Gly Val Lys Leu Leu Gln Val Ser Thr Ile
50 55 60

Ala Met Gln Gln Gln Glu Lys Leu Ile Gln Gln Glu Arg Ala Leu Leu
65 70 75 80

Asn Phe Thr Glu Trp Lys Arg Ser Cys Ala Leu Gln Met Lys Tyr Cys
85 90 95

Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Ala His Asn Ser Ser Pro
100 105 110

ORN-033PC_ST25.txt

Cys Pro Asn Asn Trp Ile Gln Asn Arg Glu Ser Cys Tyr Tyr Val Ser
115 120 125

Glu Ile Trp Ser Ile Trp His Thr Ser Gln Glu Asn Cys Leu Lys Glu
130 135 140

Gly Ser Thr Leu Leu Gln Ile Glu Ser Lys Glu Glu Met Asp Phe Ile
145 150 155 160

Thr Gly Ser Leu Arg Lys Ile Lys Gly Ser Tyr Asp Tyr Trp Val Gly
165 170 175

Leu Ser Gln Asp Gly His Ser Gly Arg Trp Leu Trp Gln Asp Gly Ser
180 185 190

Ser Pro Ser Pro Gly Leu Leu Pro Ala Glu Arg Ser Gln Ser Ala Asn
195 200 205

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Ser Thr Trp Lys Tyr Phe Ile Cys Glu Lys Tyr Ala Leu Arg Ser Ser
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<400> 23

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Gly	Arg	Ile	Phe	Ser	Val	Asn	Ala	Met	Gly
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<223> Synthetic polymer

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Gly	Ser	Phe	Ser	Ser	Ile	Asn	Val	Met	Gly
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<400> 55

Ile Asn Ala Met Gly
 1 5

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<400> 56

Val Asn Ala Met Gly
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<210> 57
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<400> 57

Ile Asn Ala Trp Gly
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Leu Asn Ser Met Ala

1 5

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Ser Ile Thr Ala Met Gly
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Ile Asn Ala Ile Gly
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Ala	Ile	Thr	Asn	Asp	Gly	Arg	Thr	Thr	Tyr	Val	Asp	Ser	Val	Lys	Gly

1 5 10 15

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Ala Val Thr Val Gly Gly Arg Tyr Ala Tyr Ala Asp Ser Ala Lys Asn
 1 5 10 15

<210> 86
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<400> 86

Ala Ile Thr Asn Gln Gly Ala Thr Thr Tyr Ala Asp Ser Val Lys Gly
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Gly Ile Thr Gly Ser Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg Gly
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<400> 88

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Ala	Ile	Thr	Asn	Gly	Gly	Arg	Thr	Thr	Tyr	Val	Asp	Ser	Val	Lys	Gly
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<400> 91

Ala	Ile	Thr	Thr	Gly	Gly	Arg	Thr	Thr	Tyr	Val	Asp	Ser	Val	Lys	Gly
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<210> 92

<211> 16

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<400> 92

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Leu	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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<210> 93

<211> 16

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<400> 93

Ala	Ile	Thr	Ser	Gly	Gly	Arg	Arg	Ala	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 94

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 94

Ala	Ile	Thr	Ser	Ala	Ser	Ala	Ser	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val
1				5					10					15	

Lys Gly

<210> 95

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 95

Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Asp	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 96
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 96

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Val	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 97
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 97

Ala	Ile	Thr	Asp	Gly	Gly	Arg	Leu	Ala	Tyr	Ala	Asp	Ser	Ala	Lys	Gly
1				5					10					15	

<210> 98
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 98

Ser	Ile	Thr	Asn	Gln	Gly	Ile	Arg	Asn	Tyr	Ser	Thr	Ser	Val	Met	Gly
1				5					10					15	

<210> 99

<211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 99

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 100
 <211> 16
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<220>
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<400> 100

Ala	Ile	Thr	Asn	Gly	Gly	Arg	Ile	Ala	Tyr	Gly	Ile	Ala	Val	Asn	Gly
1				5					10					15	

<210> 101
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 101

Ala	Ile	Thr	Asn	Gly	Gly	Arg	Ile	Ala	Tyr	Ser	Asp	Ser	Ala	Lys	Gly
1				5					10					15	

<210> 102
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 102

Gly	Ile	Thr	Ser	Asp	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	Lys	Gly

1 5 10 15

<210> 103
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 103

Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 104
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 104

Ala Ile Thr Asp Gln Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys Gly
1 5 10 15

<210> 105
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 105

Ala Ile Thr Asn Gly Gly Gln Thr Thr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 106
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 106

Ala	Ile	Thr	Thr	Gly	Gly	Arg	Thr	Ala	Tyr	Val	Asp	Ser	Val	Lys	Gly
1				5				10						15	

<210> 107

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 107

Ala	Ile	Thr	Ser	Gln	Gly	Arg	Ile	Thr	Leu	Ala	Asp	Ser	Val	Lys	Gly
1				5				10						15	

<210> 108

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 108

Ala	Ile	Thr	Val	Asp	Gly	Arg	Leu	Ala	Tyr	Ala	Asp	Ser	Ala	Lys	His
1				5				10						15	

<210> 109

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 109

Ala	Ile	Thr	Asn	Gly	Gly	Arg	Ile	Ala	Tyr	Gly	Thr	Ser	Val	Met	Gly
1				5				10						15	

<210> 110
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 110

Ala	Ile	Thr	Asn	Gly	Gly	Gln	Ile	Ala	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 111
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 111

Ala	Ile	Thr	Asp	Gln	Gly	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 112
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 112

Gly	Ile	Thr	Thr	Gln	Gly	Arg	Ile	Thr	Tyr	Gly	Asn	Ser	Val	Arg	Gly
1				5					10					15	

<210> 113
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 113

Ala	Ile	Thr	Ser	Gly	Gly	Arg	Thr	Thr	Tyr	Val	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 114
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 114

Ala	Ile	Asn	Trp	Arg	Gly	Gly	Asp	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 115
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 115

Ala	Ile	Thr	Asp	Gly	Gly	Ala	Lys	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 116
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 116

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Leu	Ser	Tyr	Val	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 117

<211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 117

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Arg	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 118
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 118

Ala	Ile	Thr	Asn	Gly	Gly	Arg	Ile	Ala	Tyr	Thr	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 119
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 119

Ala	Ile	Thr	Asn	Gly	Gly	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 120
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 120

Ala	Ile	Thr	Asp	Gly	Gly	Arg	Leu	Thr	Tyr	Ala	Asp	Ser	Ala	Lys	Gly

1 5 10 15

<210> 121
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 121

Ala Ile Ser Trp Ser Gly Gly Ser Thr Glu Tyr His Asp Ser Val Lys
1 5 10 15

Gly

<210> 122
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 122

Ala Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 123
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 123

Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser Tyr Ser Asn Ser Ala Lys
1 5 10 15

Gly

<210> 124
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 124

Ala	Ile	Thr	Gly	Gln	Gly	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 125
 <211> 16
 <212> PRT
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<220>
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<400> 125

Ala	Ile	Thr	Asn	Gly	Gly	Gln	Ile	Val	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 126
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 126

Ala	Ile	Thr	Thr	Gln	Gly	Arg	Thr	Thr	Tyr	Glu	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 127
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 127

Ala Ile Thr Ser Gly Gly Ile Thr Asn Tyr Ala Asn Ser Val Gln Gly
1 5 10 15

<210> 128
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 128

Ala Ile Thr Val Gly Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys Gly
1 5 10 15

<210> 129
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 129

Gly Ile Thr Gly Gly Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg Gly
1 5 10 15

<210> 130
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 130

Ala Ile Thr Ser Gln Gly Arg Ser Thr Tyr Ala Asp Ser Ala Lys Gly
1 5 10 15

<210> 131
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 131

Ala	Ile	Thr	Asn	Gly	Gly	Ala	Thr	Val	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 132

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 132

Ala	Ile	Thr	Asp	Gly	Gly	Arg	Leu	Thr	Tyr	Ala	Asp	Ser	Ala	Lys	Asn
1				5					10					15	

<210> 133

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 133

Ala	Ile	Asn	Trp	Ser	Ser	Gly	Gly	Ile	Ser	Tyr	Ser	Asn	Ala	Ala	Lys
1				5					10					15	

Gly

<210> 134

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<400> 134

Ala	Ile	Thr	Asn	Xaa	Gly	Arg	Thr	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 135

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 135

Ala	Ile	Trp	Trp	Ala	Ser	Gly	Gly	Ile	Ser	Tyr	Ala	Asn	Ser	Ala	Lys
1				5				10						15	

Gly

<210> 136

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 136

Ala	Ile	Thr	Asn	Gln	Gly	Ala	Pro	Thr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 137

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 137

Arg	Ile	Thr	Asn	Leu	Gly	Leu	Pro	Asn	Tyr	Ala	Asp	Ser	Val	Thr	Gly

1 5 10 15

<210> 138
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 138

Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 139

Ala Ile Thr Asn Gly Gly Ala Lys Thr
1 5

<210> 140
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 140

Ala Ile Thr Ser Gly Gly Arg Leu Ser
1 5

<210> 141
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 141

Ala Ile Thr Asn Gly Gly Gln Thr Ala
1 5

<210> 142

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 142

Ala Ile Thr Ser Gly Gly Arg Ser Thr
1 5

<210> 143

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 143

Ile Thr Asn Gln Gly Arg Ile Ala
1 5

<210> 144

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 144

Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Pro Ser Val Asn Gly
1 5 10 15

<210> 145

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 145

Ala Ile Thr Asn Asp Gly Arg Thr Thr
1 5

<210> 146

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 146

Ala Val Thr Val Gly Gly Arg Tyr Ala
1 5

<210> 147

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 147

Ala Ile Thr Asn Gln Gly Ala Thr Thr
1 5

<210> 148

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 148

Gly Ile Thr Gly Ser Gly Gln Ile Thr
1 5

<210> 149
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 149

Ala Ile Thr Asn Gly Gly Arg Thr Val
 1 5

<210> 150
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 150

Ala Ile Thr Ser Gly Gly Arg Leu Ala
 1 5

<210> 151
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 151

Ala Ile Thr Asn Gly Gly Arg Thr Thr
 1 5

<210> 152
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 152

Ala Ile Thr Thr Gly Gly Arg Thr Thr
1 5

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 153

Ala Ile Thr Asn Gln Gly Arg Leu Thr
1 5

<210> 154
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 154

Ala Ile Thr Ser Gly Gly Arg Arg Ala
1 5

<210> 155
<211> 11
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<213> Artificial Sequence

<220>
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<400> 155

Ala Ile Thr Ser Ala Ser Ala Ser Arg Thr Thr
1 5 10

<210> 156
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 156

Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr
1				5					10

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 157

Ala	Ile	Thr	Asn	Gln	Gly	Arg	Val	Thr
1				5				

<210> 158

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 158

Ala	Ile	Thr	Asp	Gly	Gly	Arg	Leu	Ala
1				5				

<210> 159

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 159

Ser	Ile	Thr	Asn	Gln	Gly	Ile	Arg	Asn
1				5				

<210> 160

<211> 9
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<220>
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<400> 160

Ala Ile Thr Asn Gln Gly Arg Thr Thr
 1 5

<210> 161
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 161

Ala Ile Thr Asn Gly Gly Arg Ile Ala
 1 5

<210> 162
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 162

Gly Ile Thr Ser Asp Gly Ser Thr Gly
 1 5

<210> 163
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 163

Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr

1

5

10

<210> 164
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 164

Ala Ile Thr Asp Gln Gly Arg Leu Ala
1 5

<210> 165
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 165

Ala Ile Thr Asn Gly Gly Gln Thr Thr
1 5

<210> 166
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 166

Ala Ile Thr Thr Gly Gly Arg Thr Ala
1 5

<210> 167
<211> 9
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<220>
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<400> 167

Ala Ile Thr Ser Gln Gly Arg Ile Thr
1 5

<210> 168

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 168

Ala Ile Thr Val Asp Gly Arg Leu Ala
1 5

<210> 169

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 169

Ala Ile Thr Asn Gly Gly Gln Ile Ala
1 5

<210> 170

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 170

Ala Ile Thr Asp Gln Gly Arg Thr Thr
1 5

<210> 171

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 171

Gly Ile Thr Thr Gln Gly Arg Ile Thr
1 5

<210> 172

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 172

Ala Ile Thr Ser Gly Gly Arg Thr Thr
1 5

<210> 173

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 173

Ala Ile Asn Trp Arg Gly Gly Asp Thr Tyr
1 5 10

<210> 174

<211> 9

<212> PRT

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<220>

<223> Synthetic polymer

<400> 174

Ala Ile Thr Asp Gly Gly Ala Lys Thr
1 5

<210> 175
 <211> 9
 <212> PRT
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<220>
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<400> 175

Ala Ile Thr Asn Gln Gly Arg Leu Ser
 1 5

<210> 176
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<220>
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<400> 176

Ala Ile Thr Asn Gln Gly Arg Arg Thr
 1 5

<210> 177
 <211> 9
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 <213> Artificial Sequence

<220>
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<400> 177

Ala Ile Thr Asp Gly Gly Arg Leu Thr
 1 5

<210> 178
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 178

Ala Ile Ser Trp Ser Gly Gly Ser Thr Glu
1 5 10

<210> 179
<211> 9
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<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 179

Ala Ile Thr Asn Gln Gly Arg Ile Ala
1 5

<210> 180
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 180

Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser
1 5 10

<210> 181
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 181

Ala Ile Thr Gly Gln Gly Arg Thr Thr
1 5

<210> 182
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 182

Ala Ile Thr Asn Gly Gly Gln Ile Val
1 5

<210> 183

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 183

Ala Ile Thr Thr Gln Gly Arg Thr Thr
1 5

<210> 184

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 184

Ala Ile Thr Ser Gly Gly Ile Thr Asn
1 5

<210> 185

<211> 9

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<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 185

Ala Ile Thr Val Gly Gly Arg Leu Ala
1 5

<210> 186

<211> 9
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<220>
 <223> Synthetic polymer

<400> 186

Gly Ile Thr Gly Gly Gly Gln Ile Thr
 1 5

<210> 187
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 <213> Artificial Sequence

<220>
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<400> 187

Ala Ile Thr Ser Gln Gly Arg Ser Thr
 1 5

<210> 188
 <211> 9
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 <213> Artificial Sequence

<220>
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<400> 188

Ala Ile Thr Asn Gly Gly Ala Thr Val
 1 5

<210> 189
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<220>
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<220>
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<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<400> 189

Ala Ile Thr Asn Xaa Gly Arg Thr Thr
1 5

<210> 190

<211> 10

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<213> Artificial Sequence

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<223> Synthetic polymer

<400> 190

Ala Ile Trp Trp Ala Ser Gly Gly Ile Ser
1 5 10

<210> 191

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 191

Ala Ile Thr Asn Gln Gly Ala Pro Thr
1 5

<210> 192

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 192

Arg Ile Thr Asn Leu Gly Leu Pro Asn
1 5

<210> 193

<211> 7
 <212> PRT
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<220>
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<400> 193

Phe Thr Arg Arg Asp Asp Tyr
 1 5

<210> 194
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 <212> PRT
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<220>
 <223> Synthetic polymer

<400> 194

Phe Gln Ser Ser Gly Ile Asp
 1 5

<210> 195
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 195

Trp Ala Ala Asp Tyr Gln Gln Tyr
 1 5

<210> 196
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 196

Trp Asn Arg Asp Arg Gln Gln Tyr

1 5

<210> 197
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 197

Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr
 1 5 10

<210> 198
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 <212> PRT
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<220>
 <223> Synthetic polymer

<400> 198

Phe Thr Arg Asp Lys Asp Tyr
 1 5

<210> 199
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<400> 199

Trp Asp Arg Asp Arg Gln Gln Tyr
 1 5

<210> 200
 <211> 7
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<220>
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<400> 200

Phe Thr Arg Thr Asp Asp Tyr
1 5

<210> 201

<211> 8

<212> PRT

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<220>

<223> Synthetic polymer

<400> 201

Tyr Asp Arg Ser Ser Thr Pro Tyr
1 5

<210> 202

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 202

Phe Thr Arg Gly Asp Asp Tyr
1 5

<210> 203

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 203

Leu Asn Ser Ala Thr Thr Tyr
1 5

<210> 204

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 204

Tyr Thr Arg Asp Glu Asp Tyr
1 5

<210> 205

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 205

Phe Thr Arg Asp Glu Asp Tyr
1 5

<210> 206

<211> 13

<212> PRT

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<220>

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<400> 206

Lys Trp Tyr Asp Pro Leu Val Ile Glu Tyr Tyr Asp Asn
1 5 10

<210> 207

<211> 7

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<213> Artificial Sequence

<220>

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<400> 207

Lys Ala Asp His Asn Asp Tyr
1 5

<210> 208
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<220>
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<400> 208

Phe Arg Ser Gly Ala Asp Asp Tyr
 1 5

<210> 209
 <211> 15
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<220>
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<400> 209

Glu Val Pro Ser Thr Tyr Ser Cys Ser Gly Phe Arg Glu Asp Tyr
 1 5 10 15

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<220>
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<400> 210

Phe Ala Ala Ser Gly Met Glu Tyr
 1 5

<210> 211
 <211> 8
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 <213> Artificial Sequence

<220>
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<400> 211

Trp Thr Thr Asp Arg Gln Gln Tyr
1 5

<210> 212
<211> 9
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<213> Artificial Sequence

<220>
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<400> 212

Phe Ala Gly Trp Gly Lys Glu Asp Tyr
1 5

<210> 213
<211> 7
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<220>
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<400> 213

Phe Ser Pro Thr Gly Asp Tyr
1 5

<210> 214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 214

Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr
1 5 10

<210> 215
<211> 13
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<220>

<223> Synthetic polymer

<400> 215

Lys	Ala	Ser	Pro	Val	Tyr	Gly	Ser	Thr	Val	Glu	Asp	Tyr
1				5					10			

<210> 216

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 216

Ser	Thr	Pro	Arg	Gly	Asp	Ser	Tyr
1				5			

<210> 217

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 217

Glu	Ala	Glu	Gly	Ser	Gly	Arg	Glu	Gly	Asn	Phe	Tyr	Glu	Arg	Ser
1				5					10					15

<210> 218

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 218

Trp	Asp	Arg	Asp	Arg	Gln	Gln	Tyr
1				5			

<210> 219

<211> 7
 <212> PRT
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<220>
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<400> 219

Phe Thr Arg Ser Asp Asp Tyr
 1 5

<210> 220
 <211> 8
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<220>
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<400> 220

Ser Thr Pro Arg Gly Asp Ser Tyr
 1 5

<210> 221
 <211> 7
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<220>
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<400> 221

Phe Thr Arg Asp Thr Asp Tyr
 1 5

<210> 222
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 222

Trp Thr Thr Leu Gly Thr Phe

1 5

<210> 223
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 223

Trp Val Arg Asp Gly Gln Gln Tyr
 1 5

<210> 224
 <211> 13
 <212> PRT
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<220>
 <223> Synthetic polymer

<400> 224

Lys Ala Ile Pro Val Tyr Gly Ser Thr Val Glu Asp Tyr
 1 5 10

<210> 225
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 <212> PRT
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<220>
 <223> Synthetic polymer

<400> 225

Lys Ala Ala Ala Thr His Leu Ser Thr Val Ala Asp Tyr
 1 5 10

<210> 226
 <211> 7
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<220>
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<400> 226

Phe Gly Arg Phe Asp Asp Tyr
1 5

<210> 227

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 227

Trp Gly Val Lys Thr Gly Pro Glu Ser Gly Ser Gly Thr Leu
1 5 10

<210> 228

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 228

Phe Thr Arg Asp Glu Asp Tyr
1 5

<210> 229

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 229

Arg Leu Thr Thr Glu Tyr Asp Tyr Ala Tyr
1 5 10

<210> 230

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 230

Phe Thr Arg Gly Asn Asp Tyr
1 5

<210> 231

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 231

Phe Gln Ser Ser Gly Ile Asp
1 5

<210> 232

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 232

Phe Ser Pro Thr Asp Asp Phe
1 5

<210> 233

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 233

Lys Ala Ile Pro Ile Tyr Gly Ser Thr Ala Glu Asp Tyr
1 5 10

<210> 234
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 234

Phe Ser Leu Thr Asp Asp Tyr
 1 5

<210> 235
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 235

Trp Thr Arg Asp Arg Gln Gln Tyr
 1 5

<210> 236
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 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 236

Phe Thr Arg Asp Glu Asp Phe
 1 5

<210> 237
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 237

Glu Val Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Gly Ala
1 5 10

<210> 238
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 238

Pro Gly Trp Asp Tyr
1 5

<210> 239
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 239

Tyr Asp Arg Ser Ala Thr Ala Tyr
1 5

<210> 240
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 240

Ala Ser Ser Val Leu Ser Gly Thr Val Asp Tyr
1 5 10

<210> 241
<211> 8
<212> PRT
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<220>

<223> Synthetic polymer

<400> 241

Phe Ala Ala Asp Gly Met Glu Tyr
1 5

<210> 242

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 242

Lys Ala Ala Ala Ser Tyr Val Ser Thr Val Ala Asp Tyr
1 5 10

<210> 243

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 243

Thr Ala Lys Asp Asp Tyr
1 5

<210> 244

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 244

Phe Thr Gly Trp Gly Lys Glu Asp Tyr
1 5

<210> 245

<211> 8
 <212> PRT
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<220>
 <223> Synthetic polymer

<400> 245

Trp Ala Ala Asp Tyr Gln Gln Tyr
 1 5

<210> 246
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 246

Tyr Asp Arg Ser Ala Thr Pro Tyr
 1 5

<210> 247
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 247

Trp Ala Arg Asp Arg Gln Gln Tyr
 1 5

<210> 248
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 248

Trp Thr Lys Asp Arg Gln Gln Tyr

1 5

<210> 249
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 249

Phe Thr Arg Thr Tyr Asp Tyr
 1 5

<210> 250
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 250

Ala Ser Ser Ile Leu Ser Gly Thr Val Asp Tyr
 1 5 10

<210> 251
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 251

Trp Ala Ala Asp Tyr Gln Gln Tyr
 1 5

<210> 252
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 252

Lys Pro Ala Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr
1 5 10

<210> 253

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 253

Phe Ala Ala Asp Gly Met Glu Tyr
1 5

<210> 254

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 254

Phe Gly Ser Gly Gly Gly
1 5

<210> 255

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 255

Ala Ser Ser Val Leu Ser Gly Thr Ala Asp Tyr
1 5 10

<210> 256

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 256

Val Ala Leu Lys Ala Glu Tyr
1 5

<210> 257

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 257

Glu Ala Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Glu Arg Ser
1 5 10 15

<210> 258

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 258

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Thr Asp Asn Ala Gly Asn Thr Val Tyr Leu

Ala Phe Gln Ser Ser Gly Ile Asp Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 260
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 260

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly

115

120

125

Ser His His His His His His
130 135

<210> 261
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 261

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ser Asp Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Ser Thr Tyr Ile Asp Ser Ala Lys
50 55 60

Gly Arg Ala Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Ala Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Asn Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 262
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 262

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Val Phe Ser Ile Asn
 20 25 30

Ala Trp Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Pro Ser Val Asn
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95

Ala Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
 115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
 130 135 140

<210> 263
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 263

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Leu Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Pro Ala Leu Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Asp Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Trp Cys Lys
85 90 95

Ala Phe Thr Arg Asp Lys Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 264

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (108)..(108)

<223> Xaa can be any naturally occurring amino acid

<400> 264

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Ser Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Ala Val Thr Val Gly Gly Arg Tyr Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Asn Arg Phe Thr Ile Ser Arg Asp Asp Ala Gln Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Asp Arg Asp Arg Gln Gln Tyr Trp Gly Xaa Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 265

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 265

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
		Ala	Ala
		25	Ser
		Gly	Arg
		Val	Phe
		30	Ser
		Ile	Asn
Ala	Met	Gly	Trp
	35	Tyr	Arg
		Gln	Ala
		40	Pro
		Gly	Lys
		45	Gln
		Arg	Glu
		Leu	Val
Ala	Ala	Ile	Thr
	50	Asn	Gln
		Gly	Ala
		55	Thr
		Thr	Tyr
		60	Ala
		Asp	Ser
		Val	Lys
Gly	Arg	Phe	Thr
65		Ile	Ser
		70	Arg
		Asp	Thr
		Ala	Gly
		75	Asn
		Thr	Val
		Tyr	Leu
		80	
Gln	Met	Asn	Ser
		85	Leu
		Arg	Pro
		Glu	Asp
		90	Thr
		Ala	Val
		His	Tyr
		95	Cys
		Lys	
Ala	Phe	Thr	Arg
		100	Thr
		Asp	Asp
		Tyr	Trp
		105	Gly
		Gln	Gly
		Thr	Gln
		110	Val
		Thr	
Val	Ser	Ser	Ala
		115	Ala
		Ala	Tyr
		120	Pro
		Tyr	Asp
		Val	Pro
		125	Asp
		Tyr	Gly
		Ser	
His	His	His	His
		130	His

<210> 266
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 266

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly
1			5				10						15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Val	Asn	Ile	Asp	Thr	Leu	Asn
		20						25					30		

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Ser Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Gly Ile Thr Gly Ser Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Ser Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Thr Leu Gln Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Tyr Asp Arg Ser Ser Thr Pro Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 267
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 267

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Val Tyr Gly Asp Ser Val Lys

50

55

60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Gly Asn Thr Val His Leu
65 70 75 80

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 268
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 268

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Phe Leu Ser Leu Ser Cys Ala Ala Ser Gly Ser Met His Ser Val Asn
20 25 30

Ser Met Ala Trp Tyr Arg Gln Val Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Leu Ala Tyr Ala Pro Ser Val Asn
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Tyr Ala Lys Asn Thr Ile His Leu
65 70 75 80

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Gln Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Leu Asn Ser Ala Thr Thr Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 269
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 269

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Asp Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp His Arg Pro Ala Arg Gly Asn Glu Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Tyr Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr

100

105

110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 270
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 270

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Arg Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asp
20 25 30

Ala Met Gly Trp Tyr Arg Pro Ala His Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 271
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 271

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Leu Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Phe Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Trp Tyr Asp Pro Leu Val Ile Glu Tyr Tyr Asp Asn Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 272

<211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 272

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Ala
 20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Arg Ala Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Glu Asn Thr Val Ala Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
 85 90 95

Ala Lys Ala Asp His Asn Asp Tyr Trp Gly Gln Gly Thr Gln Ile Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His
 130

<210> 273
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 273

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ile Gly Asn Ile Ala Ser Ile Thr
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Ala Ser Ala Ser Arg Thr Thr Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Gln Pro Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Lys Gly Phe Arg Ser Gly Ala Asp Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp
115 120 125

Tyr Gly Ser His His His His His His
130 135

<210> 274

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 274

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu His Glu Gly Val
35 40 45

Ser Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr Tyr Asp Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Glu Val Pro Ser Thr Tyr Ser Cys Ser Gly Phe Arg Glu Asp
100 105 110

Tyr Lys Gly Lys Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 275
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 275

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val

35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Val Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Ser Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 276
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 276

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Ser Ile Phe Arg Ser Tyr
20 25 30

Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys
50 55 60

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Gly Arg Phe Thr Ile Ser Arg Glu Asp Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Thr Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 277
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 277

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Trp Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Ser Ile Val Ser Ile Asn
20 25 30

Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ser Ile Thr Asn Gln Gly Ile Arg Asn Tyr Ser Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Val Lys Asn Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys

85

90

95

Gly Phe Ala Gly Trp Gly Lys Glu Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His
130 135

<210> 278
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 278

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Ala
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Glu Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Pro Thr Gly Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 279
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 279

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Leu Ala Ser Arg Ser Phe Ser Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Ile Ala Val Asn
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His

130

135

140

<210> 280
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 280

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Ala Met Gly Tyr Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Ser Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Met Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ser Pro Val Tyr Gly Ser Thr Val Glu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 281
<211> 135
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 281

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Thr Ser Phe Ser Ile Asn
20 25 30

Gly Met Ala Trp Tyr Arg Gln Ala Pro Gly Gly Gln Arg Glu Leu Val
35 40 45

Gly Gly Ile Thr Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Arg Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Thr Ser Thr Pro Arg Gly Asp Ser Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 282

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 282

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Thr Tyr
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Gly Leu Val
35 40 45

Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Glu Ala Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Glu Arg
100 105 110

Ser Trp Tyr Gln Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His
145

<210> 283
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 283

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Glu Thr Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
		25	Ala
			Ala
			Ser
			Gly
			Ser
			Ile
			Phe
			Ser
			Ile
			Asn
			30
Ala	Met	Gly	Trp
	35	Tyr	Arg
		Gln	Ala
		40	Pro
			Gly
			Lys
			Gln
			Arg
			Glu
			Leu
			Val
			45
Ala	Ala	Ile	Thr
	50	Asp	Gln
		Gly	Arg
		55	Leu
			Ala
			Tyr
			Ala
			Asp
			Ser
			Ala
			Lys
			60
Gly	Arg	Phe	Thr
65		Ile	Ser
		70	Arg
			Glu
			Asn
			Ala
			Arg
			Asn
			Thr
			Leu
			His
			Leu
			80
Gln	Met	Ser	Ser
		85	Leu
			Lys
			Ala
			Glu
			Asp
			Thr
			Ala
			Val
			Tyr
			Tyr
			Cys
			Thr
			95
Ile	Trp	Asp	Arg
		100	Asp
			Arg
			Gln
			Gln
			Tyr
			Trp
			Gly
			Gln
			Gly
			Thr
			Gln
			Val
			110
Thr	Val	Ser	Ser
		115	Ala
			Ala
			Ala
			Tyr
			Pro
			Tyr
			Asp
			Val
			Pro
			Asp
			Tyr
			Gly
			125
Ser	His	His	His
	130	His	His
		135	His

<210> 284
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 284

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5						10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ile	Phe	Asp	Ile	Asn
			20					25					30		

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Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Ser Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 285
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 285

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Thr Leu Phe Ser Ile Asn
20 25 30

Gly Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Arg Arg Glu Leu Val
35 40 45

Gly Gly Ile Thr Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys

50

55

60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Ala Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Thr Ser Thr Pro Arg Gly Asp Ser Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 286
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 286

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Asp Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Pro Ala Leu Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Ala Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ala Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

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Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Ser Cys Lys
85 90 95

Ala Phe Thr Arg Asp Thr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 287
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 287

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly
1 5 10 15

Ser Leu Gln Leu Ser Cys Ala Ala Ser Gly Arg Ala Phe Ser Thr Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Ser Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gln Gly Arg Ile Thr Leu Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Thr Lys Asn Thr Val Phe Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Trp Thr Thr Leu Gly Thr Phe Gly Gly Gln Gly Thr Gln Val Thr

100

105

110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 288
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 288

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Glu
1 5 10 15

Ser Leu Ser Leu Ser Cys Ala Val Ala Ser Gly Ser Ile Ile Ser Ile
20 25 30

Asn Ser Met Gly Trp Tyr Arg Gln Ala Pro Glu Lys Gln Arg Glu Leu
35 40 45

Val Ala Ala Ile Thr Val Asp Gly Arg Leu Ala Tyr Ala Asp Ser Ala
50 55 60

Lys His Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His
65 70 75 80

Leu His Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Trp Val Arg Asp Gly Gln Gln Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His
130 135

<210> 289
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 289

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Arg Asn Phe Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Thr Val Asp Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ile Pro Val Tyr Gly Ser Thr Val Glu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 290

<211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 290

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
 20 25 30

Ala Met Gly Trp Tyr Arg Gln Val Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Ile Ala Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Asp Val Tyr Tyr Cys Asn
 85 90 95

Ala Lys Ala Ala Ala Thr His Leu Ser Thr Val Ala Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
 115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
 130 135 140

<210> 291
 <211> 136
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 291

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Val Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Ala
85 90 95

Cys Lys Ala Phe Gly Arg Phe Asp Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His
130 135

<210> 292

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 292

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Tyr Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Gly Ile Thr Thr Gln Gly Arg Ile Thr Tyr Gly Asn Ser Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Gly Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Lys Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ser
85 90 95

Ala Trp Gly Val Lys Thr Gly Pro Glu Ser Gly Ser Gly Thr Leu Glu
100 105 110

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr
115 120 125

Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 293
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 293

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ile Gly Ile Asn
20 25 30

Ser Met Gly Tyr Tyr Arg Thr Ala Pro Gly Lys Gln Arg Glu Leu Val

35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 294
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 294

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Pro Gly Tyr
20 25 30

Val Met Ala Trp Phe Arg Gln Ser Pro Gly Gln Glu Arg Glu Phe Ala
35 40 45

Ala Ala Ile Asn Trp Arg Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Thr Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Ala Arg Leu Thr Thr Glu Tyr Asp Tyr Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
115 120 125

Asp Tyr Gly Ser His His His His His His
130 135

<210> 295
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 295

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Thr Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys

85

90

95

Ala Phe Thr Arg Gly Asn Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 296
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 296

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Val Ser Gly Arg Thr Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Leu Ser Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Ala Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Phe Gln Ser Ser Gly Ile Asp Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 297
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 297

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Ser Tyr
20 25 30

Thr Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Arg Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Pro Thr Asp Asp Phe Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His

130

<210> 298
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 298

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Phe Phe Ser Ile Asn
 20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Thr Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Asn Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
 85 90 95

Ala Lys Ala Ile Pro Ile Tyr Gly Ser Thr Ala Glu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
 115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
 130 135 140

<210> 299
 <211> 134
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 299

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Leu Thr Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 300

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 300

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Asp Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 301
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 301

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn

20

25

30

Ala Met Gly Trp Tyr Arg Pro Ala Leu Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Phe Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 302
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 302

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Arg Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Asp Leu Val
35 40 45

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Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Glu Tyr His Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Glu Val Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Gly Ala
100 105 110

Ser Trp Tyr Pro Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His
145

<210> 303
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 303

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Asp Ser Val Lys

50

55

60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Arg Pro Gly Trp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
100 105 110

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
115 120 125

His His His His
130

<210> 304
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 304

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Val Asn Ile Gly Ser Leu Asn
20 25 30

Ser Met Val Trp Tyr Arg Gln Ser Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Gly Ile Thr Gly Ser Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Ile Ala Lys Ser Thr Ala Tyr Leu
65 70 75 80

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Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Tyr Asp Arg Ser Ala Thr Ala Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 305
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 305

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Asn Tyr
20 25 30

Ala Val Gly Trp Trp Arg Gln Ala Pro Gly Lys Gln Arg Glu Phe Val
35 40 45

Ala Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser Tyr Ser Asn Ser Ala
50 55 60

Lys Gly Arg Phe Ala Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Ser Ser Val Leu Ser Gly Thr Val Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 306
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 306

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Gly Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Asp Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 307
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 307

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Ile Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ala Ala Ser Tyr Val Ser Thr Val Ala Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 308

<211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 308

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Val Phe Ser Ile Asn
 20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Glu Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Thr Gln Gly Arg Thr Thr Tyr Glu Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Gln Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
 85 90 95

Ala Trp Thr Ala Lys Asp Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His
 130

<210> 309
 <211> 136
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 309

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Arg Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ile Gly Ser Ile Phe Glu Ile Asn
20 25 30

Ser Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Ile Thr Asn Tyr Ala Asn Ser Val Gln
50 55 60

Gly Arg Ser Thr Ile Ser Arg Asp Asn Val Asn Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Thr Gly Trp Gly Lys Glu Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His
130 135

<210> 310

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 310

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Asn Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Val Gly Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 311
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 311

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Asn Ile Gly Thr Leu Asn
20 25 30

Ser Met Ala Trp Tyr Arg Glu Ala Pro Gly Lys Gln Arg Glu Leu Val

35 40 45

Ala Gly Ile Thr Gly Gly Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Ile Ala Lys Ser Thr Ala Tyr Leu
65 70 75 80

Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Tyr Asp Arg Ser Ala Thr Pro Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 312
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 312

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gln Gly Arg Ser Thr Tyr Ala Asp Ser Ala Lys
50 55 60

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Gly Arg Phe Thr Ile Ser Leu Gly Asn Ala Arg Asn Thr Val Asn Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 313
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 313

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Gly Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Met Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Thr Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Asp Leu
65 70 75 80

His Met Asn Ser Leu Arg Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys

85

90

95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 314
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 314

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Asn Arg Phe Thr Ile Ser Arg Glu Asn Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Lys Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His
 130 135

<210> 315
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 315

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Ser Ser Ile Asn
 20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Gly Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asp Asn Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
 85 90 95

Ala Phe Thr Arg Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His

130

<210> 316
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 316

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Asn Tyr
 20 25 30

Ala Val Ala Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Phe Val
 35 40 45

Ala Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser Tyr Ser Asn Ala Ala
 50 55 60

Lys Gly Arg Phe Ala Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Ala Ser Ser Ile Leu Ser Gly Thr Val Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
 115 120 125

Pro Asp Tyr Gly Ser His His His His His His
 130 135

<210> 317
 <211> 135
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 317

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Gly Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Met Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Thr Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Asp Leu
65 70 75 80

His Met Asn Ser Leu Arg Pro Glu Asp Ser Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 318

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 318

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Arg Ser Phe Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Pro Ala Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 319
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 319

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Pro Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn

20

25

30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Asp Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His
130 135

<210> 320
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (54)..(54)
<223> Xaa can be any naturally occurring amino acid

<400> 320

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ile Asn

20

25

30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Xaa Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Thr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Phe Gly Ser Gly Gly Gly Val Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
115 120 125

His His His His His
130

<210> 321
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 321

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Asn Tyr
20 25 30

Ala Val Ala Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

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Ala Ala Ile Trp Trp Ala Ser Gly Gly Ile Ser Tyr Ala Asn Ser Ala
50 55 60

Lys Gly Arg Phe Val Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Ser Ser Val Leu Ser Gly Thr Ala Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 322
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 322

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu

65		70		75		80
Gln Met Asn Ser	Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys	85	90	95		
Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr		100	105	110		
Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser		115	120	125		
His His His His His His		130				
<210> 323						
<211> 145						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> Synthetic polymer						
<400> 323						
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly		5	10	15		
1						
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr		20	25	30		
Ala Met Ala Trp Phe Arg Gln Ala Pro Gly Met Glu Arg Glu Leu Val		35	40	45		
Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val		50	55	60		
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr		65	70	75	80	
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys		85	90	95		

Ala Ala Glu Ala Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Glu Arg
100 105 110

Ser Trp Tyr Gln Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His
145

<210> 324
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 324

His His His His His His
1 5

<210> 325
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 325

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
1 5 10

<210> 326
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 326

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
1 5 10 15

His His His

<210> 327

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 327

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Thr
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

Leu Val Ala Leu Lys Ala Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser
115

<210> 328
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 328

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
 20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
 35 40 45

Ala Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Thr
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
 85 90 95

Leu Val Ala Leu Lys Ala Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 329
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 329

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Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Thr
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

Leu Val Ala Leu Lys Ala Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 330
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 330

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val

35 40 45

Ala Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

Leu Val Ala Leu Lys Ala Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 331
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 331

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Arg Ile Thr Asn Leu Gly Leu Pro Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

Leu Val Ala Leu Lys Ala Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 332
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 332

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser

115

<210> 333
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 333

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
 20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
 85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 334
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 334

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 335

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 335

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

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Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 336
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 336

Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu

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Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160

Leu Arg Ser Lys Glu
165

<210> 338
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 338

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys

100

105

110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160

Leu Arg Ser Lys Glu
165

<210> 339
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 339

Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
20 25 30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95

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His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
100 105 110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160

Thr Gly Tyr Leu Arg Asn
165

<210> 340
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 340

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile

85

90

95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 341
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 341

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln
50 55 60

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

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Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
100 105 110

Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys
115 120 125

Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln
130 135 140

<210> 342
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 342

Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu
1 5 10 15

Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln
35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln
50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu
65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp
85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu

100

105

110

Met Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile
115 120 125

Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
130 135 140

Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln
145 150 155 160

Glu Arg Leu Arg Arg Lys Glu
165

<210> 343
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 343

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

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Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Arg Leu Arg Arg Lys Glu
165

<210> 344
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 344

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu

85

90

95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Arg Leu Arg Arg Lys Glu
165

<210> 345
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 345

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser
65 70 75 80

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Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Arg Leu Arg Arg Lys Glu
165

<210> 346
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 346

Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu
1 5 10 15

Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln
35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln
50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu

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Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu
65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp
85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu
100 105 110

Met Asn Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile
115 120 125

Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
130 135 140

Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Cys Thr Asn Leu Gln
145 150 155 160

Glu Arg Leu Arg Arg Lys Glu
165

<210> 348
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 348

Glu Glu Phe Gly Asn Gln
1 5

<210> 349
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 349

Glu Glu Phe Asp Gly Asn Gln
1 5

<210> 350
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 350

Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys
1 5 10 15

Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu
20 25 30

Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys
35 40 45

Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
50 55 60

Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile
65 70 75 80

Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe
85 90 95

Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg
100 105 110

Gln Glu Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe
115 120 125

Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser
130 135 140

Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys

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Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Ser
145 150 155 160

Leu Thr Arg Lys Asp
165

<210> 352
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 352

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
1 5 10 15

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe

130

135

140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 353

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 353

Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala Arg Gln
1 5 10 15

His Pro Lys Met His Leu Ala His Ser Asn Leu Lys Pro Ala Ala His
20 25 30

Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Asn
35 40 45

Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn Asn Ser
50 55 60

Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln Val Val
65 70 75 80

Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro Leu Tyr
85 90 95

Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe His Val
100 105 110

Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln Glu Pro
115 120 125

Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr Gln Gly
130 135 140

Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val Leu Ser
145 150 155 160

Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
165 170

<210> 354
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 354

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1 5 10 15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu

130

135

140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 355
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 355

Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
1 5 10 15

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Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
20 25 30

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
35 40 45

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
50 55 60

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65 70 75 80

Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
100 105 110

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
130 135 140

Asp Phe Thr Met Gln Phe Val Ser Ser
145 150

<210> 356
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 356

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys

20

25

30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr
130

<210> 357
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 357

His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
1 5 10 15

Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile
20 25 30

Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
35 40 45

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Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
50 55 60

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
65 70 75 80

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
85 90 95

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
100 105 110

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
115 120 125

Ser

<210> 358
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 358

Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His
1 5 10 15

Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr
20 25 30

Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser
35 40 45

Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn
50 55 60

Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn

65		70		75		80									
Glu	Glu	Thr	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	Glu	Phe	Glu
			85						90					95	
Val	Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln
		100						105					110		
Ala	Arg	Ala	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln
		115					120					125			
Lys	Lys	Ala	Lys	Asn	Leu	Asp	Ala	Ile	Thr	Thr	Pro	Asp	Pro	Thr	Thr
	130					135					140				
Asn	Ala	Ser	Leu	Thr	Thr	Lys	Leu	Gln	Ala	Gln	Asn	Gln	Trp	Leu	Gln
145					150					155					160
Asp	Met	Thr	Thr	His	Leu	Ile	Leu	Arg	Ser	Phe	Lys	Glu	Phe	Leu	Gln
				165					170					175	
Ser	Ser	Leu	Arg	Ala	Leu	Arg	Gln	Met							
		180						185							
<210> 359															
<211> 114															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic polymer															
<400> 359															
Ser	Pro	Gly	Pro	Val	Pro	Pro	Ser	Thr	Ala	Leu	Arg	Glu	Leu	Ile	Glu
1				5					10					15	
Glu	Leu	Val	Asn	Ile	Thr	Gln	Asn	Gln	Lys	Ala	Pro	Leu	Cys	Asn	Gly
			20					25					30		
Ser	Met	Val	Trp	Ser	Ile	Asn	Leu	Thr	Ala	Gly	Met	Tyr	Cys	Ala	Ala
		35					40					45			

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Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
100 105 110

Phe Asn

<210> 360
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 360

Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
1 5 10 15

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
20 25 30

Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
35 40 45

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
50 55 60

Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
65 70 75 80

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met

85

90

95

Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys
100 105 110

Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
115 120 125

Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
130 135 140

His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
145 150 155 160

Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
165 170 175

Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
180 185 190

Asp Leu

<210> 361
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 361

Met Lys Pro Lys Met Lys Tyr Ser Thr Asn Lys Ile Ser Thr Ala Lys
1 5 10 15

Trp Lys Asn Thr Ala Ser Lys Ala Leu Cys Phe Lys Leu Gly Lys Ser
20 25 30

Gln Gln Lys Ala Lys Glu Val Cys Pro Met Tyr Phe Met Lys Leu Arg
35 40 45

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Ser Gly Leu Met Ile Lys Lys Glu Ala Cys Tyr Phe Arg Arg Glu Thr
50 55 60

Thr Lys Arg Pro Ser Leu Lys Thr Gly Arg Lys His Lys Arg His Leu
65 70 75 80

Val Leu Ala Ala Cys Gln Gln Gln Ser Thr Val Glu Cys Phe Ala Phe
85 90 95

Gly Ile Ser Gly Val Gln Lys Tyr Thr Arg Ala Leu His Asp Ser Ser
100 105 110

Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu Ser Thr
115 120 125

Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr Glu
130 135 140

Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys Val Leu
145 150 155 160

Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly Asp Gly
165 170 175

Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp Phe
180 185 190

Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys Cys
195 200 205

Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Met His
210 215 220

Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe Ile
225 230 235 240

Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser Ser Glu
245 250 255

Asn	Leu	Cys	Thr	Glu	Asn	Ile	Leu	Phe	Lys	Leu	Ser	Glu	Thr
			260					265					270

<210> 362
 <211> 10
 <212> PRT
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<220>
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<400> 362

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Met	Ser
1				5					10

<210> 363
 <211> 17
 <212> PRT
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<220>
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<400> 363

Thr	Ile	Asn	Trp	Asn	Gly	Gly	Ser	Ala	Glu	Tyr	Ala	Glu	Pro	Val	Lys
1				5					10					15	

Gly

<210> 364
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 364

Cys	Ile	Arg	Val	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Pro	Val	Lys
1				5					10					15	

Gly

<210> 365
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 365

Lys Asp Ala Asp Leu Val Trp Tyr Asn Leu Ser
 1 5 10

<210> 366
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 366

Lys Asp Ala Asp Leu Val Trp Tyr Asn Leu Arg
 1 5 10

<210> 367
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 367

Ala Gly Ser Leu Tyr Thr Cys Val Gln Ser Ile Val Val Val Pro Ala
 1 5 10 15

Arg Pro Tyr Tyr Asp Met Asp Tyr
 20

<210> 368
 <211> 132
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 368

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Asn Trp Asn Gly Gly Ser Ala Glu Tyr Ala Glu Pro Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Leu Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ala Asp Leu Val Trp Tyr Asn Leu Ser Thr Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
115 120 125

Asp Tyr Gly Ser
130

<210> 369

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 369

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Asn Trp Asn Gly Gly Ser Ala Glu Tyr Ala Glu Pro Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Leu Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ala Asp Leu Val Trp Tyr Asn Leu Arg Thr Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
115 120 125

Asp Tyr Gly Ser
130

<210> 370
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 370

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20

25

30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Arg Val Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Pro Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Ala Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Ser Leu Tyr Thr Cys Val Gln Ser Ile Val Val Val Pro
100 105 110

Ala Arg Pro Tyr Tyr Asp Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser
145

<210> 371
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 371

Gly Arg Ser Phe Ser Ser Tyr Thr Leu Ala
1 5 10

<210> 372
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 372

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Gly
1				5					10

<210> 373

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 373

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Ile	Met	Gly
1				5					10

<210> 374

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 374

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Gly
1				5					10

<210> 375

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 375

Gly	Arg	Thr	Ser	Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Gly
1				5									10

<210> 376
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 376

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Gly
1				5					10

<210> 377
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 377

Gly	Leu	Thr	Phe	Ser	Asn	Tyr	Ile	Met	Gly
1				5					10

<210> 378
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 378

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Gly
1				5					10

<210> 379
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 379

Gly Arg Thr Phe Ser Ser Asp Thr Met Gly
1 5 10

<210> 380
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 380

Gly Leu Thr Phe Ser Asn Tyr Ile Met Gly
1 5 10

<210> 381
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 381

Gly Phe Thr Leu Asp Tyr Tyr Gly Ile Gly
1 5 10

<210> 382
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 382

Gly His Thr Phe Ser Ser Tyr Thr Met Gly
1 5 10

<210> 383
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 383

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Val	Ile	Gly
1				5					10

<210> 384

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 384

Gly	Phe	Ala	Phe	Asp	Gly	Tyr	Ala	Ile	Gly
1				5					10

<210> 385

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 385

Gly	Phe	Ala	Phe	Gly	Phe	Phe	Asp	Met	Thr
1				5					10

<210> 386

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 386

Gly	Arg	Thr	Phe	Ser	Asn	Tyr	Val	Ile	Gly
1				5					10

<210> 387

<211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 387

Gly Ser Ile Phe Ser Ile Asn Val Met Gly
 1 5 10

<210> 388
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 388

Gly Arg Thr Phe Ser Asn Tyr Asn Val Gly
 1 5 10

<210> 389
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 389

Gly His Thr Phe Ser Ser Tyr Thr Met Gly
 1 5 10

<210> 390
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 390

Gly Arg Thr Phe Ser Thr Tyr Pro Val Gly

1

5

10

<210> 391
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 391

Gly Arg Thr Phe Ser Asn Tyr Ala Met Gly
 1 5 10

<210> 392
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 392

Gly Arg Thr Phe Ser Asp Tyr Arg Met Gly
 1 5 10

<210> 393
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 393

Gly Leu Thr Phe Ser Asn Tyr Ile Met Ala
 1 5 10

<210> 394
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 394

Gly	Arg	Thr	Phe	Ser	Asn	Ser	Val	Met	Gly
1				5					10

<210> 395

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 395

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Ile	Ile	Gly
1				5					10

<210> 396

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 396

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Val	Met	Gly
1				5					10

<210> 397

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 397

Gly	Gly	Thr	Phe	Ser	Asn	Tyr	Val	Met	Gly
1				5					10

<210> 398

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 398

Gly	Arg	Thr	Phe	Ser	Asn	Tyr	Gly	Ile	Gly
1				5					10

<210> 399

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 399

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Ile	Ala
1				5					10

<210> 400

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 400

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Thr	Val	Ala
1				5					10

<210> 401

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 401

Gly	Phe	Pro	Phe	Asp	Asp	Tyr	Ala	Ile	Ala
1				5					10

<210> 402
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 402

Gly	Arg	Thr	Phe	Ser	Ser	Tyr	Val	Met	Gly
1				5					10

<210> 403
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 403

Gly	Arg	Thr	Leu	Ser	Ser	Asn	Pro	Met	Ala
1				5					10

<210> 404
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 404

Gly	Phe	Thr	Phe	Asp	Asn	Tyr	Ala	Ile	Gly
1				5					10

<210> 405
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 405

Gly Arg Ala Phe Ser Ser Tyr Phe Met Gly
1 5 10

<210> 406
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 406

Thr Pro Thr Phe Ser Ser Tyr Asn Met Gly
1 5 10

<210> 407
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 407

Gly Phe Thr Phe Asp Asp Tyr Ala Ile Ala
1 5 10

<210> 408
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 408

Gly Gly Thr Phe Ser Gly Tyr Ile Met Gly
1 5 10

<210> 409
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 409

Gly	Arg	Ser	Phe	Ser	Ser	Tyr	Thr	Ile	Ala
1				5					10

<210> 410

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 410

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 411

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 411

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 412

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 412

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 413

<211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 413

Gly	Phe	Thr	Phe	Asp	Gln	Tyr	Thr	Ile	Ala
1				5					10

<210> 414
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 414

Gly	Phe	Ala	Phe	Asp	Gly	Tyr	Ala	Ile	Gly
1				5					10

<210> 415
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 415

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Ala
1				5					10

<210> 416
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 416

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly

1

5

10

<210> 417
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 417

Gly Phe Thr Phe Asp Asp Tyr Thr Ile Gly
1 5 10

<210> 418
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 418

Gly Phe Ser Ser Asp Asp Tyr Thr Ile Gly
1 5 10

<210> 419
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 419

Gly Phe Ser Ser Asp Asp Tyr Thr Ile Gly
1 5 10

<210> 420
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 420

Gly	Phe	Ser	Phe	Asp	Asp	Tyr	Ala	Ile	Ala
1				5					10

<210> 421

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 421

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 422

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 422

Gly	Phe	Thr	Gly	Asn	Asp	Leu	Ala	Ile	Gly
1				5					10

<210> 423

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 423

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Ala
1				5					10

<210> 424

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 424

Glu	Gly	Thr	Leu	Ser	Ser	Tyr	Gly	Ile	Gly
1				5					10

<210> 425

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 425

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Ala
1				5					10

<210> 426

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 426

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Ile	Ala
1				5					10

<210> 427

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 427

Gly	Leu	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 428
 <211> 10
 <212> PRT
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<220>
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<400> 428

Gly	Leu	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 429
 <211> 10
 <212> PRT
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<220>
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<400> 429

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 430
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 430

Gly	Phe	Ser	Phe	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 431
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 431

Gly Phe Thr Phe Asp Asp Tyr Ala Ile Ala
1 5 10

<210> 432
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 432

Gly Phe Thr Phe Asp Asp Tyr Ala Ile Gly
1 5 10

<210> 433
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 433

Gly Phe Thr Phe Gly Asp Tyr Thr Ile Gly
1 5 10

<210> 434
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 434

Glu Gly Thr Phe Ser Ser Tyr Gly Ile Gly
1 5 10

<210> 435
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 435

Gly	Phe	Ser	Ser	Asp	Asp	Tyr	Thr	Ile	Gly
1				5					10

<210> 436

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 436

Gly	Val	Ser	Ile	Gly	Asp	Tyr	Asn	Ile	Gly
1				5					10

<210> 437

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 437

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Thr	Ile	Ala
1				5					10

<210> 438

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 438

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Thr	Ile	Ala
1				5					10

<210> 439

<211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 439

Ala	Ser	Ile	Thr	Trp	Gly	Gly	Gly	Asn	Thr	Tyr
1				5					10	

<210> 440
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 440

Ala	Ala	Thr	Val	Trp	Thr	Gly	Ala	Gly	Thr	Val
1				5					10	

<210> 441
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 441

Ala	Ala	Ile	Gly	Trp	Ser	Ala	Asp	Ile	Thr	Val
1				5					10	

<210> 442
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 442

Ala	Phe	Ile	Asp	Trp	Ser	Gly	Gly	Gly	Thr	Tyr

1

5

10

<210> 443
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 443

Ala Thr Ile Thr Trp Gly Gly Gly Ser Thr Tyr
1 5 10

<210> 444
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 444

Ala Ala Ile Ser Trp Ser Gly Gly Pro Thr Val
1 5 10

<210> 445
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 445

Ala Ala Ile Thr Trp Gly Gly Gly Ser Thr Val
1 5 10

<210> 446
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 446

Ala Ala Ile Thr Trp Ser Gly Val Ser Thr Val
1 5 10

<210> 447

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 447

Gly Ala Ile Met Trp Ser Gly Ala Phe Thr His
1 5 10

<210> 448

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 448

Ala Ala Ile Thr Trp Gly Gly Gly Ser Thr Val
1 5 10

<210> 449

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 449

Ser Cys Ile Ser Ser Ser Asp Arg Asn Thr Tyr
1 5 10

<210> 450

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 450

Ala	Phe	Ile	Asp	Trp	Ser	Gly	Gly	Gly	Thr	Tyr
1				5					10	

<210> 451

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 451

Ala	Val	Ile	Thr	Trp	Ser	Gly	Asp	Ser	Thr	Tyr
1				5					10	

<210> 452

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 452

Ala	Cys	Ile	Ser	Ser	Lys	Asp	Gly	Ser	Thr	Tyr
1				5					10	

<210> 453

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 453

Ser	Gly	Ile	Asn	Ser	Ile	Gly	Gly	Ser	Thr	Thr
1				5					10	

<210> 454
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 454

Ala	Val	Val	Thr	Trp	Ser	Gly	Asp	Ser	Thr	Tyr
1				5					10	

<210> 455
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 455

Ala	Lys	Ile	Thr	Asn	Phe	Gly	Ile	Thr	Ser
1				5					10

<210> 456
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 456

Ser	Phe	Ile	Ser	Trp	Ile	Ser	Asp	Ile	Thr	Tyr
1				5					10	

<210> 457
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 457

Ala Phe Ile Asp Trp Ser Gly Gly Gly Thr Tyr
1 5 10

<210> 458
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 458

Ala Val Ile Leu Trp Ser Gly Val Ser Thr Tyr
1 5 10

<210> 459
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 459

Ala Ala Ile Val Trp Ser Gly Gly Ser Thr Tyr
1 5 10

<210> 460
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 460

Ala Ala Ile Ser Ser Ser Gly Tyr His Thr Tyr
1 5 10

<210> 461
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 461

Ser	Cys	Ile	Ser	Ser	Pro	Asp	Gly	Ser	Thr	Tyr
1				5					10	

<210> 462

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 462

Ala	Ala	Val	Leu	Trp	Ser	Gly	Val	Ser	Thr	Ala
1				5					10	

<210> 463

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 463

Val	Ala	Ile	Thr	Trp	Asp	Gly	Ser	Ala	Thr	Thr
1				5					10	

<210> 464

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 464

Ala	Ala	Ile	Gly	Trp	Asn	Gly	Gly	Ile	Thr	Tyr
1				5					10	

<210> 465

<211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 465

Gly	Phe	Ile	Thr	Trp	Ser	Gly	Ala	Ser	Thr	Tyr
1				5					10	

<210> 466
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 466

Ala	Gly	Ile	Asn	Trp	Ser	Gly	Glu	Ser	Ala	Asp
1				5					10	

<210> 467
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 467

Ser	Cys	Ile	Glu	Arg	Ser	Asp	Gly	Ser	Thr	Tyr
1				5					10	

<210> 468
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 468

Ser	Cys	Ile	Ser	Asn	Thr	Asp	Ser	Ser	Thr	Tyr

1

5

10

<210> 469
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 469

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr
1 5 10

<210> 470
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 470

Ala Gln Ile Ser Trp Ser Ala Gly Ser Ile Tyr
1 5 10

<210> 471
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 471

Ala Gly Met Ser Trp Asn Pro Gly Pro Ala Val
1 5 10

<210> 472
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 472

Ser	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr
1				5					10	

<210> 473

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 473

Ala	Asn	Ile	Gly	Trp	Thr	Gly	Asp	Met	Thr	Tyr
1				5					10	

<210> 474

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 474

Ala	Ala	Ile	Ile	Trp	Ser	Gly	Ser	Met	Thr	Tyr
1				5					10	

<210> 475

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 475

Ser	Cys	Ile	Ser	Asn	Thr	Asp	Ser	Ser	Thr	Tyr
1				5					10	

<210> 476

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 476

Ala	Ala	Asn	Thr	Trp	Ser	Gly	Gly	Pro	Thr	Tyr
1				5					10	

<210> 477

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 477

Ser	Cys	Ile	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10

<210> 478

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 478

Ser	Cys	Tyr	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 479

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 479

Ser	Cys	Ile	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10

<210> 480
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 480

Gly Cys Ile Lys Ser Ser Asp Gly Thr Thr Gly
 1 5 10

<210> 481
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 481

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr
 1 5 10

<210> 482
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 482

Ala Ala Ile Ala Trp Ser Ala Gly Ser Thr Tyr
 1 5 10

<210> 483
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 483

Ser Cys Ile Ser Ser Lys Glu Gly Ser Thr Tyr
1 5 10

<210> 484
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 484

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Gly
1 5 10

<210> 485
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 485

Ser Cys Tyr Ser Ser Arg Asp Gly Thr Thr Gly
1 5 10

<210> 486
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 486

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly
1 5 10

<210> 487
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 487

Ser	Cys	Tyr	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 488

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 488

Ser	Cys	Phe	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 489

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 489

Ser	Cys	Ile	Ser	Asn	Thr	Asp	Ser	Ser	Thr	Phe
1				5					10	

<210> 490

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 490

Ser	Cys	Tyr	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 491

<211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 491

Ser	Cys	Ile	Ser	Asn	Thr	Asp	Ser	Ser	Thr	Tyr
1				5					10	

<210> 492
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 492

Ser	Cys	Ile	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 493
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 493

Gly	Gly	Ile	Asn	Trp	Ser	Gly	Asp	Ser	Thr	Asp
1				5					10	

<210> 494
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 494

Ser	Cys	Phe	Ser	Ser	Ser	Asp	Gly	Ser	Ala	Gly

1

5

10

<210> 495
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 495

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr
1 5 10

<210> 496
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 496

Ser Cys Phe Ser Thr Arg Asp Gly Asn Ala Gly
1 5 10

<210> 497
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 497

Ser Cys Phe Ser Ser Arg Asp Gly Ser Thr Gly
1 5 10

<210> 498
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 498

Ser	Cys	Phe	Ser	Ser	Arg	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 499

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 499

Ser	Cys	Ile	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10

<210> 500

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 500

Ser	Cys	Ile	Ser	Asn	Thr	Asp	Ser	Ser	Thr	Tyr
1				5					10	

<210> 501

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 501

Ser	Cys	Ile	Ser	Ser	Pro	Asp	Gly	Ser	Thr	Tyr
1				5					10	

<210> 502

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 502

Ser	Cys	Tyr	Ser	Ser	Ser	Asp	Gly	Asn	Thr	Gly
1				5					10	

<210> 503

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 503

Gly	Gly	Ile	Asn	Trp	Ser	Gly	Asp	Ser	Thr	Asp
1				5					10	

<210> 504

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 504

Ser	Cys	Phe	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Gly
1				5					10	

<210> 505

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 505

Ser	Cys	Ile	Ser	Ser	Gly	Asp	Gly	Thr	Thr	Tyr
1				5					10	

<210> 506
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 506

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly
 1 5 10

<210> 507
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 507

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly
 1 5 10

<210> 508
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 508

Ala Lys Gly Leu Arg Asn Ser Asp Trp Asp Leu Arg Arg Gly Tyr Glu
 1 5 10 15

Tyr Asp Tyr

<210> 509
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 509

Ala	Asp	Gln	Ala	Ser	Val	Pro	Pro	Pro	Tyr	Gly	Ser	Glu	Arg	Tyr	Asp
1				5					10					15	

Ile	Ala	Ser	Pro	Ser	Glu	Tyr	Asp	Tyr
			20				25	

<210> 510

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 510

Ala	Asn	Ser	Arg	Ala	Tyr	Tyr	Ser	Ser	Ser	Tyr	Asp	Leu	Gly	Arg	Leu
1				5					10					15	

Ala	Ser	Tyr	Asp	Tyr
			20	

<210> 511

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 511

Ala	Ala	Gln	Arg	Leu	Gly	Ser	Val	Thr	Asp	Tyr	Thr	Lys	Tyr	Asp	Tyr
1				5					10					15	

<210> 512

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 512

Ala Ser Val Lys Val Val Ala Gly Ser Gly Ile Asp Ile Ser Gly Ser
1 5 10 15

Arg Asn Tyr Asp Tyr
20

<210> 513

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 513

Ala Lys Arg Leu Asp Tyr Ser Ala Thr Asp Lys Gly Val Asp Leu Ser
1 5 10 15

Asp Glu Tyr Asp Tyr
20

<210> 514

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 514

Ala Ala Gly Gly Ser Gly Arg Leu Arg Asp Leu Lys Val Gly Gln Asn
1 5 10 15

Tyr Asp Tyr

<210> 515

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 515

Ala	Asp	Ser	Pro	Pro	Arg	Thr	Tyr	Ser	Ser	Gly	Ser	Val	Asn	Leu	Glu
1				5				10						15	

Asp	Gly	Ser	Glu	Tyr	Asp	Tyr
			20			

<210> 516

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 516

Val	Ile	Pro	Gly	Arg	Gly	Ser	Ala	Leu	Pro	Ile	Asp	Val	Gly	Lys	Ser
1				5				10						15	

Asp	Glu	Tyr	Glu	Tyr
			20	

<210> 517

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 517

Ala	Ala	Gly	Ala	Ser	Gly	Arg	Leu	Arg	Asp	Leu	Lys	Val	Gly	Gln	Asn
1				5				10						15	

Tyr	Asp	Tyr

<210> 518

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 518

Ala	Asp	Gly	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Ala	Gly	Pro
1				5					10					15	

Pro	Pro	Gly	Gly	Met	Asp	Tyr
			20			

<210> 519

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 519

Ala	Ala	Gln	Arg	Leu	Gly	Ser	Val	Thr	Asp	Tyr	Thr	Lys	Tyr	Asp	Tyr
1				5					10					15	

<210> 520

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 520

Ala	Ile	Pro	Pro	Arg	Ala	Tyr	Ser	Gly	Gly	Ser	Tyr	Ser	Leu	Lys	Asp
1				5					10					15	

Gln	Ser	Lys	Tyr	Glu	Tyr
			20		

<210> 521

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 521

Ala	Asp	Gly	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Ser	Ser	Ala	Gly	Pro
1				5					10					15	

Pro	Pro	Gly	Gly	Met	Asp	Tyr
			20			

<210> 522

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 522

Lys	Ser	Arg	Ser	Ser	Tyr	Ser	Asn	Asn
1				5				

<210> 523

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 523

Ala	Met	Pro	Pro	Arg	Ala	Tyr	Thr	Gly	Arg	Ser	Val	Ser	Leu	Lys	Asp
1				5				10						15	

Gln	Ser	Lys	Tyr	Glu	Tyr
			20		

<210> 524

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 524

Leu Asp Thr Thr Gly Trp Gly Pro Pro Pro Tyr Gln Tyr
1 5 10

<210> 525

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 525

Ala His Pro Pro Asp Pro Ser Arg Gly Gly Glu Trp Arg Leu Gln Thr
1 5 10 15

Pro Ser Glu Tyr Asp Tyr
20

<210> 526

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 526

Ala Ala Gln Arg Leu Gly Ser Val Thr Asp Tyr Thr Lys Tyr Asp Tyr
1 5 10 15

<210> 527

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 527

Val Pro Arg Ser His Phe Thr Thr Ala Gln Asp Met Gly Gln Asp Met
1 5 10 15

Gly Ala Pro Ser Trp Tyr Glu Tyr
20

<210> 528
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 528

Ala Val Leu Ile Arg Tyr Tyr Ser Gly Gly Tyr Gln Gly Leu Ser Asp
1 5 10 15

Ala Asn Glu Tyr Asp Tyr
20

<210> 529
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 529

Val Val Lys Tyr Leu Ser Gly Ser Tyr Ser Tyr Ala Gly Gln Tyr Asn
1 5 10 15

Phe

<210> 530
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 530

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Val Gly Pro

1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 531
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 531

Ala His Glu Ser Thr Tyr Tyr Ser Gly Thr Tyr Tyr Leu Thr Asp Pro
1 5 10 15

Arg Arg Tyr Val Tyr
20

<210> 532
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 532

Ala Val Pro Ala Arg Gly Leu Thr Met Asp Leu Glu Asn Ser Asp Ile
1 5 10 15

Tyr Asp His

<210> 533
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 533

Ala Ala Thr Leu Gln Val Thr Gly Ser Tyr Tyr Leu Asp Leu Ser Thr
1 5 10 15

Val Asp Ile Tyr Asp Asn
20

<210> 534
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 534

Ala Thr Leu Phe Arg Ser Asn Gly Pro Lys Asp Leu Ser Ser Gly Tyr
1 5 10 15

Glu Tyr Asp Tyr
20

<210> 535
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 535

Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr
1 5 10

<210> 536
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 536

Val Gly Ser Ala Asn Ser Gly Glu Phe Arg Phe Gly Trp Val Leu Lys

1 5 10 15

Pro Asp Leu Tyr Asn Tyr
20

<210> 537
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 537

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 538
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 538

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 539
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 539

Glu Arg Gly Tyr Ala Tyr Cys Ser Asp Asp Gly Cys Gln Arg Thr Gln
1 5 10 15

Asp Tyr Asp Tyr
20

<210> 540
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 540

Gly Ala Ala Arg Ala Trp Trp Ser Gly Ser Tyr Asp Tyr Thr Arg Met
1 5 10 15

Asn Asn Tyr Asp Tyr
20

<210> 541
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 541

Ala Glu Thr Ser Ala Asp Ser Gly Glu Phe Arg Phe Gly Trp Val Leu
1 5 10 15

Lys Pro Ser Leu Tyr Asp Tyr
20

<210> 542
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 542

Ala Ala Gly Ser Ala Tyr Ser Gly Ser Tyr Trp Asn Ile Thr Met Ala
1 5 10 15

Ala Asn Tyr Asp Tyr
20

<210> 543

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 543

Ala Gln Arg Ile Phe Gly Ala Gln Pro Met Asp Leu Ser Gly Asp Tyr
1 5 10 15

Glu Tyr

<210> 544

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 544

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 545

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 545

Ala	Arg	Asp	Tyr	Arg	Gly	Ile	Lys	Asp	Leu	Asp	Leu	Lys	Gly	Asp	Tyr
1				5					10					15	

Asp Tyr

<210> 546

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 546

Ala	Asp	Phe	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Ile	Trp	Tyr
1				5					10					15	

Gly	Pro	Pro	Pro	Arg	Gly	Met	Asp	Tyr
			20					25

<210> 547

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 547

Ala	Asp	Ser	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Arg	Trp	Tyr
1				5					10					15	

Gly	Pro	Pro	Pro	Gly	Gly	Met	Ala	Tyr
			20					25

<210> 548

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 548

Ala	Asp	Phe	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Asn	Trp	Tyr
1				5					10					15	

Gly	Pro	Pro	Pro	Gly	Gly	Met	Asp	Tyr
			20					25

<210> 549

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 549

Ala	Asp	Phe	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Ile	Trp	Tyr
1				5					10					15	

Gly	Pro	Pro	Pro	Gly	Gly	Met	Asp	Tyr
			20					25

<210> 550

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 550

Ala	Asp	Gly	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Ala	Gly	Pro
1				5					10					15	

Pro	Pro	Gly	Gly	Met	Asp	Tyr
			20			

<210> 551

<211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 551

Ala	Arg	Ile	Ile	Thr	Val	Ala	Thr	Met	Arg	Leu	Asp	Ser	Asp	Tyr	Asp
1				5				10						15	

Tyr

<210> 552
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 552

Ala	Asp	Gly	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Ser	Ala	Gly	Pro
1				5					10					15	

Pro	Pro	Gly	Gly	Met	Asp	Tyr
				20		

<210> 553
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 553

Ala	Asp	Ser	Asn	Val	Trp	Ser	Pro	Pro	Ile	Cys	Gly	Arg	Thr	Trp	Tyr
1				5					10					15	

Gly	Pro	Pro	Pro	Gly	Gly	Met	Asp	Tyr
				20				25

<210> 554
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 554

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr
 1 5 10 15

Gly Pro Pro Pro Gly Gly Met Ala Tyr
 20 25

<210> 555
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 555

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Asn Trp Tyr
 1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
 20 25

<210> 556
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 556

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ser Trp Tyr
 1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr

20

25

<210> 557
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 557

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp Tyr
 1 5 10 15

Gly Pro Pro Pro Gly Gly Met Glu Tyr
 20 25

<210> 558
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 558

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
 1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
 20

<210> 559
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 559

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp Tyr
 1 5 10 15

Gly Pro Pro Pro Gly Gly Met Ala Tyr
20 25

<210> 560
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 560

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 561
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 561

Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Lys Thr Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
20 25

<210> 562
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 562

Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr

1

5

10

<210> 563
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 563

Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Thr Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Ala Tyr
20 25

<210> 564
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 564

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 565
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 565

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
20 25

<210> 566
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 566

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
20 25

<210> 567
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 567

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
20 25

<210> 568
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 568

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr

1 5 10 15

Gly Pro Pro Pro Gly Gly Met Asp Tyr
20 25

<210> 569
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 569

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 570
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 570

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Val Gly Pro
1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 571
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 571

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ser Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Ala Tyr
20 25

<210> 572
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 572

Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr
1 5 10

<210> 573
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 573

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ser Trp Tyr
1 5 10 15

Gly Pro Pro Pro Gly Gly Met Glu Tyr
20 25

<210> 574
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 574

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly Pro

1 5 10 15

Pro Pro Gly Gly Met Asp Tyr
20

<210> 575
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 575

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Ser Ser Asn Trp Tyr
1 5 10 15

Gly Pro Pro Pro Arg Gly Met Asp Tyr
20 25

<210> 576
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 576

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr
1 5 10 15

Gly Pro Pro Pro Arg Gly Met Asp Tyr
20 25

<210> 577
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 577

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ser Phe Ser Ser Tyr
20 25 30

Thr Leu Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ser Ile Thr Trp Gly Gly Gly Asn Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Lys Gly Leu Arg Asn Ser Asp Trp Asp Leu Arg Arg Gly Tyr
100 105 110

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala
115 120 125

Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His
130 135 140

His His
145

<210> 578
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 578

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Asp Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
Ala	Phe	Ser	Gly
	25	Arg	Thr
Phe	Ser	Ser	Tyr
	30		
Thr	Met	Gly	Trp
	35	Phe	Arg
Gln	Gly	Pro	Gly
	40	Lys	Glu
Arg	Glu	Phe	Val
	45		
Ala	Ala	Thr	Val
	50	Trp	Thr
Gly	Ala	Gly	Thr
	55	Val	Tyr
Ala	Asp	Ser	Val
	60		
Lys	Gly	Arg	Phe
	65	Thr	Ile
Ser	Arg	Asp	Asn
	70	Ala	Lys
Asn	Thr	Val	Tyr
	75		80
Leu	Gln	Met	Asn
	85	Ser	Leu
Arg	Pro	Glu	Asp
	90	Thr	Ala
Val	Tyr	Tyr	Cys
	95		
Ala	Ala	Asp	Gln
	100	Ala	Ser
Val	Pro	Pro	Pro
	105	Tyr	Gly
Ser	Glu	Arg	Tyr
	110		
Asp	Ile	Ala	Ser
	115	Pro	Ser
Glu	Tyr	Asp	Tyr
	120	Trp	Gly
Gln	Gly	Thr	Gln
	125		
Val	Thr	Val	Ser
	130	Ser	Ala
Ala	Ala	Ala	Tyr
	135	Pro	Tyr
Asp	Val	Pro	Asp
	140	Tyr	
Gly	Ser	His	His
	145	His	His
	150	His	His

<210> 579
 <211> 148
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 579

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Ala
1			5					10					15		

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Ile Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Gly Trp Ser Ala Asp Ile Thr Val Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Met Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Asn Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asn Ser Arg Ala Tyr Tyr Ser Ser Ser Tyr Asp Leu Gly Arg
100 105 110

Leu Ala Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
115 120 125

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
130 135 140

His His His His
145

<210> 580
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 580

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr

20

25

30

Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Phe Ile Asp Trp Ser Gly Gly Gly Thr Tyr Tyr Asp Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Gln Arg Leu Gly Ser Val Thr Asp Tyr Thr Lys Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 581
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 581

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Gly Arg Thr
20 25 30

Phe Ser Ser Tyr Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
35 40 45

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Arg Glu Phe Val Ala Thr Ile Thr Trp Gly Gly Gly Ser Thr Tyr Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn
65 70 75 80

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
85 90 95

Val Tyr Tyr Cys Ala Ala Ser Val Lys Val Val Ala Gly Ser Gly Ile
100 105 110

Asp Ile Ser Gly Ser Arg Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 582
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 582

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Leu Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Ser Trp Ser Gly Gly Pro Thr Val Tyr Ala Asp His Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Val Asn Ser Leu Lys Pro Glu Asp Thr Ala Asp Tyr Tyr Cys
85 90 95

Ala Ala Lys Arg Leu Asp Tyr Ser Ala Thr Asp Lys Gly Val Asp Leu
100 105 110

Ser Asp Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
115 120 125

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
130 135 140

His His His His
145

<210> 583
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 583

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Asn Tyr
20 25 30

Ile Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Gly Gly Gly Ser Thr Val Tyr Ala Asp Ser Val
50 55 60

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Glu Gly Arg Phe Thr Ile Ser Arg Asp Gly Thr Lys Asn Thr Val Ser
65 70 75 80

Leu Gln Met Asn Ser Leu Leu Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Gly Gly Ser Gly Arg Leu Arg Asp Leu Lys Val Gly Gln
100 105 110

Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala
115 120 125

Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His
130 135 140

His His
145

<210> 584
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 584

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Arg Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Ser Gly Val Ser Thr Val Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr

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Leu Gln Met Asn Ala Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Ile Pro Gly Arg Gly Ser Ala Leu Pro Ile Asp Val Gly Lys
100 105 110

Ser Asp Glu Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
115 120 125

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
130 135 140

His His His His
145

<210> 586
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 586

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Asn Tyr
20 25 30

Ile Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Gly Gly Gly Ser Thr Val Tyr Ala Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Gly Thr Lys Asn Thr Val Ser
65 70 75 80

Leu Gln Met Asn Ser Leu Gln Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Ala Ala Gly Ala Ser Gly Arg Leu Arg Asp Leu Lys Val Gly Gln
100 105 110

Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala
115 120 125

Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His
130 135 140

His His
145

<210> 587
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 587

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Arg Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Gly Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 588
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 588

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly His Thr Phe Ser Ser Tyr
20 25 30

Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Phe Ile Asp Trp Ser Gly Gly Gly Thr Tyr Tyr Ala Asn Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Gln Arg Leu Gly Ser Val Thr Asp Tyr Thr Lys Tyr Asp

100

105

110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 589
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 589

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Val Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Val Ile Thr Trp Ser Gly Asp Ser Thr Tyr Ser Ser Asp Ser Leu
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ala Leu Asn Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ile Pro Pro Arg Ala Tyr Ser Gly Gly Ser Tyr Ser Leu Lys
100 105 110

Asp Gln Ser Lys Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
 130 135 140

His His His His His
 145

<210> 590
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 590

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Glu Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ile Ser Gly Phe Ala Phe Asp Gly Tyr Ala
 20 25 30

Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Ala
 35 40 45

Cys Ile Ser Ser Lys Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Met Ser Val Asp Lys Thr Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Ser Ser Ala Gly Pro
 100 105 110

Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
 115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His

130

135

140

His His His His His
145

<210> 591
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 591

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Gly Phe Phe
20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Ser Ile Gly Gly Ser Thr Thr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Glu Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ser Arg Ser Ser Tyr Ser Asn Asn Trp Arg Pro Pro Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 592
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 592

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Arg Gly
 1 5 10 15

Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Asn Tyr
 20 25 30

Val Ile Gly Trp Phe Arg Gln Ala Pro Gly Glu Glu Arg Glu Phe Val
 35 40 45

Ala Val Val Thr Trp Ser Gly Asp Ser Thr Tyr Ser Ser Asp Ser Leu
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Asn Leu Asn Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Met Pro Pro Arg Ala Tyr Thr Gly Arg Ser Val Ser Leu Lys
 100 105 110

Asp Gln Ser Lys Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
 115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
 130 135 140

His His His His His
 145

<210> 593

<211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 593

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
 20 25 30

Val Met Gly Trp Tyr Arg Gln Thr Pro Gly Lys Glu Arg Glu Leu Val
 35 40 45

Ala Lys Ile Thr Asn Phe Gly Ile Thr Ser Tyr Ala Asp Ser Ala Gln
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Gly Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95

Leu Asp Thr Thr Gly Trp Gly Pro Pro Pro Tyr Gln Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
 115 120 125

Pro Asp Tyr Gly Ser His His His His His His
 130 135

<210> 594
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 594

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Ala
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Asn Tyr
20 25 30

Asn Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ser Phe Ile Ser Trp Ile Ser Asp Ile Thr Tyr Tyr Ser Asp Ser Val
50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Met Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala His Pro Pro Asp Pro Ser Arg Gly Gly Glu Trp Arg Leu Gln
100 105 110

Thr Pro Ser Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
130 135 140

His His His His His
145

<210> 595

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 595

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly His Thr Phe Ser Ser Tyr
20 25 30

Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Phe Ile Asp Trp Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Gln Arg Leu Gly Ser Val Thr Asp Tyr Thr Lys Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 596
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 596

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Thr Tyr

20

25

30

Pro Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Val Ile Leu Trp Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Pro Arg Ser His Phe Thr Thr Ala Gln Asp Met Gly Gln Asp
100 105 110

Met Gly Ala Pro Ser Trp Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 597
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 597

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Asn Tyr
20 25 30

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Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Val Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Val Leu Ile Arg Tyr Tyr Ser Gly Gly Tyr Gln Gly Leu Ser
100 105 110

Asp Ala Asn Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
130 135 140

His His His His His
145

<210> 598
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 598

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Ala
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Arg Thr Phe Ser Asp Tyr
20 25 30

Arg Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Trp Val

35

40

45

Ala Ala Ile Ser Ser Ser Gly Tyr His Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Gly Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Val Lys Tyr Leu Ser Gly Ser Tyr Ser Tyr Ala Gly Gln Tyr
100 105 110

Asn Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

<210> 599
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 599

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Asn Tyr
20 25 30

Ile Met Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Ser Pro Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Val Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 600
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 600

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Asn Ser
20 25 30

Val Met Gly Trp Phe Arg Gln Pro Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Val Leu Trp Ser Gly Val Ser Thr Ala Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr

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Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Val Pro Ala Arg Gly Leu Thr Met Asp Leu Glu Asn Ser Asp
100 105 110

Ile Tyr Asp His Trp Gly Arg Gly Thr Gln Val Thr Val Ser Ser Ala
115 120 125

Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His
130 135 140

His His
145

<210> 602
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 602

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Val Met Gly Trp Phe Arg Gln Ala Leu Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Gly Trp Asn Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Ala Ala Thr Leu Gln Val Thr Gly Ser Tyr Tyr Leu Asp Leu Ser
100 105 110

Thr Val Asp Ile Tyr Asp Asn Trp Gly Gln Gly Thr Gln Val Thr Val
115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
130 135 140

His His His His His
145

<210> 603
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 603

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr Phe Ser Asn Tyr
20 25 30

Val Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Gly Phe Ile Thr Trp Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Thr Leu Phe Arg Ser Asn Gly Pro Lys Asp Leu Ser Ser Gly
100 105 110

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
130 135 140

His His His
145

<210> 604
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (112)..(112)
<223> Xaa can be any naturally occurring amino acid

<400> 604

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Thr Cys Thr Ala Ser Gly Arg Thr Phe Ser Asn Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Gly Ile Asn Trp Ser Gly Glu Ser Ala Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr Trp Xaa
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 605
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 605

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Glu Arg Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Gly Ser Ala Asn Ser Gly Glu Phe Arg Phe Gly Trp Val Leu

100

105

110

Lys Pro Asp Leu Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
115 120 125

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
130 135 140

His His His His His
145

<210> 606
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 606

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Thr Val Ala Trp Phe Arg Gln Ser Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Ser Thr Val His
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 607
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 607

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Phe Gly Phe Pro Phe Asp Asp Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val His
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr

115

120

125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 608
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 608

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Val Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Gln Ile Ser Trp Ser Ala Gly Ser Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Asn Asp Asn Ala Lys Arg Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Arg Gly Tyr Ala Tyr Cys Ser Asp Asp Gly Cys Gln Arg Thr
100 105 110

Gln Asp Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
130 135 140

His His His
145

<210> 609
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 609

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Ser Asn
20 25 30

Pro Met Ala Trp Phe Arg Gln Ala Ala Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Gly Met Ser Trp Asn Pro Gly Pro Ala Val Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Ala Ala Arg Ala Trp Trp Ser Gly Ser Tyr Asp Tyr Thr Arg
100 105 110

Met Asn Asn Tyr Asp Tyr Trp Gly Pro Gly Thr Gln Val Thr Val Ser
115 120 125

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His

130

135

140

His His His His
145

<210> 610
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 610

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Asp Asn Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Glu Thr Ser Ala Asp Ser Gly Glu Phe Arg Phe Gly Trp Val
100 105 110

Leu Lys Pro Ser Leu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 611
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 611

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Phe Ser Ser Tyr
20 25 30

Phe Met Gly Trp Phe Arg Gln Thr Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Asn Ile Gly Trp Thr Gly Asp Met Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ala Gly Ser Ala Tyr Ser Gly Ser Tyr Trp Asn Ile Thr Met
100 105 110

Ala Ala Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
115 120 125

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
130 135 140

His His His His

145

<210> 612
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 612

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Thr Pro Thr Phe Ser Ser Tyr
 20 25 30

Asn Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45

Ala Ala Ile Ile Trp Ser Gly Ser Met Thr Tyr Tyr Ala Asp Ser Met
 50 55 60

Lys Gly Arg Phe Thr Val Ser Ile Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Gln Arg Ile Phe Gly Ala Gln Pro Met Asp Leu Ser Gly Asp
 100 105 110

Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
 115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
 130 135 140

His
 145

<210> 613
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 613

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Phe Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
 35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Ser Ala Lys Asn Thr Val His
 65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
 100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
 115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 130 135 140

His His His His His His
 145 150

<210> 614

<211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 614

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Gly Tyr
 20 25 30

Ile Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45

Ala Ala Asn Thr Trp Ser Gly Gly Pro Thr Tyr Tyr Ser Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Val Tyr Gln Cys
 85 90 95

Ala Ala Arg Asp Tyr Arg Gly Ile Lys Asp Leu Asp Leu Lys Gly Asp
 100 105 110

Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
 115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
 130 135 140

His
 145

<210> 615
 <211> 151
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 615

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Thr Ser Gly Arg Ser Phe Ser Ser Tyr
20 25 30

Thr Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr
100 105 110

Gly Pro Pro Pro Arg Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 616

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 616

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Tyr Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Tyr Ser Ser Ser Asp Gly Ser Thr Gly Phe Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Ala Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 617

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 617

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Val Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Asn Trp Tyr
100 105 110

Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 618

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 618

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Gly Cys Ile Lys Ser Ser Asp Gly Thr Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 619
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 619

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Ala Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
		25	Ala
			Ala
			Ser
			Gly
			Phe
			Thr
			Phe
			Asp
			Gln
			Tyr
			30
Thr	Ile	Ala	Trp
	35	Phe	Arg
		Gln	Ala
		40	Pro
			Gly
			Lys
			Glu
			Arg
			Glu
			Gly
			Val
			45
Ser	Cys	Ile	Ser
	50	Asn	Thr
		55	Asp
			Ser
			Ser
			Thr
			Tyr
			Tyr
			Ala
			Asp
			Ser
			Val
			60
Lys	Gly	Arg	Phe
	65	Thr	Ile
		70	Ser
			Ser
			Asp
			Asn
			Ala
			Lys
			Asn
			Thr
			Val
			Tyr
			80
Leu	Gln	Met	Ser
		85	Ser
			Leu
			Lys
			Pro
			Glu
			Asp
			Thr
			Ala
			Val
			Tyr
			Tyr
			Cys
			95
Ala	Ala	Asp	Gly
		100	Asn
			Val
			Trp
			Ser
			Pro
			Pro
			Ile
			Cys
			Gly
			Ser
			Ala
			Gly
			110
Pro	Pro	Pro	Gly
		115	Gly
			Met
			Asp
			Tyr
			Trp
			Gly
			Lys
			Gly
			Thr
			Gln
			Val
			Thr
			125
Val	Ser	Ser	Ala
	130	Ala	Ala
		135	Tyr
			Pro
			Tyr
			Asp
			Val
			Pro
			Asp
			Tyr
			Gly
			Ser
			140
His	His	His	His
	145	His	His
		150	

<210> 620
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 620

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly
1				5					10					15	

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Ala Trp Ser Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Arg Ile Ile Thr Val Ala Thr Met Arg Leu Asp Ser Asp Tyr
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 621
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 621

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asp Gly Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val

35 40 45

Ser Cys Ile Ser Ser Lys Glu Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 622
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 622

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Ala Trp Phe Arg Arg Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

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Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Ser Asp Ser Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Arg Thr Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 623
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 623

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Tyr Ser Ser Arg Asp Gly Thr Thr Gly Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Ala Tyr Trp Gly Gln Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 624
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 624

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
50 55 60

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Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Asn Trp Tyr
100 105 110

Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 625
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 625

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Tyr Ser Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr

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Leu Glu Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 627
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 627

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Phe Gly Phe Ser Phe Asp Asp Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val His
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 628
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 628

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Tyr Ser Ser Ser Asp Gly Ser Thr Gly Phe Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Ala Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 629
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 629

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Val Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ile Ser Gly Phe Thr Gly Asn Asp Leu
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Asp Gln Arg Glu Gly
35 40 45

Ile Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val
65 70 75 80

His Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala

100

105

110

Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 630
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 630

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Ala Trp Phe Arg Arg Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Thr Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Lys Thr Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 631
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 631

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Glu Gly Thr Leu Ser Ser Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Gly Gly Ile Asn Trp Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp

115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 632
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 632

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
20 25 30

Thr Ile Ala Trp Phe Arg Arg Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Phe Ser Ser Ser Asp Gly Ser Ala Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Ser Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Thr Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Ala Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 633
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 633

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His

145

150

<210> 634
 <211> 152
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 634

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Val Ser Gly Leu Ser Ser Asp Asp Tyr
 20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Phe
 35 40 45

Ser Cys Phe Ser Thr Arg Asp Gly Asn Ala Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
 100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
 115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
 130 135 140

Gly Ser His His His His His His
 145 150

<210> 635
 <211> 152
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 635

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Val Ser Gly Leu Ser Ser Asp Asp Tyr
 20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Lys Arg Glu Gly Phe
 35 40 45

Ser Cys Phe Ser Ser Arg Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
 100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
 115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
 130 135 140

Gly Ser His His His His His His
 145 150

<210> 636

<211> 152
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 636

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ser Asp Asp Tyr
 20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Phe
 35 40 45

Ser Cys Phe Ser Ser Arg Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Arg Trp
 100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
 115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
 130 135 140

Gly Ser His His His His His His
 145 150

<210> 637
 <211> 151
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 637

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Ile Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr
100 105 110

Gly Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 638

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 638

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Phe Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Asn Thr Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val His
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 639

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (19)..(19)

<223> Xaa can be any naturally occurring amino acid

<400> 639

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Xaa Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Ser Pro Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Val Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 640

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 640

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Ala
1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Gly Asp Tyr
20 25 30

Thr Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Tyr Ser Ser Ser Asp Gly Asn Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ser Trp
100 105 110

Tyr Gly Pro Pro Pro Gly Gly Met Ala Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 641

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 641

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Glu Gly Thr Phe Ser Ser Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Gly Gly Ile Asn Trp Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Glu Ser Gly Val Trp Val Gly Gly Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 642

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 642

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
		Ala	Ala
		25	Ser
		Gly	Phe
		Ser	Ser
		30	Asp
			Asp
			Tyr
Thr	Ile	Gly	Trp
	35	Phe	Arg
		Gln	Ala
		40	Pro
		Gly	Lys
		Glu	Arg
		45	Glu
			Gly
			Ile
Ser	Cys	Phe	Ser
	50	Ser	Ser
		Ser	Asp
		55	Gly
		Ser	Thr
		Gly	Phe
		60	Ala
			Asp
			Ser
			Val
Lys	Gly	Arg	Phe
	65	Thr	Ile
		Ser	Ser
		70	Asp
		Asn	Ala
		75	Thr
			Asn
			Thr
			Val
			Tyr
			80
Leu	Gln	Met	Asn
		Ser	Leu
		85	Lys
		Pro	Glu
		90	Asp
		Thr	Ala
			Val
			Tyr
			95
			Tyr
			Cys
Ala	Ala	Asp	Phe
		100	Asn
			Val
			Trp
			Ser
			105
			Pro
			Pro
			Ile
			Cys
			Gly
			110
			Ser
			Ser
			Trp
Tyr	Gly	Pro	Pro
	115	Pro	Gly
		Gly	Gly
		120	Met
		Glu	Tyr
		Trp	Gly
			125
			Lys
			Gly
			Thr
			Gln
Val	Thr	Val	Ser
	130	Ser	Ala
		Ala	Ala
		135	Tyr
		Pro	Tyr
		140	Asp
			Val
			Pro
			Asp
			Tyr
Gly	Ser	His	His
	145	His	His
		150	His

<210> 643
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 643

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Asp
1				5					10					15	

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Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Val Ser Ile Gly Asp Tyr
20 25 30

Asn Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Ser Gly Asp Gly Thr Thr Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Thr Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Gly Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ala Gly
100 105 110

Pro Pro Pro Gly Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
115 120 125

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
130 135 140

His His His His His His
145 150

<210> 644
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 644

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20

25

30

Thr Ile Ala Trp Phe Arg Gln Ala Pro Gly Gly Lys Glu Arg Glu Gly
35 40 45

Ile Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Met Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Ser Ser Asn Trp
100 105 110

Tyr Gly Pro Pro Pro Arg Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln
115 120 125

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
130 135 140

Gly Ser His His His His His His
145 150

<210> 645
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 645

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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Thr Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35 40 45

Ser Cys Ile Ser Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Phe Asn Val Trp Ser Pro Pro Ile Cys Gly Ser Ile Trp Tyr
100 105 110

Gly Pro Pro Pro Arg Gly Met Asp Tyr Trp Gly Lys Gly Thr Gln Val
115 120 125

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
130 135 140

Ser His His His His His His
145 150

<210> 646
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 646

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Asp Pro Ala Asn Asp Asn Thr Leu Tyr Ala Ser Lys Phe
50 55 60

Gln Gly Arg Ala Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Gly Tyr Gly Tyr Tyr Val Phe Asp His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 647
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 647

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Asp Asn Thr Leu Tyr Ala Ser Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Gly Tyr Tyr Val Phe Asp His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 648
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 648

Asp Val Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Arg Ser Ile Ser Gln Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln His Asn Glu Asn Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Phe Ser Met Asp
100 105 110

Tyr Tyr Ala Ile Ala

115

<210> 649
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 649

Gly	Phe	Ser	Met	Asp	Tyr	Tyr	Ala	Ile	Ala
1				5					10

<210> 650
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 650

Gly	Phe	Ser	Met	Asp	Tyr	Tyr	Ala	Ile	Ala
1				5					10

<210> 651
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 651

Gly	Phe	Ser	Val	Asp	Tyr	Tyr	Ala	Ile	Ala
1				5					10

<210> 652
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 652

Gly	Phe	Ser	Met	Asp	Tyr	Tyr	Ala	Ile	Ala
1				5					10

<210> 653

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 653

Gly	Gly	Phe	Asn	Arg	Val	Ser	Tyr	Met	Gly
1				5					10

<210> 654

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 654

Gly	Gly	Phe	Asn	Arg	Val	Ser	Tyr	Met	Gly
1				5					10

<210> 655

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 655

Gly	Ile	Ile	Lys	Ser	Ile	Asn	Phe	Met	Gly
1				5					10

<210> 656

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 656

Gly	Phe	Ile	Leu	Asp	Tyr	Tyr	Gly	Ile	Gly
1				5					10

<210> 657

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 657

Gly	Leu	Ser	Leu	Asp	Tyr	Asp	Gly	Val	Gly
1				5					10

<210> 658

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 658

Gly	Phe	Ile	Leu	Asp	Tyr	Tyr	Gly	Ile	Gly
1				5					10

<210> 659

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 659

Gly	Arg	Thr	Phe	Ser	Ser	Leu	Gly	Met	Gly
1				5					10

<210> 660
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 660

Gly	Arg	Thr	Phe	Ser	Ser	Leu	Gly	Met	Gly
1				5					10

<210> 661
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 661

Gly	Phe	Ala	Phe	Gly	Ser	Tyr	Asp	Met	Gly
1				5					10

<210> 662
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 662

Gly	Phe	Ser	Phe	Gly	Asn	Asn	Asp	Met	Ser
1				5					10

<210> 663
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 663

Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr
1 5 10

<210> 664
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 664

Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr
1 5 10

<210> 665
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 665

Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr
1 5 10

<210> 666
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 666

Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr
1 5 10

<210> 667
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 667

Ser Val Thr Ser Gly Gly Glu Ile
1 5

<210> 668

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 668

Ser Val Thr Ser Gly Gly Glu Ile
1 5

<210> 669

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 669

Ser Thr Thr Ser Asp Gly Arg Thr
1 5

<210> 670

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 670

Cys Ile Ser Ser Ser Asp Gly Ser Thr
1 5

<210> 671

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 671

Cys Ile Ser Ser Ser Asp Gly Ser Thr
 1 5

<210> 672
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 672

Cys Ile Ser Ser Ser Asp Gly Ser Thr
 1 5

<210> 673
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 673

Ala Ile Ala Trp Asn Gly Ala Ser Thr
 1 5

<210> 674
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 674

Ala Ile Ala Trp Asn Gly Ala Ser Thr

1 5

<210> 675
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 675

Gly Ile Asn Ser Gly Gly Arg Ile Thr
 1 5

<210> 676
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 676

Ala Ile Asn Ser Gly Gly Gly Ser Thr
 1 5

<210> 677
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 677

Ala Val Arg Ser Thr Ala Asn Thr Leu Cys Pro Ser His Tyr Ser Val
 1 5 10 15

Met Asp Tyr

<210> 678
 <211> 19
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 678

Ala	Val	Arg	Ser	Thr	Ala	Asn	Thr	Leu	Cys	Pro	Ser	His	Tyr	Ser	Ile
1				5				10						15	

Met Asp Tyr

<210> 679

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 679

Ala	Val	Arg	Ser	Thr	Ala	Asn	Thr	Leu	Cys	Pro	Ser	His	Tyr	Ser	Val
1				5				10						15	

Met Asp Tyr

<210> 680

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 680

Asn	Ala	Asp	Ile	Trp	Val	Ser	Asp	Ala	Arg	Met	Tyr	Asn	Tyr
1				5				10					

<210> 681

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 681

Asn	Ala	Asp	Ile	Trp	Val	Ser	Asp	Ala	Arg	Met	Tyr	Asn	Tyr
1				5					10				

<210> 682

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 682

Asn	Ala	Asp	Ile	Trp	Leu	Pro	Ser	Asp	Arg	Met	Tyr	Asn	Tyr
1				5					10				

<210> 683

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 683

Ala	Thr	Ala	Thr	Leu	Cys	Asp	Gly	Gly	Ile	Trp	Gly	Tyr
1				5					10			

<210> 684

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 684

Ala	Thr	Ala	Thr	Leu	Cys	Asp	Gly	Gly	Ile	Trp	Gly	Tyr
1				5					10			

<210> 685

<211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 685

Ala	Thr	Ala	Thr	Leu	Cys	Asp	Gly	Gly	Ile	Trp	Gly	Tyr
1				5					10			

<210> 686
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 686

Ala	Ala	Ser	Gly	Leu	Gly	Ser	Val	Val	Val	Thr	Ala	Asn	Glu	Tyr	Asp
1				5					10					15	

Tyr

<210> 687
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 687

Ala	Ala	Ser	Gly	Leu	Gly	Ser	Val	Val	Val	Thr	Ala	Asn	Glu	Tyr	Asp
1				5					10					15	

Tyr

<210> 688
 <211> 15
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 688

Ala	Gln	Gly	Asp	Arg	Ser	Ser	Trp	His	Tyr	Tyr	Gly	Met	Asp	Tyr
1				5					10					15

<210> 689

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 689

Ala	Thr	Lys	Ser	Asp	Pro	Met	Thr	Asn	Glu	Tyr	Asp	Leu
1				5					10			

<210> 690

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 690

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Met	Asp	Tyr	Tyr
			20					25					30		

Ala	Ile	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Glu	Ile
		35					40					45			

Ser	Cys	Ile	Thr	Gly	Ser	Asp	Phe	Met	Val	Asp	Thr	Tyr	Tyr	Val	Ala
	50					55					60				

Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Glu	Asn	Thr

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Gly Val Tyr
85 90 95

Phe Cys Ala Val Arg Ser Thr Ala Asn Thr Leu Cys Pro Ser His Tyr
100 105 110

Ser Val Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
130 135 140

His His His
145

<210> 692
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 692

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Ser Val Asp Tyr Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Ile
35 40 45

Ser Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr Tyr Tyr Val Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr

85

90

95

Phe Cys Ala Val Arg Ser Thr Ala Asn Thr Leu Cys Pro Ser His Tyr
100 105 110

Ser Ile Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
130 135 140

His His
145

<210> 693
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 693

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Ser Met Asp Tyr Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Ile
35 40 45

Ser Cys Ile Thr Gly Ser Asp Phe Met Val Asp Thr Tyr Tyr Val Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65 70 75 80

Ala His Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr
85 90 95

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Phe Cys Ala Val Arg Ser Thr Ala Asn Thr Leu Cys Pro Ser His Tyr
100 105 110

Ser Val Met Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
130 135 140

His His His
145

<210> 694
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 694

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Phe Asn Arg Val Ser
20 25 30

Tyr Met Gly Trp Tyr Arg Gln Ala Pro Gly Thr Lys Arg Glu Leu Val
35 40 45

Ala Ser Val Thr Ser Gly Gly Glu Ile Thr Ile Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Gly Leu Lys Pro Glu Asp Gly Ala Thr Tyr Trp Cys Asn
85 90 95

Ala Asp Ile Trp Val Ser Asp Ala Arg Met Tyr Asn Tyr Trp Gly Gln

100

105

110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His
130 135

<210> 695
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 695

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Phe Asn Arg Val Ser
20 25 30

Tyr Met Gly Trp Tyr Arg Gln Ala Pro Gly Ser Lys Arg Glu Leu Val
35 40 45

Ala Ser Val Thr Ser Gly Gly Glu Ile Thr Val Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Asn Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Gly Leu Lys Pro Glu Asp Gly Ala Thr Tyr Trp Cys Asn
85 90 95

Ala Asp Ile Trp Val Ser Asp Ala Arg Met Tyr Asn Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 696
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 696

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ile Lys Ser Ile Asn
20 25 30

Phe Met Gly Trp Tyr Arg Gln Pro Pro Gly Thr Lys Arg Glu Leu Val
35 40 45

Ala Ser Thr Thr Ser Asp Gly Arg Thr Thr Val Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Ile Tyr Leu
65 70 75 80

Glu Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Thr Tyr Trp Cys Asn
85 90 95

Ala Asp Ile Trp Leu Pro Ser Asp Arg Met Tyr Asn Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 697

<211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 697

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ile Leu Asp Tyr Tyr
 20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ala Val
 35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Leu Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Thr Ala Thr Leu Cys Asp Gly Gly Ile Trp Gly Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
 115 120 125

Pro Asp Tyr Gly Ser His His His His His His
 130 135

<210> 698
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 698

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Leu Ser Leu Asp Tyr Asp
20 25 30

Gly Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ala Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Gly Asn Ala Leu Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Ala Thr Leu Cys Asp Gly Gly Ile Trp Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 699

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 699

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ile Leu Asp Tyr Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ala Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Leu Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Ala Thr Leu Cys Asp Gly Gly Ile Trp Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 700
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 700

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Arg Thr Phe Ser Ser Leu
20 25 30

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val

35 40 45

Ser Ala Ile Ala Trp Asn Gly Ala Ser Thr Tyr Tyr Thr Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Thr Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Ala Ser Gly Leu Gly Ser Val Val Val Thr Ala Asn Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 701
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 701

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Leu
20 25 30

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ser Ala Ile Ala Trp Asn Gly Ala Ser Thr Tyr Tyr Thr Glu Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Thr Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Ala Ser Gly Leu Gly Ser Val Val Val Thr Ala Asn Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 702
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 702

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Ala Phe Gly Ser Tyr
20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Gly Ile Asn Ser Gly Gly Arg Ile Thr Asp Tyr Ala Asp Ser Val
50 55 60

Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Gln Gly Asp Arg Ser Ser Trp His Tyr Tyr Gly Met Asp Tyr Trp
100 105 110

Gly Lys Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr
115 120 125

Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 703
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (112)..(112)
<223> Xaa can be any naturally occurring amino acid

<400> 703

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Gly Asn Asn
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asn Ser Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Thr Lys Ser Asp Pro Met Thr Asn Glu Tyr Asp Leu Trp Gly Xaa
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 704
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 704

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

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Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

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Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 705
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 705

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

35

40

45

Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95

Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 706

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 706

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
115 120 125

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys
180 185 190

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Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
210 215 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225 230 235 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
245 250 255

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
275 280 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305 310 315 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
370 375 380

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
385 390 395 400

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Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 707
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 707

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly

115

120

125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 708
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 708

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Phe Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 709
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 709

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Val Ser Tyr Met
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Phe Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 710

<211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 710

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Cys Leu Thr Ile Asn Ser Leu Gln Pro Glu
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Phe Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 711
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 711

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Val Ser Tyr Met

20

25

30

His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Cys Leu Thr Ile Asn Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Phe Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 712

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 712

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
35 40 45

Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
85 90 95

Ala Lys Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 713
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 713

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
35 40 45

Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
85 90 95

Ala Lys Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser

115

<210> 714
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 714

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
 35 40 45

Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
 50 55 60

Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
 85 90 95

Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 715
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 715

Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
35 40 45

Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Asn Thr Ala Tyr
65 70 75 80

Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
85 90 95

Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 716

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 716

Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Val Asn Thr Ala Tyr
65 70 75 80

Leu Gln Ile Thr Ser Leu Asn Ala Glu Asp Thr Gly Met Tyr Phe Cys
85 90 95

Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 717
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 717

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln

65		70		75		80									
Tyr	Gln	Cys	Ile	Ile	Ile	Tyr	Gly	Val	Ala	Trp	Asp	Tyr	Lys	Tyr	Leu
			85						90				95		
Thr	Leu	Lys	Val	Lys	Ala	Ser	Tyr	Arg	Lys	Ile	Asn	Thr	His	Ile	Leu
			100					105					110		
Lys	Val	Pro	Glu	Thr	Asp	Glu	Val	Glu	Leu	Thr	Cys	Gln	Ala	Thr	Gly
		115						120				125			
Tyr	Pro	Leu	Ala	Glu	Val	Ser	Trp	Pro	Asn	Val	Ser	Val	Pro	Ala	Asn
	130					135					140				
Thr	Ser	His	Ser	Arg	Thr	Pro	Glu	Gly	Leu	Tyr	Gln	Val	Thr	Ser	Val
145					150					155					160
Leu	Arg	Leu	Lys	Pro	Pro	Pro	Gly	Arg	Asn	Phe	Ser	Cys	Val	Phe	Trp
			165						170					175	
Asn	Thr	His	Val	Arg	Glu	Leu	Thr	Leu	Ala	Ser	Ile	Asp	Leu	Gln	Ser
			180					185					190		
Gln	Met	Glu	Pro	Arg	Thr	His	Pro	Thr	Trp	Leu	Leu	His	Ile	Phe	Ile
		195						200				205			
Pro	Phe	Cys	Ile	Ile	Ala	Phe	Ile	Phe	Ile	Ala	Thr	Val	Ile	Ala	Leu
	210					215					220				
Arg	Lys	Gln	Leu	Cys	Gln	Lys	Leu	Tyr	Ser	Ser	Lys	Asp	Thr	Thr	Lys
225					230					235					240
Arg	Pro	Val	Thr	Thr	Thr	Lys	Arg	Glu	Val	Asn	Ser	Ala	Ile		
			245					250							

<210> 718
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 718

Met Ile Phe Leu Leu Leu Met Leu Ser Leu Glu Leu Gln Leu His Gln
1 5 10 15

Ile Ala Ala Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile
20 25 30

Glu His Gly Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser
35 40 45

His Val Asn Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn
50 55 60

Asp Thr Ser Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu
65 70 75 80

Pro Leu Gly Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp
85 90 95

Glu Gly Gln Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr
100 105 110

Lys Tyr Leu Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr
115 120 125

His Ile Leu Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln
130 135 140

Ala Thr Gly Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val
145 150 155 160

Pro Ala Asn Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val
165 170 175

Thr Ser Val Leu Arg Leu Lys Pro Pro Pro Gly Arg Asn Phe Ser Cys
180 185 190

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Val Phe Trp Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp
195 200 205

Leu Gln Ser Gln Met Glu Pro Arg Thr His Pro Thr Trp Glu Pro Lys
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 719
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 719

Ser Asn Thr Ser Glu Ser Phe Lys Ser Asn Thr Ser Glu Ser Phe Phe
1 5 10 15

Arg Val Thr Gln Leu Ala Pro Lys Ala Gln Ile Lys Glu
20 25

<210> 720
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 720

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

Met Glu Ile Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ile Tyr Asp Gly Ser Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ala Leu Thr Val Ser Ser
115

<210> 721
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 721

Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Cys Ala Ser Gln Gly
1 5 10 15

Gly Lys Val Thr Val Thr Cys Lys Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Met Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
35 40 45

His Tyr Thr Ser Thr Leu Leu Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro

Phe Gly Gly Gly
100

<210>	722
<211>	6
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 722

Thr Lys Leu Glu Ile Lys
1 5

<210>	723
<211>	116
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 723

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly His Ile Asn Pro Ser Ser Gly Phe Thr Thr Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr

65		70		75		80
Met	Gln	Leu	Ser	Ser	Leu	Thr
			85			
				Asp	Ser	Ala
				90		
					Val	Tyr
						Phe
						95
Ala	Arg	Glu	Asp	Tyr	Asp	Val
			100			
				Tyr	Trp	Gly
				105		
					Gln	Gly
						Thr
						110
Thr	Val	Ser	Ser			
			115			
<210> 724						
<211> 100						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> Synthetic polymer						
<400> 724						
Asp	Ile	Val	Met	Thr	Gln	Ser
1				5		
					Gln	Lys
						Phe
						10
						Met
						Ser
						Thr
						Ser
						Val
						15
Asp	Arg	Val	Ser	Val	Thr	Cys
			20			
						Lys
						Ala
						25
						Ser
						Gln
						Ser
						Val
						Asp
						30
Val	Ala	Trp	Tyr	Gln	Gln	Lys
						35
						Pro
						40
						Gly
						Gln
						Ser
						Pro
						45
Phe	Ser	Ala	Ser	Tyr	Arg	Tyr
						50
						55
						Ser
						Gly
						Val
						Pro
						60
						Asp
						Arg
						Phe
						Thr
						Gly
Ser	Gly	Ser	Gly	Thr	Asp	Phe
65						70
						Thr
						Leu
						75
						Ile
						Asn
						Ser
						Val
						Gln
						80
Glu	Asp	Leu	Ala	Glu	Tyr	Phe
						85
						Cys
						Gln
						90
						Tyr
						Asn
						Ser
						Val
						Gln
						95
						Pro
						Tyr
Thr	Phe	Gly	Ser			
			100			

<210> 725
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 725

Gly Thr Lys Leu Glu Ile Lys
 1 5

<210> 726
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 726

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Ser Gly Ser Tyr Thr Ile Tyr Tyr Thr Asp Thr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe
 65 70 75 80

Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Arg Gly Tyr Gly Ser Phe Tyr Glu Tyr Tyr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 727
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 727

Gln Ile Val Leu Thr Gln Ser Pro Ala Leu Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 728
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 728

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile His
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Ser Gly Gly Ile Thr Tyr Tyr Glu Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Asp Arg Ala Glu Ser Ser Trp Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser
115

<210> 729
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 729

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ala Ser Ile His
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val

35 40 45

Ala Val Ile Thr Trp Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Gly Asp Lys His Gln Ser Ser Trp Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser
115

<210> 730
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 730

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile His
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Leu
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Gly Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Asp Arg Ala Gln Ser Ser Trp Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser
115

<210> 731
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 731

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Gly Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Leu Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Glu Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Asp Arg Val Asp Ser Asn Trp Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser

115

<210> 732
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 732

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Phe Ser Ser Gly
 20 25 30

Thr Met Gly Trp Phe Arg Arg Ala Pro Gly Lys Glu Arg Glu Phe Val
 35 40 45

Ala Ser Ile Pro Trp Ser Gly Gly Arg Ile Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Val Lys Glu Arg Ser Thr Gly Trp Asp Phe Ala Ser Trp Gly Gln
 100 105 110

Cys Thr Gln Val Thr Val Ser Ser
 115 120

<210> 733
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 733

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Gln Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Ser
20 25 30

Trp Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Thr Gly Phe Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 734

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 734

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Gln Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Ser
20 25 30

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Trp Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Thr Gly Phe Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 735
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 735

Gln Val Gln Leu Val Gln Ser Gly His Glu Val Lys Gln Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Ser
20 25 30

Trp Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Thr Gly Phe Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210>	736
<211>	121
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 736

Gln Val Gln Leu Val Gln Ser Gly His Glu Val Lys Gln Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Ser
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Thr Gly Phe Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 737
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 737

Gln Val Gln Leu Val Gln Ser Gly His Glu Val Lys Gln Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Ser
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Thr Gly Phe Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 738
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 738

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Thr Leu Ser Pro Gly
1 5 10 15

Gln Arg Leu Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro
35 40 45

Lys Leu Leu Ile Lys Phe Gly Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 739

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 739

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Gln Arg Leu Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro

35

40

45

Lys Leu Leu Ile Lys Phe Gly Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 740
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 740

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Gln Arg Leu Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro
35 40 45

Lys Leu Leu Ile Lys Phe Gly Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 741
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 741

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Gln Arg Leu Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro
35 40 45

Lys Leu Leu Ile Lys Phe Gly Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 742
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 742

Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Gly
1 5 10

<210> 743
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 743

Gly Thr Ile Phe Ser Ile Asn His Met Asp
1 5 10

<210> 744
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 744

Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser
1 5 10

<210> 745
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 745

Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Asn
1 5 10

<210> 746
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 746

Gly	Thr	Ile	Phe	Ser	Ile	Asn	Arg	Met	Asp
1				5					10

<210> 747

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 747

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5					10

<210> 748

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 748

Gly	Lys	Ile	Phe	Ser	Gly	Asn	Asp	Met	Gly
1				5					10

<210> 749

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 749

Gly	Thr	Ile	Phe	Ser	Ile	Asn	Arg	Met	Asp
1				5					10

<210> 750

<211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 750

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5					10

<210> 751
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 751

Gly	Phe	Thr	Phe	Asn	Asp	Tyr	Ala	Met	Ser
1				5					10

<210> 752
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 752

Gly	Phe	Asn	Leu	Asp	Pro	Tyr	Ala	Ile	Ala
1				5					10

<210> 753
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 753

Gly	Phe	Thr	Phe	Thr	Ala	Tyr	Ala	Met	Ser

1 5 10

<210> 754
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 754

Gly Phe Thr Phe Asp Tyr Tyr Ala Ile Gly
 1 5 10

<210> 755
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 755

Gly Phe Asn Leu Asp Pro Tyr Ala Ile Ala
 1 5 10

<210> 756
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 756

Gly Thr Ile Phe Ser Ile Asn Arg Met Asp
 1 5 10

<210> 757
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 757

Gly	Thr	Ile	Phe	Ser	Ile	Asn	Arg	Met	Asp
1				5					10

<210> 758

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 758

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5					10

<210> 759

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 759

Gly	Phe	Asn	Leu	Asp	Pro	Tyr	Ala	Ile	Gly
1				5					10

<210> 760

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 760

Gly	Phe	Asn	Leu	Asp	Pro	Tyr	Ala	Ile	Ala
1				5					10

<210> 761

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 761

Glu	Ser	Ile	Phe	Ser	Ile	Glu	Ala	Met	Gly
1				5					10

<210> 762

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 762

Gly	Lys	Ile	Phe	Ser	Gly	Asn	Asp	Met	Gly
1				5					10

<210> 763

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 763

Gly	Phe	Thr	Leu	Asp	Tyr	Tyr	Ala	Ile	Gly
1				5					10

<210> 764

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 764

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5					10

<210> 765
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 765

Gly	Thr	Ile	Phe	Ser	Ile	Asn	Arg	Met	Asp
1				5					10

<210> 766
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 766

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5					10

<210> 767
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 767

Gly	Phe	Asn	Leu	Asp	Pro	Tyr	Ala	Ile	Ala
1				5					10

<210> 768
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 768

Gly Arg Thr Phe Ser Ile Ser Ala Met Gly
1 5 10

<210> 769
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 769

Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Asn
1 5 10

<210> 770
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 770

Gly Phe Thr Phe Ser Ser Tyr Gly Met Ser
1 5 10

<210> 771
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 771

Gly Phe Thr Phe Asn Asp Tyr Ala Met Ser
1 5 10

<210> 772
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 772

Gly	Phe	Thr	Leu	Asp	Tyr	Tyr	Ala	Ile	Gly
1				5					10

<210> 773

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 773

Ile	Ser	Ser	Ser	Asp	Gly	Ser	Thr	Tyr
1				5				

<210> 774

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 774

Ile	Thr	Ser	Asp	Gly	Phe	Pro	Thr
1				5			

<210> 775

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 775

Ile	Arg	Trp	Asn	Gly	Gly	Ser	Thr	Asn
1				5				

<210> 776

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 776

Ile Ser Ser Ser Asp Gly Ser Thr Tyr
 1 5

<210> 777
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 777

Ile Thr Ser Asp Gly Thr Pro Thr
 1 5

<210> 778
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 778

Ile Asp Ser Gly Gly Gly Ser Thr Ser
 1 5

<210> 779
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 779

Ile Thr Ser Gly Gly Ile Thr Asp

1 5

<210> 780
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 780

Ile Thr Ser Asp Gly Thr Pro Thr
 1 5

<210> 781
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 781

Ile Asp Ser Gly Gly Gly Ser Thr Ser
 1 5

<210> 782
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 782

Ile Arg Ser Asn Gly Gly Tyr Thr Asn
 1 5

<210> 783
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 783

Ile Ser Ser Ser Asp Val Gly Thr Tyr
1 5

<210> 784

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 784

Ile Asn Ser Ser Asp Gly Ser Thr Tyr
1 5

<210> 785

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 785

Ile Ser Gly Ser Asp Ser Ser Thr Tyr
1 5

<210> 786

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 786

Ile Ser Ser Ser Asp Val Gly Thr Tyr
1 5

<210> 787

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 787

Ile Thr Ser Asp Gly Thr Pro Thr
1 5

<210> 788

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 788

Ile Thr Ser Asp Gly Thr Pro Ala
1 5

<210> 789

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 789

Ile Asp Ser Gly Gly Gly Ser Thr Ser
1 5

<210> 790

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 790

Ile Ser Ser Gly Asp Gly Ser Lys Tyr
1 5

<210> 791
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 791

Ile Ser Ser Ser Asp Val Gly Thr Tyr
 1 5

<210> 792
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 792

Ile Phe Gly Gly Gly Phe Thr Asn
 1 5

<210> 793
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 793

Ile Thr Ser Gly Gly Ile Thr Asp
 1 5

<210> 794
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 794

Ile Ser Ser Ser Asp Gly Ser Thr Tyr
1 5

<210> 795
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 795

Ile Asp Ser Gly Gly Gly Ser Thr Ser
1 5

<210> 796
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 796

Ile Thr Ser Asp Gly Thr Pro Thr
1 5

<210> 797
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 797

Ile Asp Ser Gly Gly Gly Ser Thr Ser
1 5

<210> 798
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 798

Ile Ser Ser Ser Asp Val Gly Thr Tyr
1 5

<210> 799

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 799

Ile Thr Trp Ser Gly Gly Ser Thr Ser
1 5

<210> 800

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 800

Ile Ser Ser Ser Asp Gly Ser Thr Tyr
1 5

<210> 801

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 801

Ile Asp Ser Gly Gly Gly Ser Thr Ser
1 5

<210> 802

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 802

Ile Arg Ser Asn Gly Gly Tyr Thr Asn
 1 5

<210> 803
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 803

Ile Ser Ser Ser Asp Gly Ser Thr Tyr
 1 5

<210> 804
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 804

Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu Tyr Trp
 1 5 10 15

<210> 805
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 805

Ser Ser Gly Val Tyr Asn Tyr Trp

1 5

<210> 806
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 806

Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Pro Arg
1 5 10

<210> 807
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 807

Ser Gly Trp Arg Leu Cys Arg Pro Thr Asp Glu Tyr Asp Tyr Ser Tyr
1 5 10 15

Trp

<210> 808
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 808

Ser Ser Gly Val Tyr Asn Tyr Trp
1 5

<210> 809
<211> 14
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 809

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Ser	Asp	Tyr	Trp
1				5					10				

<210> 810

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 810

Arg	Asp	Arg	Thr	Ile	Trp	Trp
1				5		

<210> 811

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 811

Ser	Ser	Gly	Val	Tyr	Asn	Tyr	Trp
1				5			

<210> 812

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 812

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Ser	Asp	Tyr	Trp
1				5					10				

<210> 813
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 813

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Tyr	Pro
1				5					10		

<210> 814
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 814

Asp	Gly	Tyr	Tyr	Tyr	Cys	Ser	Asp	Tyr	Pro	His	Pro	Leu	Tyr	Trp
1				5					10					15

<210> 815
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 815

Asp	Gly	Trp	Arg	Asp	Cys	Thr	Trp	Ser	Asn	Glu	Tyr	Ala	Tyr	Trp
1				5					10					15

<210> 816
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 816

Thr Gly Trp Arg Thr Cys Arg Gly Leu Asn Glu Tyr Asp Tyr Trp
1 5 10 15

<210> 817
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 817

Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr Trp
1 5 10 15

<210> 818
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 818

Ser Ser Gly Val Tyr Asn Tyr Trp
1 5

<210> 819
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 819

Ser Ser Gly Val Tyr Asn Tyr Trp
1 5

<210> 820
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 820

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Ser	Asp	Tyr	Trp
1				5					10				

<210> 821

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 821

Asp	Gly	Tyr	Tyr	Tyr	Cys	Ser	Asp	Tyr	Pro	His	Pro	Leu	Tyr	Trp
1				5					10					15

<210> 822

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 822

Asp	Gly	Tyr	Tyr	Tyr	Cys	Ser	Asp	Tyr	Pro	His	Pro	Leu	Tyr	Trp
1				5					10					15

<210> 823

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 823

Asp	Leu	Val	Ser	Gly	Ser	Ser	Arg	Leu	Tyr	Asp	Tyr	Trp
1				5					10			

<210> 824

<211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 824

Arg Asp Arg Thr Ile Trp Trp
 1 5

<210> 825
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 825

Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu Tyr Trp
 1 5 10 15

<210> 826
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 826

Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp
 1 5 10

<210> 827
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 827

Ser Ser Gly Val Tyr Asn Tyr Trp

1 5

<210> 828
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 828

Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp
1 5 10

<210> 829
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 829

Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr Trp
1 5 10 15

<210> 830
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 830

Met Gly Arg Thr Asn Tyr Gly Val Ile Tyr Asp Pro Asn Met Tyr Asn
1 5 10 15

Tyr Trp

<210> 831
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 831

Ser	Gly	Trp	Arg	Leu	Cys	Arg	Pro	Thr	Asp	Glu	Tyr	Asp	Tyr	Leu	Tyr
1				5					10					15	

Trp

<210> 832

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 832

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Ser	Asp	Tyr	Trp
1				5					10				

<210> 833

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 833

Gln	Gly	Tyr	Tyr	Cys	Ser	Gly	Tyr	Gly	Cys	Tyr	Pro
1				5					10		

<210> 834

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 834

Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu Tyr Trp
1 5 10 15

<210> 835
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 835

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asn
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 836

<211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 836

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
 20 25 30

His Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Leu Ile Thr Ser Asp Gly Phe Pro Thr Tyr Ala Asp Ser Ala Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
 85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His
 130

<210> 837
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 837

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Arg Trp Asn Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Pro Arg Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
115 120 125

Asp Tyr Gly Ser His His His His His His
130 135

<210> 838

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 838

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Ala Ile Asn Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Ser Gly Trp Arg Leu Cys Arg Pro Thr Asp Glu Tyr Asp Tyr
100 105 110

Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 839
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 839

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
20 25 30

Arg Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val

35 40 45

Ala Leu Ile Thr Ser Asp Gly Thr Pro Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 840
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 840

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 841
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 841

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Lys Ile Phe Ser Gly Asn
20 25 30

Asp Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Gly Ile Ile Thr Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ala Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Met Met Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn

85

90

95

Met Arg Asp Arg Thr Ile Trp Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
115 120 125

His His His His His
130

<210> 842
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 842

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
20 25 30

Arg Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Leu Ile Thr Ser Asp Gly Thr Pro Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His
 130

<210> 843
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 843

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
 35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Thr Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
 115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His

130

135

140

<210> 844
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 844

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Arg Ser Asn Gly Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Tyr Pro Gly Gln Gly
 100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
 115 120 125

Asp Tyr Gly Ser His His His His His His
 130 135

<210> 845
 <211> 142
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 845

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Leu Asp Pro Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Val Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 846

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 846

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ala Tyr
20 25 30

Ala Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Asn Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Thr Asp Gly Trp Arg Asp Cys Thr Trp Ser Asn Glu Tyr Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 847
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 847

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Tyr Tyr

20

25

30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Gly Ser Asp Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Val Arg Asp Asn Ala Gln Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Val Thr Gly Trp Arg Thr Cys Arg Gly Leu Asn Glu Tyr Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 848
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 848

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Leu Asp Pro Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

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Ser Cys Ile Ser Ser Ser Asp Val Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 849
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 849

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
20 25 30

Arg Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Leu Ile Thr Ser Asp Gly Thr Pro Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu

65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val	Ser	Ser	Ala	Ala	Ala	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Gly	Ser
		115					120					125			

His His His His His His
130

<210>	850
<211>	134
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 850

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
20 25 30

Arg Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Leu Ile Thr Ser Asp Gly Thr Pro Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 851
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 851

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp

115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 852
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 852

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Leu Asp Pro Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Gly Asp Gly Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 853
 <211> 142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 853

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Asn Leu Asp Pro Tyr
 20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
 35 40 45

Ser Cys Ile Ser Ser Ser Asp Val Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Thr Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr
 100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
 115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
 130 135 140

<210> 854
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 854

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Ser Ile Phe Ser Ile Glu
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Phe Gly Gly Gly Phe Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Arg Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Asp Leu Val Ser Gly Ser Ser Arg Leu Tyr Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
115 120 125

Pro Asp Tyr Gly Ser His His His His His His
130 135

<210> 855

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 855

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20	Ser	Cys
		Ala	Ala
		25	Ser
		Gly	Lys
		Ile	Phe
		30	Ser
		Gly	Asn
Asp	Met	Gly	Trp
	35	Tyr	Arg
		Gln	Ala
		40	Pro
		Gly	Lys
		Gln	Arg
		45	Glu
		Leu	Val
Gly	Ile	Ile	Thr
	50	Ser	Gly
		Gly	Ile
		55	Thr
		Asp	Tyr
		60	Ala
		Asp	Ala
		Val	Lys
Gly	Arg	Phe	Thr
	65	Ile	Ser
		70	Arg
		Asp	Asn
		Ala	Lys
		75	Asn
		Met	Met
		Tyr	Leu
		80	
Gln	Met	Asn	Ser
	85	Leu	Lys
		Pro	Glu
		Asp	Thr
		90	Ala
		Val	Tyr
		Tyr	Cys
		95	Asn
Met	Arg	Asp	Arg
	100	Thr	Ile
		Trp	Trp
		105	Gly
		Gln	Gly
		Thr	Gln
		110	Val
		Thr	Val
Ser	Ser	Ala	Ala
	115	Ala	Tyr
		Pro	Tyr
		120	Asp
		Val	Pro
		Asp	Tyr
		125	Gly
		Ser	His
His	His	His	His
	130	His	

<210> 856
 <211> 143
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 856

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Leu	Asp	Tyr	Tyr
	20							25					30		

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Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asn
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 857
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 857

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 858

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 858

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Thr Ile Phe Ser Ile Asn
20 25 30

Arg Met Asp Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Leu Ile Thr Ser Asp Gly Thr Pro Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Lys Thr Val Ser Leu
65 70 75 80

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Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

Val Ser Ser Gly Val Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His
130

<210> 859
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 859

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly

100

105

110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 860
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 860

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Leu Asp Pro Tyr
20 25 30

Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Val Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Tyr Tyr Tyr Cys Ser Asp Tyr Pro His Pro Leu Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro
115 120 125

Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 861
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (13)..(13)
<223> Xaa can be any naturally occurring amino acid

<400> 861

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Xaa Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ile Ser
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Ile Thr Trp Ser Gly Gly Ser Thr Ser Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Met Gly Arg Thr Asn Tyr Gly Val Ile Tyr Asp Pro Asn Met
100 105 110

Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His
145

<210> 862
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 862

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Ala Ile Asn Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Ser Gly Trp Arg Leu Cys Arg Pro Thr Asp Glu Tyr Asp Tyr
100 105 110

Leu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His

130

135

140

<210> 863
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 863

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Met Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

Ser Ala Ile Asp Ser Gly Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 864
<211> 138
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 864

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Thr Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Arg Ser Asn Gly Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gln Gly Tyr Tyr Cys Ser Gly Tyr Gly Cys Tyr Pro Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
115 120 125

Asp Tyr Gly Ser His His His His His His
130 135

<210> 865

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 865

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Thr
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asn
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Asp Gly Trp Ser Ser Cys Arg His Gly Ile Asn Glu Tyr Leu
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His
130 135 140

<210> 866
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 866

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr

20

25

30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly

225		230		235		240
Gly	Pro	Ser	Val	Phe	Leu	Met
				245		255
Ile	Ser	Arg	Thr	Pro	Glu	His
						270
Glu	Asp	Pro	Glu	Val	Lys	Val
						285
His	Asn	Ala	Lys	Thr	Lys	Tyr
						300
Arg	Val	Val	Ser	Val	Leu	Gly
						320
Lys	Glu	Tyr	Lys	Cys	Lys	Ile
						335
Glu	Lys	Thr	Ile	Ser	Lys	Val
						350
Tyr	Thr	Leu	Pro	Pro	Ser	Ser
						365
Leu	Thr	Cys	Leu	Val	Lys	Glu
						380
Trp	Glu	Ser	Asn	Gly	Gln	Pro
						400
Val	Leu	Asp	Ser	Asp	Gly	Ser
						415
Asp	Lys	Ser	Arg	Trp	Gln	Gln
						430
His	Glu	Ala	Leu	His	Asn	His

435

440

445

Pro Gly Lys
450

<210> 867
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 867

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

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Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 868
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 868

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 869
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 869

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 870
<211> 448
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 870

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180

185

190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp

385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 871
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 871

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 872
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 872

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

260

265

270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 873

<211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 873

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
 85 90 95

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
 100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
 145 150 155 160

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175

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Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 874
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 874

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Asp Thr Phe Ser Thr Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Lys Ala His Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 875
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 875

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 876
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 876

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Thr Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Phe Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 877
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 877

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 878
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 878

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Val His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Leu His Ala Asp Thr Gly Ile Thr Lys Phe Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Ile Gln Leu Trp Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser
115

<210> 879
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 879

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 880
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 880

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Ile Phe Ser Thr Tyr
20 25 30

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn His Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Gly Ile Ala Ala Ala Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 881

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 881

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 882
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 882

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Val Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Gly Asn Ser Gly Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys

85

90

95

Ala Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 883
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 883

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 884
<211> 123
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 884

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Asp Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Arg Ala His Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 885

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 885

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 886
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 886

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Lys Ala His Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr Thr Ala Tyr

<210> 888
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 888

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Ser Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Ala Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ser Ser Gly Trp Ser Arg Tyr Tyr Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 889
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 889

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 890
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 890

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Glu Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asn Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Leu Phe Gly Ile Ala His Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Tyr Ser Tyr Val Ser Gly Ser Pro Phe Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 891

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 891

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Thr
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 892
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 892

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Asp Asp Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Arg Gly Arg Ile Glu Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Gly Arg Phe Arg Tyr Phe Asp Trp Phe Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 893
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 893

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 894

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 894

Glu Val Lys Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Val

35 40 45

Gly Tyr Ile Ser Tyr Thr Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Tyr Gly Gly Trp Leu Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 895
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 895

Asp Ile Val Met Thr Gln Ser His Lys Leu Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Asp Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
100 105

<210> 896
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 896

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

Ser Ile Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Met Trp Ala Gly Gly Gly Thr Asn Ser Asn Ser Val Leu Lys
50 55 60

Ser Arg Leu Ile Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
85 90 95

Arg Tyr Tyr Gly Asn Ser Pro Tyr Tyr Ala Ile Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 897

<211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 897

Asp Ile Val Thr Thr Gln Ser His Lys Leu Met Ser Thr Ser Val Gly
 1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
 65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Asp Ser Ser Tyr Pro Leu
 85 90 95

Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
 100 105

<210> 898
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 898

Glu Val Lys Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Ile Ser Asp

20

25

30

Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Leu
35 40 45

Gly Tyr Ile Ser Tyr Thr Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Arg Gly Gly Trp Leu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 899
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 899

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15

Glu Lys Val Ser Met Gly Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Asp Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110

Lys

<210> 900
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 900

Glu Val Lys Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Phe Pro Arg Asp Asn Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Lys Glu Asn Trp Val Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Thr Leu Thr Leu Ser Ser
115

<210> 901
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 901

Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Arg Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Ser
35 40 45

Asp Thr Ser Lys Leu Thr Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ala Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Trp Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 902
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 902

Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Thr Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Gln Ala Ser Gly Tyr Thr Phe Pro Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asp Pro Asn Tyr Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Ile Leu Thr Val Asp Arg Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Leu Thr Asp Trp Gly Gln Gly Thr Ser Leu Thr Val
100 105 110

Ser Ser

<210> 903

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 903

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30

Tyr Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Phe Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Thr Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Asn Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 904
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 904

Glu Val Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Tyr Val Asn Pro Phe Asn Asp Gly Thr Lys Tyr Asn Glu Met Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ser Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gln Ala Trp Gly Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 905
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 905

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Tyr Val Asn Pro Phe Asn Asp Gly Thr Lys Tyr Asn Glu Met Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ser Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Ala Trp Gly Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 906
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 906

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Val Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
 35 40 45

Gly Tyr Val Asn Pro Phe Asn Asp Gly Thr Lys Tyr Asn Glu Met Phe
 50 55 60

Lys Gly Arg Ala Thr Leu Thr Ser Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gln Ala Trp Gly Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 907
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 907

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Tyr Val Asn Pro Phe Asn Asp Gly Thr Lys Tyr Asn Glu Met Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ser Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Ala Trp Gly Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 908
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 908

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile

35 40 45

Gly Tyr Val Asn Pro Phe Asn Asp Gly Thr Lys Tyr Asn Glu Met Phe
50 55 60

Lys Gly Arg Ala Thr Ile Thr Ser Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Ala Trp Gly Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 909
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 909

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Glu Ser Val Glu Tyr Tyr
20 25 30

Gly Thr Ser Leu Val Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Val Asp Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Ser Leu Glu Glu Glu Asp Ala Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Arg Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 910
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 910

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Glu Ser Val Glu Tyr Tyr
20 25 30

Gly Thr Ser Leu Val Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Val Asp Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Ser Leu Glu Ala Glu Asp Ala Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Arg Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 911
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 911

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Glu Ser Val Glu Tyr Tyr
20 25 30

Gly Thr Ser Leu Val Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Val Asp Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Ser Leu Glu Ala Glu Asp Ala Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Arg Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 912

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 912

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Glu Ser Val Glu Tyr Tyr
20 25 30

Gly Thr Ser Leu Val Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro

35

40

45

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Val Asp Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Arg Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 913
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 913

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Asp Leu Val Thr Ser Met Val Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ser Tyr Glu Leu Thr Gln Pro Pro
115 120 125

Ser Val Ser Val Ser Pro Gly Gln Ala Ala Arg Ile Thr Cys Ser Gly
130 135 140

Asp Ala Leu Pro Gln Lys Tyr Val Phe Trp Tyr Gln Gln Lys Ser Gly
145 150 155 160

Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly
165 170 175

Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu
180 185 190

Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr Tyr Cys Tyr
195 200 205

Ser Thr Asp Arg Ser Gly Asn His Arg Val Phe Gly Gly Gly Thr Arg
210 215 220

Leu Thr Val Leu
225

<210> 914
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 914

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Gly Glu Gln Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Asn Tyr Gly Tyr Tyr Asp Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Glu Ile Val Leu Thr Gln Ser Pro
115 120 125

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
130 135 140

Ala Ser Gln Ser Val Ser Ser Asn Tyr Leu Ala Trp Phe Gln Gln Lys
145 150 155 160

Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Thr Ser Ser Arg Ala
165 170 175

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
195 200 205

Cys Gln Gln Tyr Gly Ser Ser Ile Phe Thr Phe Gly Pro Gly Thr Lys
210 215 220

Val Asp Ile Lys

225

<210> 915
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 915

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 916
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 916

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Glu Val Glu Ile Lys
100 105

<210> 917

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 917

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Arg Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Leu His Tyr Asp Ser Ser Gly Tyr Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 918
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 918

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ile Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu

85

90

95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 919
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 919

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Gly Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Gln Leu Tyr Ser Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 920
<211> 107
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 920

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Leu Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 921

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 921

Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Phe Thr Phe Ser Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Ser Ala Val Tyr Ser Cys
85 90 95

Ala Lys Val Leu Val Gly Phe Asn Asn Gly Cys Trp Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 922
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 922

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210>	923
<211>	120
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 923

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Val Thr Ser Met Val Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 924
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 924

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Gln Lys Tyr Val
 20 25 30

Phe Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Arg Ser Gly Asn His
 85 90 95

Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 925
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 925

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 926
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 926

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 927
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 927

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 928
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 928

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 929
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 929

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 930

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 930

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Ser Tyr

20

25

30

Trp Met Tyr Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 931
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 931

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

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Lys Asn Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 932
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 932

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 933
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 933

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 934
<211> 120
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 934

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 935

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 935

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Tyr Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Asn Ser Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Arg Lys Gly Leu Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 936
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 936

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Ile Pro Ala Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 937
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 937

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 938
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 938

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
 20 25 30

Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 939
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 939

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1 5 10 15

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Glu Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 940
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 940

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210>	941
<211>	107
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 941

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

$\langle 210 \rangle$	942
$\langle 211 \rangle$	107
$\langle 212 \rangle$	PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 942

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 943

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 943

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

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Val Ala Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 944
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 944

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 945
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 945

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Asp Cys Ala
85 90 95

Arg Gly Tyr Asp Ser Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Glu
115

<210> 946
<211> 116
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 946

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Lys Gly Tyr Asp Ser Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Ile Val Ser Ala
115

<210> 947

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 947

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser
115

<210> 948
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 948

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Val Thr Asp Tyr Asn Ala Ala Phe Ile

50

55

60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser
115

<210> 949
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 949

Glu Val Lys Leu Phe Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Asp Phe Ser Thr Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Asn Pro Asp Ser Thr Thr Ile Asn Tyr Ala Pro Ser Leu
50 55 60

Lys Asp Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Pro Gly Asp Tyr Gly Tyr Asp Phe Asp Cys Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 950
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 950

Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Met
35 40 45

Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Ser Leu Leu Trp Phe Ser Thr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 951

<211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 951

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
 20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Lys
 50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
 65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Phe Cys Ala
 85 90 95

Arg Leu Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
 100 105 110

Thr Val Ser Ser
 115

<210> 952
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 952

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Gly Met Ser Trp Ala Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Leu Gly Ser Val Gln
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Arg Gly Tyr Asp Ala Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Ser Val Ser Glu
115

<210> 953
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 953

Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly
20 25 30

Tyr Trp Thr Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Met
35 40 45

Gly Tyr Ile Ser Tyr Thr Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Tyr Tyr Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Gln Arg Asp Trp Leu Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ala
115

<210> 954
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 954

Glu Glu Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Ile Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala

85

90

95

Arg Gly Tyr Asp Ala Gly Phe Ala Phe Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Ala Ser Ala
115

<210> 955
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 955

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Thr Tyr
20 25 30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Thr Lys Asp Asn Ser Lys Asn Gln Val Val Leu
65 70 75 80

Thr Met Asn Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 956
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 956

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Ser Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Asp Cys Ala
 85 90 95

Arg Gly Tyr Asp Ser Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 957
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 957

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Ser Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

<210> 958
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 958

Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Ser Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala

50

55

60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 959

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 959

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Ala Ala Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ile Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Thr Ser Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 960
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 960

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
 20 25 30

Val Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Ala Ser Asn Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
 65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Thr Ser Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 961
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 961

Asp Val Leu Met Thr Gln Thr Pro Leu Tyr Leu Pro Val Ser Leu Gly
 1 5 10 15

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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ile Ile Val His Ser
20 25 30

Asn Ala Asn Thr Tyr Leu Glu Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 962
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 962

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Tyr Leu Tyr Trp Asn Gln Gln Lys Pro Gly Ser Ser Pro Lys Val Trp
35 40 45

Ile Tyr Asn Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu

Pro Thr Leu Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210>	963
<211>	106
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 963

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Asn Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gly Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

$\langle 210 \rangle$	964
$\langle 211 \rangle$	111
$\langle 212 \rangle$	PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 964

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Asn Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 965

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 965

Asp Ile Val Met Thr Gln Thr Pro Ser Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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Ser Asn Gln Lys Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Asn Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Ser Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110

Lys

<210> 966
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 966

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His

65		70		75		80									
Pro	Val	Glu	Glu	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Trp
				85					90					95	
Glu	Ile	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
			100					105					110		
<210> 967 <211> 107 <212> PRT <213> Artificial Sequence <220> <223> Synthetic polymer <400> 967															
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Ser	Asn	Asp
			20					25					30		
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Tyr	Ala	Ala	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Thr	Ser	Pro	Tyr
				85					90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

<210> 968
 <211> 111
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 968

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1 5 10 15

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Ser Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 969

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 969

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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Trp Met His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 970
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 970

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65		70		75		80									
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Thr	Arg	Trp	Thr	Thr	Gly	Thr	Gly	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												
<210> 971															
<211> 117															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic polymer															
<400> 971															
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	Tyr
			20					25					30		
Trp	Met	His	Trp	Ile	Arg	Gln	Ser	Pro	Ser	Arg	Gly	Leu	Glu	Trp	Leu
		35				40						45			
Gly	Asn	Ile	Tyr	Pro	Gly	Thr	Gly	Gly	Ser	Asn	Phe	Asp	Glu	Lys	Phe
	50					55					60				
Lys	Asn	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Thr	Arg	Trp	Thr	Thr	Gly	Thr	Gly	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		

Val Thr Val Ser Ser
115

<210> 972
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 972

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 973
<211> 113
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 973

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 974

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 974

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser

20

25

30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Ile
50 55 60

Pro Pro Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 975
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 975

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 976
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 976

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100

105

110

Lys

<210> 977
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 977

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
 35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
 65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

<210> 978
 <211> 113
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 978

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 979

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 979

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 980
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 980

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50

55

60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 981
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 981

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 982
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 982

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 983

<211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 983

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 984
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 984

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr

20

25

30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Trp Ala
35 40 45

Ser Ser Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Ser Cys
85 90 95

Ala Ala Ser Gln Ala Pro Ile Thr Ile Ala Thr Met Met Lys Pro Phe
100 105 110

Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 985
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 985

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Ala Lys Cys Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Trp Val
35 40 45

Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Ala Arg His Gly Gly Pro Leu Thr Val Glu Tyr Phe Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 986
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 986

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Tyr Tyr
20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Ala Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Gly Gly Asp Asn Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Gly Gly Trp Lys Tyr Cys Ser Gly Tyr Asp Pro Glu Tyr Ile

100

105

110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 987
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 987

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ser Gln Tyr
20 25 30

Asp Val Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Phe Ser Ser Ser Gly Gly Arg Thr Ile Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Phe Ser Arg Asp Asn Thr Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Thr Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ile Asp Trp Tyr Leu Asn Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser
115

<210> 988
<211> 114
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 988

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Asp Ala Ser Asn Ser
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Trp Val
35 40 45

Ala Arg Ile Thr Gly Gly Gly Leu Ile Ala Tyr Thr Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Thr Ile Asn Ser Arg Asp Gly Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser

<210> 989

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 989

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

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Ser Leu Thr Ile Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Asp Ser
20 25 30

Ile Val Ser Trp Tyr Arg Arg Ala Arg Gly Lys Gln Arg Glu Trp Val
35 40 45

Ala Gly Ile Ser Asn Gly Gly Thr Thr Lys Tyr Ala Glu Ser Val Leu
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Val Tyr Leu
65 70 75 80

Gln Met Asn Gly Leu Asn Pro Glu Asp Thr Ala Val Tyr Leu Cys Lys
85 90 95

Val Arg Gln Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
100 105 110

<210> 990
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 990

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Ser Thr Val Leu Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu

65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Asp Val Tyr Pro Gln Asp Tyr Gly Leu Gly Tyr Val Glu Gly Lys
100 105 110

Val Tyr Tyr Gly His Asp Tyr Trp Gly Thr Gly Thr Leu Val Thr Val
115 120 125

Ser Ser
130

<210>	991
<211>	119
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 991

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ser Asn Tyr
20 25 30

Val Ser Asn Tyr Ala Met Gly Trp Gly Arg Gln Ala Pro Gly Thr Gln
35 40 45

Arg Glu Leu Val Ala Ser Ile Ser Asn Gly Asp Thr Thr Asn Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Phe Glu His Gln Val Ala Gly Leu Thr Trp Gly Gln Gly
 100 105 110

Thr Gln Val Thr Val Ser Ser
 115

<210> 992
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (27)..(27)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (32)..(32)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (75)..(75)
 <223> Xaa can be any naturally occurring amino acid

<400> 992

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Xaa Ala Leu Lys Ile Xaa
 20 25 30

Val Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Thr Asn Tyr Ser Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Gly Asp Asn Ala Xaa Asn Thr Val Tyr Leu

65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Arg
 85 90 95

Glu Trp Asn Ser Gly Tyr Pro Pro Val Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser
115

<210>	993
<211>	120
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polymer

<400> 993

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Gly
20 25 30

Thr Met Gly Trp Phe Arg Arg Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ser Ile Pro Trp Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Thr Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Lys Glu Arg Ser Thr Gly Trp Asp Phe Ala Ser Trp Gly Gln
100 105 110

Gly Ile Gln Val Thr Val Ser Ser
115 120

<210> 994
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 994

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Gly Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Phe Ile Ser Gly Ser Asp Gly Ser Thr Tyr Tyr Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Asp Pro Trp Gly Pro Pro Ser Ile Ala Thr Met Thr Ser Tyr
100 105 110

Glu Tyr Lys His Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 995
<211> 113
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 995

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Thr Met Ile Trp Leu Arg Arg Ala Pro Gly Lys Gly Phe Glu Trp Val
35 40 45

Ser Thr Ile Asp Lys Asp Gly Asn Thr Asn Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Ala Val Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Thr
85 90 95

Lys His Gly Ser Ser Ala Arg Gly Gln Gly Thr Arg Val Thr Val Ser
100 105 110

Ser

<210> 996

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 996

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Asn Ser Gly Gly Gly Ile Thr Tyr Arg Gly Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Glu
85 90 95

Asn Gly Gly Ser Ser Tyr Arg Arg Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser

<210> 997
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 997

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe
50 55 60

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Lys Asp Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 998
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 998

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

100

105

110

Ser Ser

<210> 999
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 999

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

Ser Ser

<210> 1000
 <211> 114
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1000

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 1001

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1001

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Thr Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 1002
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1002

Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Thr Val Thr Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50

55

60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 1003

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1003

Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 1004
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1004

Asp Ile Val Met Thr Gln Ser Pro Ala Phe Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 1005

<211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1005

Asp Ile Val Met Thr Gln Ser Pro Ala Phe Leu Ser Val Thr Pro Gly
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 100 105 110

Lys

<210> 1006
 <211> 504
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1006

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys

1	5	10	15
Leu	Leu	Leu	Ala
	20	Ala	Ser
		Cys	Ala
		Trp	Ser
		Gly	Val
		Ala	Gly
		Glu	Glu
		30	
Glu	Leu	Gln	Val
	35	Ile	Gln
		Pro	Asp
		Lys	Ser
		Val	Leu
		Val	Ala
		Ala	Gly
		45	
Glu	Thr	Ala	Thr
	50	Leu	Arg
		Cys	Thr
		Ala	Thr
		Ser	Leu
		Ile	Pro
		Val	Gly
		60	
Pro	Ile	Gln	Trp
	65	Phe	Arg
		Gly	Ala
		Gly	Pro
		Gly	Arg
		Glu	Leu
		Ile	Tyr
		80	
Asn	Gln	Lys	Glu
		Gly	His
		85	Phe
		Pro	Arg
		Val	Thr
		Thr	Val
		Ser	Asp
		95	Leu
Thr	Lys	Arg	Asn
		100	Asn
		Met	Asp
		Phe	Ser
		105	Ile
		Arg	Ile
		Gly	Asn
		110	Ile
		Thr	
Pro	Ala	Asp	Ala
		115	Gly
		Thr	Tyr
		Tyr	Cys
		Val	Lys
		Phe	Arg
		125	Lys
		Gly	Ser
Pro	Asp	Asp	Val
		130	Glu
		Phe	Lys
		135	Ser
		Gly	Ala
		Gly	Thr
		140	Glu
		Leu	Ser
		Val	
Arg	Ala	Lys	Pro
		145	Ser
		Ala	Pro
		Val	Val
		Ser	Gly
		155	Pro
		Ala	Ala
		Arg	Ala
		160	
Thr	Pro	Gln	His
		165	Thr
		Val	Ser
		Phe	Thr
		Cys	Glu
		170	Ser
		His	Gly
		175	Phe
		Ser	
Pro	Arg	Asp	Ile
		180	Thr
		Leu	Lys
		Trp	Phe
		185	Lys
		Asn	Gly
		Asn	Glu
		190	Leu
		Ser	
Asp	Phe	Gln	Thr
		195	Asn
		Val	Asp
		Pro	Val
		Gly	Glu
		Ser	Val
		205	Ser
		Tyr	Ser
Ile	His	Ser	Thr
		Ala	Lys
		Val	Val
		Leu	Thr
		Arg	Glu
		Asp	Val
		His	Ser

210

215

220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu

420

425

430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 1007

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1007

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

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Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
165 170 175

Tyr Ser Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val
180 185 190

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
275 280 285

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Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
305 310 315 320

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
325 330 335

Ser Asn Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu
340 345 350

Leu Val Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln
355 360 365

Lys Lys Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu
370 375 380

Lys Asn Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala
385 390 395 400

Asp Leu Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu
405 410 415

Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro
420 425 430

Ala Ser Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu
435 440 445

Asn Arg Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser
450 455 460

Glu Tyr Ala Ser Val Gln Val Pro Arg Lys
465 470

<210> 1008
<211> 508
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1008

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser

180

185

190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys

385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Val Gln Ser Leu Asp Thr Asn Asp Ile Thr
420 425 430

Tyr Ala Asp Leu Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala
435 440 445

Ala Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro
450 455 460

Gln Pro Ala Ser Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val
465 470 475 480

His Leu Asn Arg Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser
485 490 495

Phe Ser Glu Tyr Ala Ser Val Gln Val Pro Arg Lys
500 505

<210> 1009
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1009

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45

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Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195 200 205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
245 250 255

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Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
290 295 300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 1010
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1010

Gly Gly Gly Gly Ser
1 5

<210> 1011
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1011

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 1012
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1012

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

<210> 1013
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1013

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 1014
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1014

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 1015
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1015

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25 30

<210> 1016
 <211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1016

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser
 35

<210> 1017
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1017

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser
 35 40

<210> 1018
 <211> 16
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1018

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 1019

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1019

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 1020

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1020

Gly Gly Gly Gly Gly Gly
1 5

<210> 1021

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1021

Glu Ala Ala Ala Lys
1 5

<210> 1022
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1022

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
 1 5 10

<210> 1023
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1023

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
 1 5 10 15

<210> 1024
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1024

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
 1 5 10

<210> 1025
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1025

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Ala

<210> 1026
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1026

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala
20

<210> 1027
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1027

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
20 25

<210> 1028
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1028

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 1029

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1029

Pro Ala Pro Ala Pro
1 5

<210> 1030

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1030

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15

Leu Asp

<210> 1031

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1031

Glu	Gly	Lys	Ser	Ser	Gly	Ser	Gly	Ser	Glu	Ser	Lys	Ser	Thr
1				5					10				

<210> 1032

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1032

Gly	Ser	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Gly	Glu	Phe
1				5					10		

<210> 1033

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1033

Gly	Gly	Ser
1		

<210> 1034

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1034

Gly	Gly	Ser	Gly	Gly	Ser
1				5	

<210> 1035

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1035

Gly Gly Ser Gly Gly Ser Gly Gly Ser
 1 5

<210> 1036
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1036

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 1 5 10

<210> 1037
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1037

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 1 5 10 15

<210> 1038
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1038

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly

1 5 10 15

Gly Ser

<210> 1039
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1039

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 1 5 10 15

Gly Ser Gly Gly Ser
 20

<210> 1040
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1040

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser
 20

<210> 1041
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1041

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
20 25

<210> 1042
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1042

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
20 25 30

<210> 1043
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1043

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser

<210> 1044
<211> 36
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1044

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser
35

<210> 1045

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1045

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser
35

<210> 1046

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1046

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly

1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40

<210> 1047
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1047

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40 45

<210> 1048
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1048

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser

35

40

45

<210> 1049
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1049

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40 45

Gly Gly Ser
50

<210> 1050
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1050

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40 45

Gly Gly Ser Gly Gly Ser

50

<210> 1051
 <211> 57
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1051

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 35 40 45

Gly Gly Ser Gly Gly Ser Gly Gly Ser
 50 55

<210> 1052
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1052

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 35 40 45

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser

50

55

60

<210> 1053
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1053

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40 45

<210> 1054
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1054

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser
50

<210> 1055

<211> 55
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1055

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser
 50 55

<210> 1056
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1056

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 50 55 60

<210> 1057

<211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1057

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 50 55 60

Ser
 65

<210> 1058
 <211> 70
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1058

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

50

55

60

Ser Gly Gly Gly Gly Ser
65 70

<210> 1059
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1059

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75

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<223> Synthetic polymer

<400> 1060

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

20

25

30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

<210> 1061

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1061

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser
85

<210> 1062

<211> 90

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1062

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

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20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90

<210> 1063

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<400> 1063

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1 5 10 15

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20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

<210> 1064
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<220>
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<400> 1064

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
85 90 95

Gly Gly Gly Ser
100

<210> 1065

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<400> 1065

Gly Gly Gly Ser Glu
 1 5

<210> 1066
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<220>
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<400> 1066

Gly Ser Glu Ser Gly
 1 5

<210> 1067
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1067

Gly Ser Glu Gly Ser
 1 5

<210> 1068
 <211> 35
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<400> 1068

Gly Glu Gly Gly Ser Gly Glu Gly Ser Ser Gly Glu Gly Ser Ser Ser

1 5 10 15

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
20 25 30

Gly Gly Ser
35

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<400> 1069

Cys Pro Pro Cys
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<210> 1070
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 1070
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<210> 1071
<211> 29
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<213> Artificial Sequence

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<400> 1072
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<210> 1073
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<212> DNA
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<220>
<223> Synthetic polymer

<400> 1073
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<210> 1074
<211> 24
<212> DNA
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<220>
<223> Synthetic polymer

<400> 1074
cgccagggtt ttcccagtca cgac 24

<210> 1075
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
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cctgtctacg ggtcgacggt tggggactac tggggccagg ggacccagggt caccgtctcc	360
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 <213> Artificial Sequence

<220>
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tag	423

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<220>
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tag	423

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<220>
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tag	423

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cctatctacg ggtcgacggc agaggactac tggggccagg ggacccagggt caccgtctcc	360
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tag	423

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<220>
 <223> Synthetic polymer

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<220>
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<210> 1083
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

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ccaggggaagc agcgcgagtt ggtcgcagct attactaatg gaggtagaac aacctatgca	180
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tag	423

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<220>
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tag 423

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tag 423

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<212> DNA
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<220>
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<220>
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<210> 1090
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<220>
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<400> 1090
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<210> 1091
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 <212> DNA
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<220>
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<400> 1091
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<213> Artificial Sequence

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<223> Synthetic polymer

<400> 1092

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ccagggaagc agcgcgagtt ggtcgcagct attactaatt agggtaggac aacgtatgca	180
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<210> 1093

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1093

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ggacggttcg atgactactg gggccagggg acccaggtca cctctcctc agcggccgca	360
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<211> 405

<212> DNA

<213> Artificial Sequence

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<223> Synthetic polymer

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<220>
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<210> 1096
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acatatgact actggggcca ggggaccag gtcaccgtct cctcagcggc cgcataccgc	360
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<210> 1097
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1097	
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ccaggaaagc agcgcgagct ggtcgcagca attactaatc aagggtgccac aacctatgca	180
gactccgtga agggccgatt caccatctcc agagacaccg ccgggaacac ggtgtatctg	240
caaatgaaca gcctgagacc tgaggacacg gccgtccatt actgtaaagc ctttacgagg	300
actgatgact actggggcca ggggaccag gtcaccgtct cctcagcggc cgcataccgc	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1098
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1098	
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tcctgtgcag cctctggaag aatcttcagt gtcaatgcca tgggttggtta ccgccaggct	120
ccaggaaagc agcgcgagtt ggtcgcagct attactaatc aagggtgccc aacctatgca	180

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gactccgtga agggccgatt caccatctcc agagacaacg ccgggaacac ggtgtatctg	240
caaatgaaca gcctgagacc tgaggacacg gccgtctatt actgtaaagc ctttacgagg	300
ggagatgact attggggcca ggggaccag gtcaccgtct cctcagcggc cgcataccg	360
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<210> 1099
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1099	
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ccaggaaagc agcgcgagtt ggtcgcagct attactaatg gtggtcagac aacgtatgca	180
gactccgtga agggccgatt caccatctcc agagacaacg ccgggaacac ggtgtatctg	240
caaatgaaca gtttgagacc tgaggacacg gccgtctatt actgtaaagc ctttacgagg	300
agcgatgact actggggcca ggggaccag gtcaccgtct cctcagcggc cgcataccg	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1100
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1100	
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tcctgtgcag cctctggaag aatcggcagt atcaattcta tgggctggta ccgccaggct	120
ccaggaaagc agcgcgaaat ggtcgcagct attactaatg gtggtgccac agtctatgca	180
gactccgtga agggccgatt caccatctcc agagacaacg ccgggaacac ggtagatctg	240
cacatgaaca gcctgagacc tgaggactcg gccgtctatt actgtaaagc ctttacgagg	300

ggagatgact actggggcca ggggacccag gtcaccgtct cctcagcggc cgcatacccg 360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1101
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1101
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ccaggaaagc agcgcgaaat ggtcgcagct attactaatg gtggtgccac agtctatgca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccgggaacac ggtagatctg 240
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gattatcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
ccgtacgacg ttccggacta cggttccac caccatcacc atcactag 408

<210> 1102
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1102
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tcctgtgcag cctctggagg aatttccagt atcaattcca tgggctggta ccgccaggct 120
ccaggaaatc agcgcgaaat ggtcgcaggc attactaatg gtggtaggac agtgtatgga 180
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caaatggaca gcctgagacc tgaggacact ggcgtgtatt actgtaaaagc ctttacgagg 300
ggagatgact actggggcca ggggacccag gtcaccgtct cctcagcggc cgcatacccg 360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1103
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1103
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 ccagggaagc agcgcgagtt ggtcgcggct attactgatg gtggcagatt aacctatgca 180
 gactccgcga agggccgatt caccatctcc agagagaaca cccggaacac ggtgcatctg 240
 caaatgagta gcctgaaagc cgaggacaca gccgactatt actgtacaat atggaccagg 300
 gatcggcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
 ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag 408

<210> 1104
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1104
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 ccagggaagc agcgcgagtt ggtcgcggct attactgatg gtggcagatt aacctatgca 180
 gactccgcga agaaccgatt caccatctcc agagagaaca cccgcaacac ggtgcatctg 240
 caaatgagta gcctgaaagc cgaggacaca gccgtctatt actgtacaat atggacaaaa 300
 gatcggcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
 ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag 408

<210> 1105
 <211> 408
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1105

caggtgcagc tgcaggagtc tggaggaggc ttggtggaga ctgggggggc tctgagactc	60
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ccagggaagc agcgcgagtt ggtcgcggct attactgatc aaggtagatt agcctacgca	180
gactccgcga agggccggtt caccatctcc agagagaacg cccggaacac gctgcatctg	240
caaatgagta gcctgaaagc cgaggacaca gccgtctatt actgtacaat atgggacagg	300
gatcggcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttccac caccatcacc atcactag	408

<210> 1106

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1106

caggtgcagc tgcaggagtc tgggggaggc ttggtgcagg ctggggaatc tctgagactc	60
tcctgtgcag cctctgtaag catcttccgc agttatttca tgggctggta ccgtcaggct	120
ccagggaagc agcgagagtt ggtcgcggct attactgatg gtggcagatt ggcctatgca	180
gactccgcga agggccgatt caccatctcc agagaagaca cccggaacac ggtgcatctg	240
caaatgagta gcctgaaagc cgaggacaca gccgtctatt actgtacaat atggaccacg	300
gatcggcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttccac caccatcacc atcactag	408

<210> 1107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1107
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tcctgtgcag cctctggaag gttcttcaga gtcaatgcc a tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgcagct attactaatg gtggacaaac agcctatgca 180
gactccgtga agggccgatt caccatctcc aaggagagcg cccggaacac ggtgcatctg 240
caaatgagta gcctgaaacc cgaagacaca gccgtctatt actgtacaat atgggcagcg 300
gattatcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
ccgtacgacg ttccggacta cggttccac caccatcacc atcactag 408

<210> 1108
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1108
caggtgcagc tgcaggagtc tgggggaggc ttggtgcaga ctgggggggtc tctgagactc 60
tcctgtgcag cctctggaag catcttcaat atcaattcca tgggctggta ccgccaggct 120
ccagggaagc agcgcgaatt ggtcgcggct attactgttg gtggcagatt agcctatgca 180
gactccgcga agggccgatt caccatctcc aaggagagcg cccggaacac ggtgcatctg 240
caaatgagta gcctgaaacc cgaagacaca gccgtctatt actgtacaat atgggcagcg 300
gattatcaac agtattgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
ccgtacgacg ttccggacta cggttccac caccatcacc atcactag 408

<210> 1109
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1109
caggtgcagc tgcaggagtc tgggggaggc ttggtgcaga ctgggggggtc tctgagactc 60

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tcctgtgcag cctctggaag catcttcagt atcaactcca tgggctggta ccgccaggct	120
ccagggaagc agcgcgagtt ggtcgcggct attactagtc aaggtagatc aacttatgca	180
gactccgcga agggccgatt caccatctcc ttagggaacg cccggaacac ggtgaatctg	240
caaatgagta gcctgaaaac tgaggacaca gccgtctatt actgtacaat ctgggccagg	300
gatcggcaac agtactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag	408

<210> 1110
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1110 caggtgcagc tgcaggagtc tggaggaggc ttggtgcaga ctggggagtc tctgagcctc	60
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gctccagaga agcagcgcga attggtcgcg gctattactg ttgatggcag attagcctat	180
gcagactccg cgaagcaccg attcaccatc tccaaagaga gcgcccggaa cacggtgcat	240
ctgcacatga gtagtttgaa acccgaggac acagccgtct attactgtac aatctgggtc	300
agggatgggc aacagtattg gggccagggg acccaggtca ccgtctcctc agcggccgca	360
tacccgtacg acgttccgga ctacggttcc caccaccatc accatcacta g	411

<210> 1111
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1111 caggtgcagc tgcaggagtc tgggggaggc ttggtgcaga ccggggggtc tctgagactc	60
tcctgtgcag cctctgtaag catcagcagt atcaattcca tgggctggta ccgccaggct	120
ccagggaagg agcgcgagtt ggtcgcggca gtcactgttg gcggcagata tgcctacgca	180

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gactccgcga agaaccgatt caccatctcc agagacgacg cccagaacac ggtacatctg	240
caaatgagta gcctgagagc cgaggacaca gccgtctatt actgtacaat atgggacagg	300
gatcggcaac agtattgggg ctaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag	408

<210> 1112
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1112	
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cacggggaac agcgcgagtt ggtcgcagct attactactg gtggtaggac aacatatgta	180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg	240
caaatgaaca gcctgaaacc tgaggatata gccgtctatt tctgtaaagc attcactaga	300
gatgaagact actggggcca ggggaccag gtcaccgtct cctcagcggc cgcatacccg	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1113
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1113	
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tcctgtgcag cctctggaag catcttcagt atcaatgcca tgggctggta ccgcccggct	120
ctaggggagc agcgcgagtt ggtcgcagct attactactg gtggtaggac aacatatgta	180
gactccgtga agggccgatt cagcatctcc agagacaacg ccaagaacac ggtgtatcta	240
caaatgaaca gcctgaaacc tgaggacaca gccgtctact tctgtaaagc attcactagg	300

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gatgaagact tctggggcca ggggacccag gtcaccgtct cctcagcggc cgcatacccg	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1114
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1114	
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tcctgtgcag cctctggaag catcgacagt atcaatgcc a tgggctggta ccgcccggct	120
ctagggggagc agcgcgagtt ggtcgcagct attactactg gtggtaggac ggcgtatgta	180
gactccgtga agggccgatt caccatctcc agagacgccg ccaagaacac ggtgtatctg	240
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gatacagact actggggcca ggggacccag gtcaccgtct cctcagcggc cgcatacccg	360
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<210> 1115
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1115	
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ccagggaagc agcgcgagtt ggttgcagct attactagtgt gtggtaggac aacatatgta	180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg	240
caaatgaaca gcctgaaacc tgaggacaca gccgtctatt tctgtaaagc atttactaga	300
gatgaagact actggggcca ggggacccag gtcaccgtct cctcagcggc cgcatacccg	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1116
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1116
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 cgggggaacg agcgcgagtt ggtcgcagct attactaatg gtggtaggac cacatatgta 180
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 tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1117
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1117
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 ctagggaacc agcgcgagtt ggtcgcagct attactaacg atggaaggac cacatatgta 180
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 tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1118
 <211> 408
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1118

caggtgcagc tgcaggagtc tgggggaggc ttggtgcagg ctggggaatc tctgagactc	60
tcctgtgcag cctctggatc gagcgacagt atcaatgcc a tgggctggta ccgccaggct	120
ccagggaagc agcgcgagtt ggtcgcggcg attactagtg gtgggagatc aacctatata	180
gactccgcga agggccgagc gaccatctcc agagacaacg cccggaacac ggcgtatttg	240
caaatgagta gcctgaaagc tgaggacaca gccgtctatt actgtacaat atggaacagg	300
gatcggcaac aatactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag	408

<210> 1119

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1119

caggtgcagc tgcaggagtc tggaggaggc ttggtgcagg ctggggggtc tctgaggctc	60
tcctgtgcag cctctggaag catcaccagt atcaatgcc a tgggctggta ccgccaggct	120
ccagggaagc agcgcgagtt ggtcgcagct attactagtg gtggtagatt aagctatgca	180
gactccgtga agggccgatt caccatctcc agagacaacg ccgagagcac ggtggctctg	240
caaatgaaca gcctgaaacc tgaggacaca gccgtctata gctgtgcagc ctttcaaagc	300
agcggaatag actggggcca ggggaccag gtcaccgtct cctcagcggc cgcatacccg	360
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<210> 1120

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1120
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ccagggaagc agcgcgagtt ggtcgcagcg attactaatc aaggtaggct aagctatgta 180
gactccgtga agggccgatt caccatctcc agagacaacg ccgcgaacac ggtgtatctg 240
caaatgaaca gcctgaaacc tgaggacaca gccgtctatt actgtgcagc ctttcaaagc 300
agcggaatag actggggcca ggggaccag gtcaccgtct cctcagcggc cgcatacccg 360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1121
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1121
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tcctgtgcag cctatggaag catcttcagt atcaacgccca tgggctggta ccgccaggct 120
ccagggaagg agcgcgagtt ggtcgcaggt attactacac aaggtaggat aacgtatgga 180
aactccgtga ggggccgatt caccatctcc ggagacaacg ccaagaacac ggtatatctg 240
caaatgaaaa gcctgaaacc tgaggacacg gccgtctatt actgtagtgc ctgggggtgta 300
aagacggggc ctgaatccgg tagcggtagc ttggaaggcc aggggacca ggtcaccgtc 360
tcctcagcgg ccgcataccc gtacgacgtt ccggactacg gttcccacca ccatcaccat 420
cactag 426

<210> 1122
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1122

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ccaggggggc agcgcgagtt ggtcggaggt attactagt atggtagcac aggctatgca	180
gactccgtga agggccgatt caccgtctcc agagacaacg ccaagaacac ggtgtatctg	240
caaatgaaca gactgaaacc tgaggacaca gccgtctatt actgtgggac tagtacacct	300
cgtggtgata gctactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag	408

<210> 1123
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1123	
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ccaggaagc gccgcgagtt ggtcggaggt attacgtctg atggtagcac aggctatgca	180
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caaatgaaca gcctgaaacc tgaggacaca gccgtttatt actgtgggac tagtacacct	300
cgtggtgata gctactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac	360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag	408

<210> 1124
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1124	
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gactccgtga agggccgatt caccatctcc agcgacaaca ccaagaacac ggtgtttctg	240
caaatgaaca gtctgaaacc tgaggacacg gccgtctatt actgtaatgc ctggactaca	300
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 <212> DNA
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<220>
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tatgcagact ccgtgaaggg ccgattcacc atctccagag acaacgcca gaacacgggtg	240
tatctgcaaa tgaatagtct gcaacctgag gatacggccg tctattactg taagggtttc	300
cgatctgggg cgcatgacta ctggggccag gggaccagc tcaccgtctc ctgagcggcc	360
gcatacccgat acgacgttcc ggactacggt tcccaccacc atcaccatca ctag	414

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 <211> 411
 <212> DNA
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<220>
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<400> 1126	
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ccaggaagc agcgcggaatt ggtcgcaagt attactaatc aaggtattag aaattattca	180
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ORN-033PC_ST25.txt

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tggggtaaag aggactactg gggccagggg acccaggtca ccgtctcctc agcggccgca	360
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<210> 1127
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1127	
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aactccgtgc agggccgac caccatctcc agagacaacg tcaacaacac ggtgtatctt	240
caaatgaaca gcctaaaacc tgaggactcg gccgtctatt actgtaaagg atttacgggt	300
tggggtaaag aggactactg gggccagggg acccaggtca ccgtctcctc agcggccgca	360
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<210> 1128
 <211> 438
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1128	
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ccagggaagg agcgtgggct tgttgcagct attagctgga gtggtggtag cacatattat	180
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ctgcaaatga acagcctgaa gcctgaggac acggccgttt attactgtgc tgcagaggcc	300
gaaggagtg gccgagaggg aaacttttac gaacgtagct ggtaccaggg acaggggacc	360

caggtcaccg tctcctcagc ggccgcatac ccgtacgacg ttccggacta cggttcccac	420
caccatcacc atcactag	438

<210> 1129
 <211> 438
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1129	
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gcagactccg tgaagggccg attcaccatc tccagagaca acgccgagaa cacggtgtat	240
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gaagggagtg gccgagaggg aaacttttac gaacgtagct ggtaccaggg acaggggacc	360
caggtcaccg tctcctcagc ggccgcatac ccgtacgacg ttccggacta cggttcccac	420
caccatcacc atcactag	438

<210> 1130
 <211> 438
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1130	
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ccaggggaagg agcgtgacct tgtagcagct attagctgga gtggtggttc cacagagtat	180
cacgactccg tgaagggccg attcactatc tccagagaca acaccaagaa cacggtgtat	240
ctgcaaatga acagcctgaa agctgaggac acggccgttt attactgtgc agcagaggtc	300
gaagggagtg gccgagaggg aaacttttac ggtgctagct ggtacccggg acaggggacc	360

caggtcaccg tctcctcagc ggccgcatac ccgtacgacg ttccggacta cggttcccac	420
caccatcacc atcactag	438

<210> 1131
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1131	
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ccagggcagg agcgtgagtt tgccgcagct attaatggc gtggtggaga cacatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca acgtcaagaa cacggtgttt	240
ctgcaaatac acagcctgaa acctgaggac acggccgttt atttctgtgc agcccggctt	300
actactgaat atgactatgc ctactggggc caggggaccc aggtcaccgt ctctcagcg	360
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<210> 1132
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1132	
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gcgaccacat actgggggtca ggggaccag gtcaccgtct cctcagcggc cgcataccgc	360
tacgacgttc cggactacgg ttcccaccac catcaccatc actag	405

<210> 1133
 <211> 405
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1133
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 ccagagaaac aacgcgagtt ggtcgtgct attactactc agggtagaac aacatatgaa 180
 gactccgtga agggccgatt caccatctcc agagacggcg ccagaaacac ggtataccta 240
 caaatggaca gcctgaaacc cgaggatacg gccgtctatt attgtaaagc gtggacggct 300
 aaggatgact actggggcaa agggaccag gtcaccgtct cctcagcggc cgcatacccg 360
 tacgacgttc cggactacgg ttcccaccac catcaccatc actag 405

<210> 1134
 <211> 420
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<400> 1134
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 ccagggaagc agcgtgagtt tgtagcagca attaaactgga gtagtggtgg aatttcgtat 180
 tcaaactccg cgaagggccg attcgccctc tctagagata acgccaagaa cacggtgtat 240
 ctgcaaattg acagcctgaa acctgaggac acggccgttt attactgtgc agcggccagt 300
 tcggtcttaa gtggaactgt tgactactgg ggccagggga ccaggtcac cgtctcctca 360
 gcggccgcat acccgtacga cgttcgggac tacggttccc accaccatca ccatcactag 420

<210> 1135
 <211> 420
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1135

caggtgcagc tgcaggagtc tggaggaggc ttggtgcagg ctgggggttc tctgagagtc	60
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ccaggaaagc agcgtgagtt tgtagcagcg attaactgga gtagtggtgg gatttcgtat	180
tcaaacgccg cgaagggccg attcgccctc tctcgagata acgccaagaa cacggtgtat	240
ctgcaaattg acagcctgaa acctgaggac acggccgttt attactgtgc agcggccagt	300
tcgatcttaa gtggaactgt tgactactgg ggccagggga cccaggtcac cgtctcctca	360
gcggccgcat acccgtaga cgttccggac tacggttccc accaccatca ccatcactag	420

<210> 1136

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1136

caggtgcagc tgcaggagtc tggaggagga ttggtgcagg ctgggggttc tctgagactc	60
tcctgtgcag cttccggacg caccctcagt aactatgccg tagcctgggtt ccgccaggct	120
ccagggaagc agcgtgagct tgtagctgcg atttggtggg ctagtggtgg catatcgtat	180
gcaaactccg cgaagggccg attcgtcctc tccagagaca acgccaagaa cacggtgtat	240
ctgcaaattg acagcctgaa acctgaggac acggccgttt attactgtgc agcggccagt	300
tcggtcttaa gtggaactgc tgactactgg ggccagggga cccaggtcac cgtctcctca	360
gcggccgcat acccgtaga cgttccggac tacggttccc accaccatca ccatcactag	420

<210> 1137

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<400> 1137
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aactccgtga ggggccgatt caccgtctcc cgggacaacg ccaagagcac ggtgtatctg 240
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agtagtactc cgtactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag 408

<210> 1138
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1138
caggtgcagc tgcaggagtc tgggggagga ttggtgcagg ctgggggctc tctgagactc 60
tcctgtgcag cctctgtaaa catcggcact ctcaatagca tggcctggta ccgcgaggct 120
ccagggaagc agcgcgagtt ggtcgcaggt attactgggg gtggtcaaataaacctatgcg 180
aactccgtga ggggccgatt caccgtctcc cgggacatcg ccaagagcac ggcgtatctg 240
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agtgctactc cgtactgggg ccaggggacc caggtcaccg tctcctcagc ggccgcatac 360
ccgtacgacg ttccggacta cggttcccac caccatcacc atcactag 408

<210> 1139
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<400> 1139
caggtgcagc tgcaggagtc tgggggaggc ttagtgcagg ctggggggctc tctgagactc 60

ORN-033PC_ST25.txt

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<210> 1140
 <211> 432
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

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gacgactccg tgaagggccg attcaccatc tccagtgaca acgccaagaa cacggtgtat	240
ctgcaaatga acagcctgaa acctgaggac acggccgttt attactgtgc agcagaagtc	300
ccatctactt actcctgctc aggcttccgc gaggactaca aaggcaaagg gaccaggtc	360
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caccatcact ag	432

<210> 1141
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (135)..(135)
 <223> Xaa can be any naturally occurring amino acid

<400> 1141

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Val Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Thr Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val His Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Thr Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1142

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1142

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Ala Pro Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1143

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1143

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Asp Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Ser Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1144

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1144

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Thr Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Arg Asp Asp Tyr Trp Gly Gln Gly Thr Gln Ile Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1145

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1145

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Asn Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1146

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1146

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Ala Lys Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Thr Asp Asn Ala Gly Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asn Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1147

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1147

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Ile Ser Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Val Tyr Gly Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Gly Asn Thr Val His Leu
65 70 75 80

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1148

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1148

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Gly Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Met Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Thr Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Asp Leu
65 70 75 80

His Met Asn Ser Leu Arg Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Phe Thr Arg Gly Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1149

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1149

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Gly Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Met Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Ala Thr Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Thr Val Asp Leu
65 70 75 80

His Met Asn Ser Leu Arg Pro Glu Asp Ser Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1150

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1150

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Val Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Ser Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1151

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1151

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Gly Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Asp Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1152

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (137)..(137)

<223> Xaa can be any naturally occurring amino acid

<400> 1152

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Val Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Ala
85 90 95

Cys Lys Ala Phe Gly Arg Phe Asp Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His Xaa
130 135

<210> 1153

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1153

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Leu Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Phe Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Trp Tyr Asp Pro Leu Val Ile Glu Tyr Tyr Asp Asn Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1154

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (133)..(133)

<223> Xaa can be any naturally occurring amino acid

<400> 1154

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Phe Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Arg Pro Gly Trp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
100 105 110

Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His
115 120 125

His His His His Xaa
130

<210> 1155

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1155

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Ala
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Glu Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Pro Thr Gly Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1156

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1156

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Leu Thr Asp Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1157

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (54)..(54)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (134)..(134)

<223> Xaa can be any naturally occurring amino acid

<400> 1157

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Xaa Gly Arg Thr Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Thr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Phe Gly Ser Gly Gly Gly Val Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His
115 120 125

His His His His His Xaa
130

<210> 1158

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1158

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Ser Tyr
20 25 30

Thr Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Arg Thr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Ser Pro Thr Asp Asp Phe Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1159

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1159

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Leu Ala Ser Arg Ser Phe Ser Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Ile Ala Val Asn
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1160

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1160

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Arg Ser Phe Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Pro Ala Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1161

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1161

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Arg Asn Phe Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Gly Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Thr Val Asp Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ile Pro Val Tyr Gly Ser Thr Val Glu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His Xaa
130 135 140

<210> 1162

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1162

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Val Phe Ser Ile Asn
20 25 30

Ala Trp Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Ile Ala Tyr Ala Pro Ser Val Asn
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Pro Thr Pro Val Tyr Gly Ser Thr Val Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His Xaa
130 135 140

<210> 1163

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1163

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Ser Phe Ser Ser Ile Asn
20 25 30

Ala Met Gly Tyr Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Ser Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Met Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ser Pro Val Tyr Gly Ser Thr Val Glu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1164

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1164

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Phe Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Ile Ala Tyr Thr Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Asn Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ile Pro Ile Tyr Gly Ser Thr Ala Glu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1165

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1165

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Asp Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1166

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1166

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Phe Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Asn Arg Phe Thr Ile Ser Arg Glu Asn Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Lys Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1167

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1167

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Glu Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gln Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Arg Asn Thr Leu His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Asp Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1168

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1168

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Ser Ile Phe Arg Ser Tyr
20 25 30

Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asp Gly Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Glu Asp Thr Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Thr Thr Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1169

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1169

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gln Gly Arg Ser Thr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Leu Gly Asn Ala Arg Asn Thr Val Asn Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1170

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1170

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Val Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Ile Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Asp Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ala Ala Thr His Leu Ser Thr Val Ala Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His Xaa
130 135 140

<210> 1171

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (141)..(141)

<223> Xaa can be any naturally occurring amino acid

<400> 1171

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Ile Val Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Ala Ala Ser Tyr Val Ser Thr Val Ala Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp
115 120 125

Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1172

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1172

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Pro Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Val Phe Ala Ala Asp Gly Met Glu Tyr Trp Gly Lys Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1173

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1173

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Phe Phe Arg Val Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Gln Thr Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1174

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1174

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Asn Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Val Gly Gly Arg Leu Ala Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Ala Ala Asp Tyr Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1175

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa can be any naturally occurring amino acid

<400> 1175

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ser Asp Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Ser Thr Tyr Ile Asp Ser Ala Lys
50 55 60

Gly Arg Ala Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Ala Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Ile Trp Asn Arg Asp Arg Gln Gln Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
115 120 125

Ser His His His His His His Xaa
130 135

<210> 1176

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (138)..(138)

<223> Xaa can be any naturally occurring amino acid

<400> 1176

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ile Gly Asn Ile Ala Ser Ile Thr
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Ala Ser Ala Ser Arg Thr Thr Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Gln Pro Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Lys Gly Phe Arg Ser Gly Ala Asp Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp
115 120 125

Tyr Gly Ser His His His His His His Xaa
130 135

<210> 1177

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1177

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Ala
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Arg Ala Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Glu Asn Thr Val Ala Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Asp Val Tyr Tyr Cys Asn
85 90 95

Ala Lys Ala Asp His Asn Asp Tyr Trp Gly Gln Gly Thr Gln Ile Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1178

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1178

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Arg Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asp
20 25 30

Ala Met Gly Trp Tyr Arg Pro Ala His Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1179

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1179

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Pro Ala Leu Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Phe Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1180

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1180

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Leu Ser Ile Asn
20 25 30

Ser Met Gly Trp Tyr Arg Pro Ala Leu Gly Asn Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Asp Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Trp Cys Lys
85 90 95

Ala Phe Thr Arg Asp Lys Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1181

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1181

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Asp Ile Ser Ser Ile Asn
20 25 30

Ala Met Gly Trp His Arg Pro Ala Arg Gly Asn Glu Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Tyr Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1182

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1182

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Asp Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Pro Ala Leu Gly Glu Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gly Gly Arg Thr Ala Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ala Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Ser Cys Lys
85 90 95

Ala Phe Thr Arg Asp Thr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1183

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1183

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ile Gly Ile Asn
20 25 30

Ser Met Gly Tyr Tyr Arg Thr Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Thr Thr Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys Lys
85 90 95

Ala Phe Thr Arg Asp Glu Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1184

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (137)..(137)

<223> Xaa can be any naturally occurring amino acid

<400> 1184

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Glu
1 5 10 15

Ser Leu Ser Leu Ser Cys Ala Val Ala Ser Gly Ser Ile Ile Ser Ile
20 25 30

Asn Ser Met Gly Trp Tyr Arg Gln Ala Pro Glu Lys Gln Arg Glu Leu
35 40 45

Val Ala Ala Ile Thr Val Asp Gly Arg Leu Ala Tyr Ala Asp Ser Ala
50 55 60

Lys His Arg Phe Thr Ile Ser Lys Glu Ser Ala Arg Asn Thr Val His
65 70 75 80

Leu His Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Trp Val Arg Asp Gly Gln Gln Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His Xaa
130 135

<210> 1185

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1185

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Val Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Glu Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Thr Gln Gly Arg Thr Thr Tyr Glu Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Gly Ala Gln Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
85 90 95

Ala Trp Thr Ala Lys Asp Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1186

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>
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 <222> (108)..(108)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (136)..(136)
 <223> Xaa can be any naturally occurring amino acid

<400> 1186

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Ser Ile Ser Ser Ile Asn
 20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
 35 40 45

Ala Ala Val Thr Val Gly Gly Arg Tyr Ala Tyr Ala Asp Ser Ala Lys
 50 55 60

Asn Arg Phe Thr Ile Ser Arg Asp Asp Ala Gln Asn Thr Val His Leu
 65 70 75 80

Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
 85 90 95

Ile Trp Asp Arg Asp Arg Gln Gln Tyr Trp Gly Xaa Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

<210> 1187
 <211> 135
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1187

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Thr Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Leu Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Ser Thr Val Ala Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Ser Cys Ala
85 90 95

Ala Phe Gln Ser Ser Gly Ile Asp Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1188

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (135)..(135)

<223> Xaa can be any naturally occurring amino acid

<400> 1188

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Val Ser Gly Arg Thr Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Asn Gln Gly Arg Leu Ser Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Ala Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Phe Gln Ser Ser Gly Ile Asp Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
115 120 125

His His His His His His Xaa
130 135

<210> 1189

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (142)..(142)

<223> Xaa can be any naturally occurring amino acid

<400> 1189

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Tyr Gly Ser Ile Phe Ser Ile Asn
20 25 30

Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35 40 45

Ala Gly Ile Thr Thr Gln Gly Arg Ile Thr Tyr Gly Asn Ser Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Gly Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Lys Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ser
85 90 95

Ala Trp Gly Val Lys Thr Gly Pro Glu Ser Gly Ser Gly Thr Leu Glu
100 105 110

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr
115 120 125

Asp Val Pro Asp Tyr Gly Ser His His His His His His Xaa
130 135 140

<210> 1190

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (137)..(137)

<223> Xaa can be any naturally occurring amino acid

<400> 1190

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Trp Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Ser Ile Val Ser Ile Asn
20 25 30

Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ser Ile Thr Asn Gln Gly Ile Arg Asn Tyr Ser Thr Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Val Lys Asn Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys
85 90 95

Gly Phe Ala Gly Trp Gly Lys Glu Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
115 120 125

Gly Ser His His His His His His Xaa
130 135

<210> 1191

<211> 146

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polymer

<220>

<221> misc_feature

<222> (146)..(146)

<223> Xaa can be any naturally occurring amino acid

<400> 1191

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Thr Tyr
20 25 30

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Gly Leu Val
35 40 45

Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ala Glu Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Glu Ala Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Glu Arg
100 105 110

Ser Trp Tyr Gln Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His Xaa
145

<210> 1192
 <211> 146
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (146)..(146)
 <223> Xaa can be any naturally occurring amino acid

<400> 1192

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ala Trp Phe Arg Gln Ala Pro Gly Met Glu Arg Glu Leu Val
 35 40 45

Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Glu Ala Glu Gly Ser Gly Arg Glu Gly Asn Phe Tyr Glu Arg
 100 105 110

Ser Trp Tyr Gln Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ala Ala
 115 120 125

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
 130 135 140

His Xaa
145

<210> 1193
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (146)..(146)
<223> Xaa can be any naturally occurring amino acid

<400> 1193

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Phe	Ser	Thr	Tyr
			20					25					30		

Ala	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Asp	Leu	Val
		35					40					45			

Ala	Ala	Ile	Ser	Trp	Ser	Gly	Gly	Ser	Thr	Glu	Tyr	His	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr	Val	Tyr
65					70					75					80

Leu	Gln	Met	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Ala	Glu	Val	Glu	Gly	Ser	Gly	Arg	Glu	Gly	Asn	Phe	Tyr	Gly	Ala
			100					105					110		

Ser	Trp	Tyr	Pro	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ala
		115					120					125			

Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His
130 135 140

His Xaa
145

<210> 1194
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polymer

<220>
<221> misc_feature
<222> (136)..(136)
<223> Xaa can be any naturally occurring amino acid

<400> 1194

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Thr Ser Phe Ser Ile Asn
20 25 30

Gly Met Ala Trp Tyr Arg Gln Ala Pro Gly Gly Gln Arg Glu Leu Val
35 40 45

Gly Gly Ile Thr Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Arg Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
85 90 95

Thr Ser Thr Pro Arg Gly Asp Ser Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

<210> 1195
 <211> 136
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (136)..(136)
 <223> Xaa can be any naturally occurring amino acid

<400> 1195

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Thr Leu Phe Ser Ile Asn
 20 25 30

Gly Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Arg Arg Glu Leu Val
 35 40 45

Gly Gly Ile Thr Ser Asp Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Ala Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly
 85 90 95

Thr Ser Thr Pro Arg Gly Asp Ser Tyr Trp Gly Gln Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

<210> 1196
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (139)..(139)
 <223> Xaa can be any naturally occurring amino acid

<400> 1196

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Pro Gly Tyr
 20 25 30

Val Met Ala Trp Phe Arg Gln Ser Pro Gly Gln Glu Arg Glu Phe Ala
 35 40 45

Ala Ala Ile Asn Trp Arg Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Thr Val Phe
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Ala Arg Leu Thr Thr Glu Tyr Asp Tyr Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro
 115 120 125

Asp Tyr Gly Ser His His His His His His Xaa
 130 135

<210> 1197
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (137)..(137)
 <223> Xaa can be any naturally occurring amino acid

<400> 1197

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Arg Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ile Gly Ser Ile Phe Glu Ile Asn
 20 25 30

Ser Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Ile Thr Asn Tyr Ala Asn Ser Val Gln
 50 55 60

Gly Arg Ser Thr Ile Ser Arg Asp Asn Val Asn Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Ser Ala Val Tyr Tyr Cys Lys
 85 90 95

Gly Phe Thr Gly Trp Gly Lys Glu Asp Tyr Trp Gly Gln Gly Thr Gln
 100 105 110

Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr
 115 120 125

Gly Ser His His His His His His Xaa
 130 135

<210> 1198
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (144)..(144)
 <223> Xaa can be any naturally occurring amino acid

<400> 1198

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu His Glu Gly Val
 35 40 45

Ser Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr Tyr Asp Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Glu Val Pro Ser Thr Tyr Ser Cys Ser Gly Phe Arg Glu Asp
 100 105 110

Tyr Lys Gly Lys Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr
 115 120 125

Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His His His His Xaa
 130 135 140

<210> 1199
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (135)..(135)
 <223> Xaa can be any naturally occurring amino acid

<400> 1199

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly
 1 5 10 15

Ser Leu Gln Leu Ser Cys Ala Ala Ser Gly Arg Ala Phe Ser Thr Asn
 20 25 30

Ser Met Gly Trp Tyr Arg Gln Ala Ser Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gln Gly Arg Ile Thr Leu Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Ser Asp Asn Thr Lys Asn Thr Val Phe Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95

Ala Trp Thr Thr Leu Gly Thr Phe Gly Gly Gln Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His Xaa
 130 135

<210> 1200
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (135)..(135)
 <223> Xaa can be any naturally occurring amino acid

<400> 1200

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Phe Leu Ser Leu Ser Cys Ala Ala Ser Gly Ser Met His Ser Val Asn
 20 25 30

Ser Met Ala Trp Tyr Arg Gln Val Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Arg Leu Ala Tyr Ala Pro Ser Val Asn
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Tyr Ala Lys Asn Thr Ile His Leu
 65 70 75 80

Gln Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Leu Asn Ser Ala Thr Thr Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 115 120 125

His His His His His His Xaa
 130 135

<210> 1201
 <211> 136
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polymer

<220>
 <221> misc_feature
 <222> (136)..(136)
 <223> Xaa can be any naturally occurring amino acid

<400> 1201

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Asn Ile Asp Thr Leu Asn
 20 25 30

Ser Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Gly Ile Thr Gly Ser Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
 50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Ser Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Thr Leu Gln Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Tyr Asp Arg Ser Ser Thr Pro Tyr Trp Gly Gln Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

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<220>
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 <223> Xaa can be any naturally occurring amino acid

<400> 1202

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Asn Ile Gly Thr Leu Asn
 20 25 30

Ser Met Ala Trp Tyr Arg Glu Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Gly Ile Thr Gly Gly Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
 50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Ile Ala Lys Ser Thr Ala Tyr Leu
 65 70 75 80

Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Tyr Asp Arg Ser Ala Thr Pro Tyr Trp Gly Gln Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

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<220>
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<220>
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 <223> Xaa can be any naturally occurring amino acid

<400> 1203

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Val Asn Ile Gly Ser Leu Asn
 20 25 30

Ser Met Val Trp Tyr Arg Gln Ser Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Gly Ile Thr Gly Ser Gly Gln Ile Thr Tyr Ala Asn Ser Val Arg
 50 55 60

Gly Arg Phe Thr Val Ser Arg Asp Ile Ala Lys Ser Thr Ala Tyr Leu
 65 70 75 80

Gln Met Asn Thr Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Tyr Asp Arg Ser Ala Thr Ala Tyr Trp Gly Gln Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly
 115 120 125

Ser His His His His His His Xaa
 130 135

<210> 1204
 <211> 140
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 <213> Artificial Sequence

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 <222> (140)..(140)
 <223> Xaa can be any naturally occurring amino acid

<400> 1204

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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 20 25 30

Ala Val Gly Trp Trp Arg Gln Ala Pro Gly Lys Gln Arg Glu Phe Val
 35 40 45

Ala Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser Tyr Ser Asn Ser Ala
 50 55 60

Lys Gly Arg Phe Ala Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Ala Ser Ser Val Leu Ser Gly Thr Val Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
 115 120 125

Pro Asp Tyr Gly Ser His His His His His His Xaa
 130 135 140

<210> 1205
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 <223> Xaa can be any naturally occurring amino acid

<400> 1205

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Asn Tyr
 20 25 30

Ala Val Ala Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Phe Val
 35 40 45

Ala Ala Ile Asn Trp Ser Ser Gly Gly Ile Ser Tyr Ser Asn Ala Ala
 50 55 60

Lys Gly Arg Phe Ala Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Ala Ser Ser Ile Leu Ser Gly Thr Val Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ala Ala Tyr Pro Tyr Asp Val
 115 120 125

Pro Asp Tyr Gly Ser His His His His His His Xaa
 130 135 140

<210> 1206
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<220>
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<400> 1206

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Leu Ser Asn Tyr
 20 25 30

Ala Val Ala Trp Phe Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Trp Trp Ala Ser Gly Gly Ile Ser Tyr Ala Asn Ser Ala
 50 55 60

Lys Gly Arg Phe Val Leu Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ala Ala Ser Ser Val Leu Ser Gly Thr Ala Asp Tyr Trp Gly Gln
 100 105 110

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Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Tyr	Pro	Tyr	Asp	Val
		115					120					125			

Pro	Asp	Tyr	Gly	Ser	His	His	His	His	His	His	Xaa
	130					135					140