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PD-L1 variant immunomodulatory proteins and uses thereof

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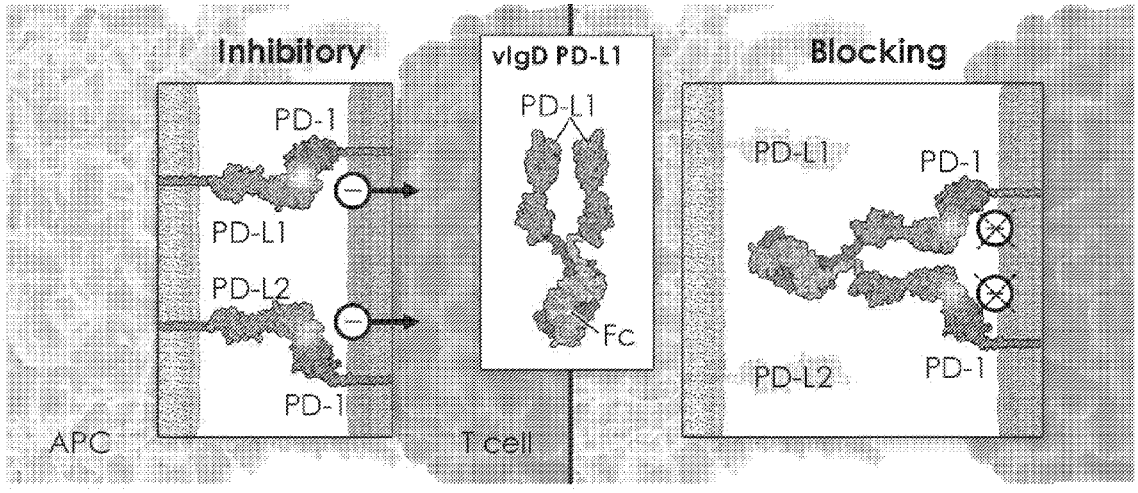
FIG. 2



(57) Abstract: Provided herein are immunomodulatory proteins comprising variant PD-L1 and nucleic acids encoding such proteins. The immunomodulatory proteins provide therapeutic utility for a variety of immunological and oncological conditions. Compositions and methods for making and using such proteins are provided.

[Continued on next page]

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— *of inventorship (Rule 4.17(iv))*

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— *with sequence listing part of description (Rule 5.2(a))*

PD-L1 VARIANT IMMUNOMODULATORY PROTEINS AND USES THEREOF

Cross-Reference to Related Applications

[0001] This application claims priority from U.S. provisional application No. 62/472,554 filed March 16, 2017, entitled "PD-L1 Variant Immunomodulatory Proteins and Uses Thereof," U.S. provisional application No. 62/475,076 filed March 22, 2017, entitled "PD-L1 Ligand Variant Immunomodulatory Proteins and Uses Thereof," U.S. provisional application No. 62/537,923 filed July 27, 2017, entitled "PD-L1 Ligand Variant Immunomodulatory Proteins and Uses Thereof," and U.S. provisional application No. 62/582,249 filed November 6, 2017, entitled "PD-L1 Ligand Variant Immunomodulatory Proteins and Uses Thereof," the contents of each of which are incorporated by reference in their entirety.

Incorporation by Reference of Sequence Listing

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled 761612001040SeqList.TXT, created February 24, 2018 which is 3,329,416 bytes in size. The information in the electronic format of the Sequence Listing is incorporated by reference in its entirety.

Field

[0003] The present disclosure relates to therapeutic compositions for modulating immune response in the treatment of cancer and immunological diseases. In some aspects, the present disclosure relates to particular variants of PD-L1 that exhibit improved binding, such as improved binding affinity or selectivity, for one or more of the cognate binding partner proteins PD-1 and CD80.

Background

[0004] Modulation of the immune response by intervening in the processes that occur in the immunological synapse (IS) formed by and between antigen-presenting cells (APCs) or target cells and lymphocytes is of increasing medical interest. Mechanistically, cell surface proteins in the IS can involve the coordinated and often simultaneous interaction of multiple protein targets with a single protein to which they bind. IS interactions occur in close association with the junction of two cells, and a single protein in this structure can interact with both a protein on the

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same cell (cis) as well as a protein on the associated cell (trans), likely at the same time. Although therapeutics are known that can modulate the IS, improved therapeutics are needed. Provided are immunomodulatory proteins, including soluble proteins or transmembrane immunomodulatory proteins capable of being expressed on cells, that meet such needs.

[0004a] Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of common general knowledge in the field.

[0004b] Unless the context clearly requires otherwise, throughout the description and the claims, the words "comprise", "comprising", and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to".

Summary

[0004c] In one aspect, the present disclosure provides a variant PD-L1 polypeptide, comprising an IgV domain or both an IgV domain and an IgC domain, wherein the variant PD-L1 polypeptide comprises an amino acid substitution N45D in an unmodified human PD-L1 with reference to the numbering of SEQ ID NO:30; wherein the variant PD-L1 polypeptide comprises a sequence of amino acids that exhibits at least 90% sequence identity to SEQ ID NO:30; wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity compared to the binding of the unmodified human PD-L1 to the ectodomain of PD-1; wherein the unmodified PD-L1 comprises the sequence of amino acids set forth in SEQ ID NO:30 or a portion thereof comprising the IgV domain or the IgV domain and the IgC domain.

[0004d] In another aspect, the present disclosure provides an immunomodulatory protein, comprising a variant PD-L1 polypeptide of the invention, directly or indirectly via a linker, to a second polypeptide comprising an immunoglobulin superfamily (IgSF) domain of an IgSF family member.

[0004e] In another aspect, the present disclosure provides an immunomodulatory protein comprising a variant PD-L1 polypeptide of the invention linked to an Fc domain or a variant thereof with reduced effector function.

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[0004f] In another aspect, the present disclosure provides a conjugate that is a fusion protein, comprising a variant PD-L1 polypeptide of the invention, or an immunomodulatory protein of the invention linked to a targeting moiety that specifically binds to a molecule on the surface of a cell.

[0004g] In another aspect, the present disclosure provides a nucleic acid molecule, encoding a variant PD-L1 polypeptide of the invention, an immunomodulatory protein of the invention, or a conjugate of the invention.

[0004h] In another aspect, the present disclosure provides a vector, comprising a nucleic acid molecule of the invention.

[0004i] In another aspect, the present disclosure provides a cell comprising or engineered by the vector of the invention, wherein the cell is isolated.

[0004j] In another aspect, the present disclosure provides a method of producing a variant PD-L1 polypeptide or an immunomodulatory protein, comprising introducing a nucleic acid molecule of the invention or vector of the invention into a host cell under conditions to express the protein in the cell, wherein the method is *ex vivo*.

[0004k] In another aspect, the present disclosure provides a pharmaceutical composition, comprising a variant PD-L1 polypeptide of the invention, an immunomodulatory protein of the invention, a conjugate of the invention, a nucleic acid of the invention, a vector of the invention, or a cell of the invention.

[0004l] In another aspect, the present disclosure provides an article of manufacture comprising a pharmaceutical composition of the invention in a vial.

[0004m] In another aspect, the present disclosure provides a kit comprising a pharmaceutical composition of the invention or an article of manufacture of the invention, and instructions for use.

[0004n] In another aspect, the present disclosure provides use of a pharmaceutical composition in the manufacture of a medicament for modulating an immune response in a subject, wherein the pharmaceutical composition comprises a variant PD-L1 polypeptide of the invention, an immunomodulatory protein of the invention, a conjugate of the invention, a nucleic acid of the invention, a vector of the invention, or a cell of the invention.

[0004o] In another aspect, the present disclosure provides a method of modulating an immune response in a subject comprising administering to the subject a variant PD-L1 polypeptide of the invention, an immunomodulatory protein of the invention, a conjugate of the invention, a nucleic acid of the invention, a vector of the invention, or a cell of the invention.

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[0005] Provided herein is a variant PD-L1 polypeptide, containing an IgV domain or a specific binding fragment thereof, an IgC domain or a specific binding fragment thereof, or both, wherein the variant PD-L1 polypeptide contains one or more amino acid modifications in an unmodified PD-L1 or a specific binding fragment thereof corresponding to position(s) selected from 6, 10, 11, 14, 15, 16, 17, 18, 19, 20, 22, 23, 26, 27, 28, 33, 35, 36, 40, 41, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 60, 64, 65, 68, 71, 72, 73, 74, 75, 78, 79, 83, 85, 87, 89, 90, 93, 97, 98, 99, 101, 102, 103, 104, 106, 110, 111, 112, 113, 117, 119, 120, 121, 124, 129, 130, 131, 134, 137, 138, 144, 148, 149, 150, 155, 158, 160, 163, 165, 167, 170, 171, 173, 175, 176, 177, 179, 180, 183, 185, 188, 189, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 207, 213, or 221, with reference to the numbering of SEQ ID NO:30 or 1728. In some cases, the amino acid modification is an amino acid substitution, insertion or deletion.

[0006] In some embodiments, the unmodified PD-L1 is a mammalian PD-L1 or a specific binding fragment thereof. In some embodiments, the unmodified PD-L1 is a human PD-L1 or a specific binding fragment thereof. In some of any such embodiments, the unmodified PD-L1 contains (i) the sequence of amino acids set forth in SEQ ID NO:30 or 1728, (ii) a sequence of amino acids that has at least 95% sequence identity to SEQ ID NO:30 or 1728; or (iii) a portion thereof including an IgV domain or IgC domain or specific binding fragments thereof or both.

[0007] In some of any such embodiments, the specific binding fragment of the IgV domain or IgC domain has a length of at least 50, 60, 70, 80, 90, 100, 110 or more amino acids; or the specific binding fragment of the IgV domain contains a length that is at least 80% of the length of the IgV domain set for as amino acids 24-130 of SEQ ID NO:3 and/or the specific binding fragment of the IgC domain contains a length that is at least 80% of the length of the IgC domain set forth as amino acids 133-225 of SEQ ID NO:3. In some of any such embodiments, the variant PD-L1 contains up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid modifications, optionally amino acid substitutions, insertions and/or deletions. In some of any such embodiments, the variant PD-L1 polypeptide contains a sequence of amino

acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:30, 1728, or a specific binding fragment thereof.

[0008] In some of any such embodiments, the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of PD-1 compared to the binding of the unmodified PD-L1 to the ectodomain of PD-1. In some embodiments, the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of CD80 compared to the binding of the unmodified PD-L1 to the ectodomain of CD80. In some of any such embodiments, the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of PD-1 compared to the unmodified PD-L1. In some embodiments, the altered binding is altered binding affinity and/or altered binding selectivity.

[0009] In some of any such embodiments, the one or more amino acid modifications are selected from P6S, Y10F, V11A, V11E, Y14S, G15A, S16G, N17D, M18I, M18T, M18V, T19A, T19I, I20L, C22R, K23E, K23N, K23R, E26A, E27D, E27G, K28E, K28I, K28N, K28R, A33D, L35P, I36S, I36T, E40G, M41K, M41V, D43G, D43V, K44E, N45D, N45I, N45T, I46V, I47T, F49S, V50A, H51N, H51R, H51Y, G52R, G52V, E53G, E53V, E54G, D55G, D55N, D55S, D55V, L56Q, K57E, K57R, V58A, V58D, H60R, R64S, Q65L, R68L, K71E, D72G, Q73R, L74P, S75P, N78I, N78S, A79T, I83T, D85E, Q89R, D90G, V93E, M97I, M97K, M97L, I98L, I98T, I98V, S99G, G101D, G101G-ins (G101GG), G102D, A103V, D104G, K106E, K106R, V110M, K111E, K111T, V112A, N113Y, N117S, I119T, N120S, Q121L, L124S, V129A, V129D, T130A, S131F, E134G, C137R, Q138R, K144E, K144Q, I148V, W149R, T150A, Q155H, S158G, K160M, T163I, K163N, N165Y, K167R, K167T, E170G, K171R, F173I, F173L, K173Y, V175A, S177C, L179P, R180S, T183A, T183I, T185A, I188V, F189L, F189S, T192S, F193S, R194G, R194W, R195G, R195S, R195T, L196S, D197G, P198S, P198T, E199G, E200K, E200N, N201D, N201Y, H202Q, T203A, A204T, L206F, V207A, L213P, T221L or a conservative amino acid substitution thereof. In some of any such embodiments, the one or more amino acid modifications are selected from among K28N/M41V/N45T/H51N/K57E, I20L/I36T/N45D/I47T, I20L/M41K/K44E, P6S/N45T/N78I/I83T, N78I, M41K/N78I, N45T/N78I, I20L/N45T, N45T, M41K, I20L/I36T/N45D, N17D/N47T/V50A/D72G, I20L/F49S, N45T/V50A, I20L/N45T/N78I, I20L/N45T/V50A, M41V/N45T, M41K/N45T, A33D/S75P/D85E, M18I/M41K/D43G/H51R/N78I, V11E/I20L/I36T/N45D/H60R/S75P, A33D/V50A, S16G/A33D/K71E/S75P, E27G/N45T/M97I, E27G/N45T/K57R, A33D/E53V,

D43G/N45D/V58A, E40G/D43V/N45T/V50A, Y14S/K28E/N45T, A33D/N78S, A33D/N78I, A33D/N45T, A33D/N45T/N78I, E27G/N45T/V50A, N45T/V50A/N78S, I20L/N45T/V110M, I20L/I36T/N45T/V50A, N45T/L74P/S75P, N45T/S75P, S75P/K106R, S75P, A33D/S75P, A33D/S75P/D104G, A33D/S75P, I20L/E27G/N45T/V50A, I20L/E27G/D43G/N45D/V58A/N78I, I20L/D43G/N45D/V58A/N78I, I20L/A33D/D43G/N45D/V58A/N78I, I20L/D43G/N45D/N78I, E27G/N45T/V50A/N78I, N45T/V50A/N78I, V11A/I20L/E27G/D43G/N45D/H51Y/S99G, I20L/E27G/D43G/N45T/V50A, I20L/K28E/D43G/N45D/V58A/Q89R, I20L/I36T/N45D, I20L/K28E/D43G/N45D/E53G/V58A/N78I, A33D/D43G/N45D/V58A/S75P, K23R/D43G/N45D, I20L/D43G/N45D/V58A/N78I/D90G/G101D, D43G/N45D/L56Q/V58A/G101G-ins (G101GG), I20L/K23E/D43G/N45D/V58A/N78I, I20L/K23E/D43G/N45D/V50A/N78I, T19I/E27G/N45I/V50A/N78I/M97K, I20L/M41K/D43G/N45D, K23R/N45T/N78I, I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG), K57R/S99G, K57R/S99G/F189L, M18V/M97L/F193S/R195G/E200K/H202Q, I36S/M41K/M97L/K144Q/R195G/E200K/H202Q/L206F, C22R/Q65L/L124S/K144Q/R195G/E200N/H202Q/T221L, M18V/I98L/L124S/P198T/L206F, S99G/N117S/I148V/K171R/R180S, I36T/M97L/A103V/Q155H, K28I/S99G, R195S, A79T/S99G/T185A/R195G/E200K/H202Q/L206F, K57R/S99G/L124S/K144Q, K57R/S99G/R195G, D55V/M97L/S99G, E27G/I36T/D55N/M97L/K111E, E54G/M97L/S99G, G15A/I36T/M97L/K111E/H202Q, G15A/I36T/V129D, G15A/I36T/V129D/R195G, G15A/V129D, I36S/M97L, I36T/D55N/M97L/K111E/A204T, I36T/D55N/M97L/K111E/V129A/F173L, I36T/D55S/M97L/K111E/I148V/R180S, I36T/G52R/M97L/V112A/K144E/V175A/P198T, I36T/I46V/D55G/M97L/K106E/K144E/T185A/R195G, I36T/I83T/M97L/K144E/P198T, I36T/M97L/K111E, I36T/M97L/K144E/P198T, I36T/M97L/Q155H/F193S/N201Y, I36T/M97L/V129D, L35P/I36S/M97L/K111E, M18I/I36T/E53G/M97L/K144E/E199G/V207A, M18T/I36T/D55N/M97L/K111E, M18V/M97L/T176N/R195G, M97L/S99G, N17D/M97L/S99G, S99G/T185A/R195G/P198T, V129D/H202Q, V129D/P198T, V129D/T150A, V93E/V129D, Y10F/M18V/S99G/Q138R/T203A, N45D, K160M/R195G, N45D/K144E, N45D/P198S, N45D/P198T, N45D/R195G, N45D/R195S, N45D/S131F, N45D/V58D, V129D/R195S, I98T/F173Y/L196S, N45D/E134G/L213P, N45D/F173I/S177C, N45D/I148V/R195G, N45D/K111T/R195G, N45D/N113Y/R195S, N45D/N165Y/E170G,

N45D/Q89R/I98V, N45D/S131F/P198S, N45D/S75P/P198S, N45D/V50A/R195T, E27D/N45D/T183A/I188V, F173Y/T183I/L196S/T203A, K23N/N45D/S75P/N120S, N45D/G102D/R194W/R195G, N45D/G52V/Q121L/P198S, N45D/I148V/R195G/N201D, N45D/K111T/T183A/I188V, N45D/Q89R/F189S/P198S, N45D/S99G/C137R/V207A, N45D/T163I/K167R/R195G, N45D/T183A/T192S/R194G, N45D/V50A/I119T/K144E, T19A/N45D/K144E/R195G, V11E/N45D/T130A/P198T, V26A/N45D/T163I/T185A, K23N/N45D/L124S/K167T/R195G, K23N/N45D/Q73R/T163I, K28E/N45D/W149R/S158G/P198T, K28R/N45D/K57E/I98V/R195S, K28R/N45D/V129D/T163N/R195T, M41K/D43G/N45D/R64S/R195G, M41K/D43G/N45D/R64S/S99G, N45D/R68L/F173L/D197G/P198S, N45D/V50A/I148V/R195G/N201D, M41K/D43G/K44E/N45D/R195G/N201D, or N45D/V50A/L124S/K144E/L179P/R195G.

[0010] In some of any such embodiments, the one or more amino acid modifications correspond to position(s) selected from 20, 27, 28, 33, 36, 41, 43, 45, 50, 58, 71, 75 or 78. In some embodiments, the one or more amino acid substitutions are selected from I20L,E27G, K28E, A33D, I36T, M41K, D43G, N45D, N45T, V50A, V58A, K71E, S75P, N78I, or a conservative amino acid substitution thereof.

[0011] In some of any such embodiments, the one or more amino acid modifications correspond to position(s) selected from 20, 27, 33, 36, 43, 45, 50, 58, 75, 78, 97, 99, or 195. In some embodiments, the one or more amino acid substitutions are selected from I20L,E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide contains amino acid modifications I20L/I36T, I20L/D43G, I20L/N45D, I20L/N45T, I20L/N45T, I20L/V50A, I20L/V58A, I20L/S75P, I20L/N78I, I36T/D43G, I36T/N45D, I36T/N45T, I36T/V50A, I36T/V58A, I36T/S75P, I36T/N78I, D43G/N45D, D43G/N45T, D43G/V50A, D43G/V58A, D43G/S75P, D43G/N78I, N45D/V50A, N45D/V58A, N45D/S75P, N45D/N78I, N45T/V50A, N45T/V58A, N45T/S75P, N45T/N78I, V50A/V58A, V50A/S75P, V50A/N78I, V58A/S75P, V58A/N78I, or S75P/N78I. In some particular embodiments, the variant PD-L1 polypeptide contains amino acid modifications D43G/N45D/V58A. In some aspects, the variant PD-L1 polypeptide contains amino acid modifications D43G/N45D/L56Q/V58A/G101G-ins (G101GG) or I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG).

[0012] In some of any such embodiments, the variant PD-L1 polypeptide contains the variant PD-L1 polypeptide comprises or consists of the PD-L1 extracellular domain (ECD); and/or the variant PD-L1 polypeptide comprises or consists of the IgV domain or a specific fragment thereof and the IgC domain or a specific fragment thereof. In some of any such embodiments, the variant PD-L1 polypeptide includes the sequence of amino acids set forth in any of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008 or a specific binding fragment thereof, or a sequence of amino acids that exhibits at least 95% sequence identity to any of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008 or a specific binding fragment thereof and that contains the one or more of the amino acid substitutions.

[0013] In some of any such embodiments, the variant PD-L1 polypeptide contains the IgV domain or a specific binding fragment thereof. In some of any such embodiments, the IgV domain or specific binding fragment thereof is the only PD-L1 portion of the variant PD-L1 polypeptide. In some embodiments, the IgC domain or specific binding fragment thereof is the only PD-L1 portion of the variant PD-L1 polypeptide.

[0014] In some of any such embodiments, the variant PD-L1 polypeptide contains the sequence of amino acids set forth in any of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937 or a specific binding fragment thereof, a sequence of amino acids that exhibits at least 95% sequence identity to any of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937 or a specific binding fragment thereof and that contains the one or more of the amino acid substitutions. In some embodiments, the IgC domain or specific binding fragment thereof is the only PD-L1 portion of the variant PD-L1 polypeptide.

[0015] In some of any such embodiments, the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 or CD80 with increased affinity compared to the binding of the unmodified PD-L1 to the same ectodomain of PD-1 or CD80. In some of any such embodiments, the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity compared to the binding of the unmodified PD-L1 to the ectodomain of PD-1. In some of any such embodiments, the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 and the ectodomain of CD80 each with increased affinity compared to the binding of the unmodified PD-L1 to the same ectodomains. In some of any such embodiments, the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity and specifically binds to the ectodomain of CD80 with decreased affinity compared to the binding of the unmodified PD-L1 to the same ectodomains.

[0016] In some of any such embodiments, the increased affinity to the ectodomain of PD-1 is increased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold or 60-fold compared to the unmodified PD-L1. In some aspects, the increased affinity to the ectodomain of CD80 is increased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold or 60-fold compared to the unmodified PD-L1. In some cases, the decreased affinity to the ectodomain of CD80 is decreased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold or 60-fold compared to the unmodified PD-L1.

[0017] In some of any such embodiments, the variant polypeptide specifically binds to the ectodomain of PD-1 with increased selectivity compared to the unmodified PD-L1. In some instances, the increased selectivity comprises a greater ratio of binding of the variant polypeptide for PD-1 versus CD80 compared to the ratio of binding of the unmodified PD-L1 polypeptide for the same ectodomains of PD-1 versus CD80. In some examples, the ratio is greater by at least or at least about 1.5-fold, 2.0-fold, 3.0-fold, 4.0-fold, 5-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold or more.

[0018] In some of any such embodiments, the PD-1 is a human PD-1. In some of any such embodiments, the CD80 is a human CD80.

[0019] In some of any such embodiments, the binding activity is altered (increased or decreased) more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold compared to the unmodified PD-L1.

[0020] In some of any such embodiments, the variant PD-L1 polypeptide is a soluble protein. In some of any such embodiments, the variant PD-L1 polypeptide lacks the PD-L1 transmembrane domain and intracellular signaling domain; and/or the variant PD-L1 polypeptide is not capable of being expressed on the surface of a cell. In some of any such embodiments, the variant PD-L1 polypeptide is linked to a multimerization domain. In some of any such embodiments, the variant PD-L1 polypeptide is a multimeric polypeptide, optionally a dimeric polypeptide, comprising a first variant PD-L1 polypeptide linked to a multimerization domain and a second variant PD-L1 polypeptide linked to a multimerization domain. In some embodiments, the first variant PD-L1 polypeptide and the second variant PD-L1 polypeptide are the same or different.

[0021] In some of any such embodiments, the multimerization domain is an Fc domain or a variant thereof with reduced effector function. In some of any such embodiments, the variant PD-L1 polypeptide is linked to a moiety that increases biological half-life of the polypeptide. In some of any such embodiments, the variant PD-L1 polypeptide is linked to an Fc domain or a variant thereof with reduced effector function.

[0022] In some of any such embodiments, the Fc domain is mammalian, optionally human; or the variant Fc domain comprises one or more amino acid modifications compared to an unmodified Fc domain that is mammalian, optionally human. In some of any such embodiments, the Fc domain or variant thereof contains the sequence of amino acids set forth in SEQ ID NO:187 or SEQ ID NO:188 or a sequence of amino acids that exhibits at least 85% sequence identity to SEQ ID NO:187 or SEQ ID NO:188. In some embodiments, the Fc domain comprises one or more amino acid modifications selected from among E233P, L234A, L234V, L235A, L235E, G236del, G237A, S267K, N297G, R292C, V302C, and K447del, each by EU numbering. In some embodiments, the Fc domain comprises the amino acid modification C220S by EU numbering. In some of any such embodiments, the Fc domain comprises the sequence of amino acids set forth in any of SEQ ID NOS: 1155, 1157, 1158, 1159, 1715, 1938, 1939, and 1940 or a sequence of amino acids that exhibits at least 85% sequence identity to any of SEQ ID NOS:1155, 1157, 1158, 1159, 1715, 1938, 1939, and 1940 and exhibits reduced effector function.

[0023] In some of any such embodiments, the variant PD-L1 polypeptide is linked indirectly via a linker, optionally a G4S linker. In some of any such embodiments, the variant PD-L1 polypeptide is a transmembrane immunomodulatory protein further containing a transmembrane domain linked to the extracellular domain (ECD) or specific binding fragment thereof of the variant PD-L1 polypeptide.

[0024] In some of any such embodiments, the transmembrane domain contains the sequence of amino acids set forth as residues 239-259 of SEQ ID NO:3 or a functional variant thereof that exhibits at least 85% sequence identity to residues 239-259 of SEQ ID NO:3. In some embodiments, the variant PD-L1 polypeptide further contains a cytoplasmic signaling domain linked to the transmembrane domain. In some instances, the cytoplasmic signaling domain contains the sequence of amino acids set forth as residues 260-290 of SEQ ID NO:3 or a functional variant thereof that exhibits at least 85% sequence identity to residues 260-290 of SEQ ID NO:3.

[0025] In some of any of the provided embodiments, the variant PD-L1 polypeptide modulates a response of an immune cell, such as a T cell. In some embodiments, the response, e.g. T cell response, is increased or is decreased. In some of any such embodiments, the variant PD-L1 increases IFN-gamma (interferon-gamma) expression relative to the unmodified PD-L1 in an in vitro T-cell assay. In some of any such embodiments, the variant PD-L1 decreases IFN-gamma (interferon-gamma) expression relative to the unmodified PD-L1 in an *in vitro* T-cell assay.

[0026] In some of any such embodiments, the variant PD-L1 polypeptide is deglycosylated.

[0027] In some embodiments of any one of the variant PD-L1 polypeptides described herein, the variant PD-L1 polypeptide increases T cell signaling relative to the unmodified PD-L1, such as determined using a reporter assay involving a T cell (e.g. Jurkat) engineered with a reporter (e.g. luciferase) operably connected to an IL-2 promoter. In some embodiments of any one of the variant PD-L1 polypeptides described herein, the variant PD-L1 polypeptide decreases T cell signaling relative to the unmodified PD-L1, such as determined using a reporter assay involving a T cell (e.g. Jurkat) engineered with a reporter (e.g. luciferase) operably connected to an IL-2 promoter. In some of any such embodiments, the variant PD-L1 polypeptide is provided in any of a variety of formats, such as soluble or immobilized (e.g. plate-bound).

[0028] Also provided is an immunomodulatory polypeptide containing the variant PD-L1 according to any of the provided embodiments linked, directly or indirectly via a linker, to a second polypeptide comprising an immunoglobulin superfamily (IgSF) domain. In some cases, the IgSF domain is affinity modified and exhibits altered binding to one or more of its cognate binding partner(s) compared to the unmodified or wild-type IgSF domain to the same one or more cognate binding partner(s). In some embodiments, the affinity-modified IgSF domain contains one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member. In some instances, the IgSF domain exhibits increased binding to one or more of its cognate binding partner(s) compared to the unmodified or wild-type IgSF domain of the IgSF family member to the same one or more cognate binding partner(s). In some examples, the IgSF domain is affinity modified and exhibits altered binding to one or more of its cognate binding partner(s) compared to the binding of the unmodified or wild-type IgSF domain of the IgSF family member to the same one or more cognate binding partner(s). In some embodiments, the variant PD-L1 is a first PD-L1 variant and the IgSF domain of the second

polypeptide is an IgSF domain from a second variant PD-L1 wherein the first and second PD-L1 variant are the same or different.

[0029] In some embodiments, the variant PD-L1 polypeptide is capable of specifically binding to PD-1 or CD80 and the IgSF domain of the second polypeptide is capable of binding to a cognate binding partner other than one specifically bound by the PD-L1 variant polypeptide. In some embodiments, the IgSF domain is from a member of the B7 family. In some cases, the IgSF domain is a tumor-localizing moiety that binds to a ligand expressed on a tumor or to an inflammatory-localizing moiety that binds to a cell or tissue associated with an inflammatory environment. In some embodiments, the IgSF domain is a tumor-localizing moiety that binds to a ligand expressed on a tumor. In some cases, the ligand is B7H6. In some embodiments, the IgSF domain is from NKp30.

[0030] In some embodiments, the IgSF domain or affinity-modified IgSF domain thereof, optionally of the second or third polypeptide, is or contains an IgV domain. In some embodiments, the variant PD-L1 polypeptide is or contains an IgV domain. In some embodiments, the immunomodulatory protein comprises a multimerization domain linked to one or both of the variant PD-L1 polypeptide of the IgSF domain. In some instances, the multimerization domain is an Fc domain or a variant thereof with reduced effector function. In some embodiments, the immunomodulatory protein is dimeric. In some embodiments, the immunomodulatory protein is homodimeric. In some embodiments, the immunomodulatory protein is heterodimeric.

[0031] In some of any such embodiments, the IgSF domain of the second polypeptide is an IgSF domain of a ligand that binds to an inhibitory receptor, or is an affinity-modified IgSF domain thereof. In some instances, the affinity-modified IgSF domain exhibits increased binding affinity and/or binding selectivity for the inhibitory receptor compared to binding of the unmodified IgSF domain to the same inhibitory receptor. In some embodiments, the inhibitory receptor is TIGIT, PD-1 or CTLA-4; or the ligand of the inhibitory receptor is PD-L2, CD155, CD112 or CD80.

[0032] In some of any such embodiments, the IgSF domain of the second polypeptide is an affinity-modified IgSF domain comprising: (i) a wildtype CD155 comprising an IgSF set forth in any of SEQ ID NOS: 47, 310, or 353, or a variant CD155 polypeptide comprising an IgSF domain of any of SEQ ID NOS set forth in Table 5, optionally any of the SEQ ID NOs: 311-352, 354-665, 1505-1576, 1551-1714; (ii) a wildtype CD112 comprising an IgSF domain set forth in

any of SEQ ID NOS: 48, 666, or 761, or a variant CD112 polypeptide comprising an IgSF domain of any of SEQ ID NOS set forth in Table 4, optionally any of the SEQ ID NOs: 667-760, 762-931, 1433-1504; (iii) a wildtype CD80 comprising an IgSF domain set forth in any of SEQ ID NOS: 28, 1005, or 2030, or a variant CD80 polypeptide comprising an IgSF of any of SEQ ID NOS: set forth in Table 3, optionally any of the SEQ ID NOs: 932-964, 966-1038, 1040-1078, 1080-1112, 1114-1152; (iv) a wildtype PD-L2 comprising an IgSF domain set forth in any of SEQ ID NOS: 31, 1203, or 1263, or a variant PD-L2 polypeptide comprising an IgSF domain of any of SEQ ID NOS set forth in Table 3, optionally any of the SEQ ID NOs: 1204-1254, 1256-1331, 1333-1407, 1409-1432; (v) a sequence of amino acids that exhibits at least 95% sequence identity to any of the SEQ ID NOSs in (i)-(iv) and that comprises the amino acid substitution; or (vi) a specific binding fragment of any of (i)-(v).

[0033] In some embodiments, the immunomodulatory protein further contains a third polypeptide comprising an IgSF domain of an IgSF family member or an affinity-modified IgSF domain thereof, said affinity-modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member. In some cases, the third polypeptide is the same as the first and/or second polypeptide or the third polypeptide is different from the first and/or second polypeptide. In some examples, the third polypeptide is selected from (i) a wildtype CD155 comprising an IgSF set forth in any of SEQ ID NOS: 47, 310, or 353, or a variant CD155 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS:311-352, 354-665, 1505-1576, 1551-1714; (ii) a wildtype CD112 comprising an IgSF domain set forth in any of SEQ ID NOS: 48, 666, or 761, or a variant CD112 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 667-760, 762-931, 1433-1504; (iii) a wildtype CD80 comprising an IgSF domain set forth in any of SEQ ID NOS: 28, 1005, or 2030, or a variant CD80 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 932-964, 966-1038, 1040-1078, 1080-1112, 1114-1152; (iv) a wildtype PD-L2 comprising an IgSF domain set forth in any of SEQ ID NOS: 31, 1203, or 1263, or a variant PD-L2 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 1204-1254, 1256-1331, 1333-1407, 1409-1432; (v) a sequence of amino acids that exhibits at least 95% sequence identity to any of the SEQ ID NOSs in (i)-(iv) and that comprises the amino acid substitution; or (vi) a specific binding fragment of any of (i)-(v). In some instances, the IgSF domain or affinity-modified IgSF domain thereof, optionally of the second or third polypeptide, is or contains an IgV domain. In some cases, the variant PD-L1 polypeptide is or contains an IgV domain.

[0034] In some embodiments, the immunomodulatory protein further contains at least one additional polypeptide comprising an IgSF domain of an IgSF family member or an affinity-modified IgSF domain thereof, said affinity-modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member. In some embodiments, the immunomodulatory protein further contains a multimerization domain linked to at least one of the variant PD-L1 polypeptide, or the second polypeptide. In some aspects, the immunomodulatory protein further contains a multimerization domain linked to at least one of the variant PD-L1 polypeptide, the second polypeptide and/or the third polypeptide. In some cases, the multimerization domain is an Fc domain or a variant thereof with reduced effector function. In some embodiments, the multimerization domain promotes heterodimer formation.

[0035] Provided is an immunomodulatory protein containing a first variant PD-L1 polypeptide in which the multimerization domain is a first multimerization domain and a second variant PD-L1 polypeptide in which the multimerization domain is a second multimerization domain, wherein the first and second multimerization domains interact to form a multimer containing the first and second variant PD-L1 polypeptide, optionally wherein the first and second variant PD-L1 polypeptide are the same. In some cases, the multimerization domain is a first multimerization domain and interacts with a second multimerization domain to form a multimer comprising the immunomodulatory protein. In some examples, the immunomodulatory protein is a first immunomodulatory protein and a second immunomodulatory protein is linked directly or indirectly via a linker to the second multimerization domain, wherein the multimer comprises the first and second immunomodulatory protein. In some embodiments, the second immunomodulatory protein is any of the immunomodulatory proteins described and the multimerization domain is the second multimerization domain. In some cases, the multimer is dimer. In some embodiments, the second polypeptide is a variant CD155 polypeptide and the first and/or second immunomodulatory protein includes the sequence set forth in any of SEQ ID NOS: 1716-1721, or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of SEQ ID NOS: 1716-1721; or the second polypeptide is CD112 or CD155 and the third polypeptide is the other of CD112 or CD155 and the first and/or second immunomodulatory portin comprise the sequence set forth in any of SEQ ID NOS: 1722-1724, or a sequence of amino acids that exhibits

at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of SEQ ID NOS: 1716-1721.

[0036] In some cases, the immunomodulatory protein is a homodimer. In some aspects, the immunomodulatory protein is a heterodimer, optionally wherein the first and second multimerization domain are different and/or are capable of interacting to mediate heterodimer formation.

In some embodiments, the first and/or second multimerization domain is an Fc domain or a variant thereof with reduced effector function, optionally wherein the Fc domain is of an immunoglobulin protein that is human and/or the Fc region is human, optionally wherein the Fc region is of an immunoglobulin G1 (IgG1) or an immunoglobulin G2 (IgG2), optionally set forth in SEQ ID NO:187 or SEQ ID NO:188, optionally wherein the Fc region exhibits one or more effector functions; or the variant Fc domain comprises one or more amino acid substitutions in a wildtype Fc region, optionally wherein the reduced effector function is reduced compared to a wildtype Fc region, optionally wherein the wildtype human Fc is of human IgG1. In some cases, the the first and second multimerization domain is the same or different.

[0037] In some embodiments, the variant Fc region contains the amino acid substitutions E233P, L234A, L234V, L235A, L235E, G236del, G237A, S267K, or N297G, with residue numbering according to the EU index of Kabat; or the amino acid substitutions R292C/N297G/V302C or L234A/L235E/G237A, with residue numbering according to the EU index of Kabat. In some examples, the Fc region or variant Fc region contains the amino acid substitution C220S, with residue numbering according to the EU index of Kabat. In some cases, the Fc region or variant Fc region contains K447del, with residue numbering according to the EU index of Kabat.

[0038] Also provided is a conjugate containing a variant PD-L1 according to any of the provided embodiments, or an immunomodulatory polypeptide according to any of the provided embodiments linked to a moiety. In some instances, the moiety is a targeting moiety that specifically binds to a molecule on the surface of a cell. In some aspects, the targeting moiety specifically binds to a molecule on the surface of an immune cell.

[0039] In some embodiments, the immune cell is an antigen presenting cell or a lymphocyte. In some cases, the targeting moiety is a tumor-localizing moiety that binds to a molecule on the surface of a tumor. In some examples, the moiety is a protein, a peptide, nucleic acid, small molecule or nanoparticle. In some embodiments, the moiety is an antibody or antigen-binding

fragment. In some of any such embodiments, the conjugate is divalent, tetravalent, hexavalent or octavalent. In some aspects, the conjugate is a fusion protein

[0040] Also provided is a nucleic acid molecule, encoding a variant PD-L1 polypeptide according to any of the provided embodiments, or an immunomodulatory polypeptide or conjugate that is a fusion protein according to any of the provided embodiments. In some embodiments, the nucleic acid molecule is synthetic nucleic acid. In some embodiments, the nucleic acid molecule is cDNA.

[0041] Also provided is a vector containing the nucleic acid molecule according to any of the provided embodiments. In some cases, the vector is an expression vector. In some aspects, the vector is a mammalian expression vector or a viral vector.

[0042] Also provided is a cell, comprising the vector according to any of the provided embodiments. In some instances, the cell is a mammalian cell. In some aspects, the cell is a human cell.

[0043] Also provided is a method of producing a variant PD-L1 polypeptide or an immunomodulatory protein, comprising introducing the nucleic acid molecule according to any of the provided embodiments or vector according to any of the provided embodiments into a host cell under conditions to express the protein in the cell. In some instances, the method further includes isolating or purifying the variant PD-L1 polypeptide or immunomodulatory protein from the cell. Also provided is a method of engineering a cell expressing a variant PD-L1 variant polypeptide including introducing a nucleic acid molecule encoding the variant PD-L1 polypeptide according to any of the provided embodiments into a host cell under conditions in which the polypeptide is expressed in the cell.

[0044] Also provided is an engineered cell, expressing the variant PD-L1 polypeptide according to any of the provided embodiments, the immunomodulatory protein according to any of the provided embodiments, the conjugate that is a fusion protein according to any of the provided embodiments, the nucleic acid molecule according to any of the provided embodiments or the vector according to any of the provided embodiments. In some cases, the variant PD-L1 polypeptide or immunomodulatory protein comprises a signal peptide. In some cases, the variant PD-L1 polypeptide or immunomodulatory protein is encoded by a nucleic acid including a sequence of nucleotides encoding comprises a signal peptide. In some embodiments, the variant PD-L1 polypeptide or immunomodulatory protein does not contain a transmembrane domain and/or is not expressed on the surface of the cell.

[0045] In some embodiments of the engineered cell, the variant PD-L1 polypeptide or immunomodulatory protein is secreted or capable of being secreted from the engineered cell. In some embodiments, the engineered cell contains a variant PD-L1 polypeptide that contains a transmembrane domain and/or is the transmembrane immunomodulatory protein according to any of the provided embodiments. In some embodiments, the variant PD-L1 polypeptide is expressed on the surface of the cell.

[0046] In some embodiments of the engineered cell, the cell is an immune cell. In some instances, the immune cell is an antigen presenting cell (APC) or a lymphocyte. In some embodiments, the cell is a primary cell. In some embodiments, the cell is a mammalian cell. In some embodiments, the cell is a human cell. In some embodiments, the lymphocyte is a T cell. In some embodiments, the APC is an artificial APC. In some examples, the cell is a lymphocyte and the lymphocyte is a T cell. In some aspects, the cell is an APC and the APC is an artificial APC. In some of any such embodiments, the engineered cell further contains a chimeric antigen receptor (CAR) or an engineered T-cell receptor.

[0047] Also provided is an infectious agent, containing a nucleic acid molecule encoding a variant PD-L1 polypeptide according to any of the provided embodiments, a conjugate that is a fusion protein of any of the provided embodiments, or an immunomodulatory polypeptide according to any of the provided embodiments. In some instances, the encoded variant PD-L1 polypeptide or immunomodulatory polypeptide does not contain a transmembrane domain and/or is not expressed on the surface of a cell in which it is expressed. In some embodiments, the encoded variant PD-L1 polypeptide or immunomodulatory polypeptide is secreted or capable of being secreted from a cell in which it is expressed. In some instances, the encoded variant PD-L1 polypeptide contains a transmembrane domain. In some embodiments, the encoded variant PD-L1 polypeptide is expressed on the surface of a cell in which it is expressed.

[0048] In some of any such embodiments, the infectious agent is a bacterium or a virus. In some embodiments, the virus is a lentiviral or retroviral construct or a hybrid thereof. In some aspects, the virus is an oncolytic virus. In some examples, the oncolytic virus is an adenovirus, adeno-associated virus, herpes virus, Herpes Simplex Virus, Vesticular Stomatic virus, Reovirus, Newcastle Disease virus, parvovirus, measles virus, vesticular stomatitis virus (VSV), Coxsackie virus or a Vaccinia virus. In some cases, the virus specifically targets dendritic cells (DCs) and/or is dendritic cell-tropic. In some examples, the virus is a lentiviral vector that is pseudotyped with a modified Sindbis virus envelope product. In some of any such embodiments,

the infectious agent further contains a nucleic acid molecule encoding a further gene product that results in death of a target cell or that can augment or boost an immune response. In some examples, the further gene product is selected from an anticancer agent, anti-metastatic agent, an antiangiogenic agent, an immunomodulatory molecule, an immune checkpoint inhibitor, an antibody, a cytokine, a growth factor, an antigen, a cytotoxic gene product, a pro-apoptotic gene product, an anti-apoptotic gene product, a cell matrix degradative gene, genes for tissue regeneration or reprogramming human somatic cells to pluripotency.

[0049] Also provided is a pharmaceutical composition containing the variant PD-L1 polypeptide according to any of the provided embodiments, an immunomodulatory protein according to any of the provided embodiments, a conjugate according to any of the embodiments, an engineered cell according to any of the provided embodiments or an infectious agent according to any of the provided embodiments. In some cases, the pharmaceutical composition contains a pharmaceutically acceptable excipient. In some embodiments, the pharmaceutical composition is sterile.

[0050] Also provided is an article of manufacture containing the pharmaceutical composition according to any of the provided embodiments in a vial. In some cases, the vial is sealed.

[0051] Also provided is a kit containing the pharmaceutical composition according to any of the provided embodiments and instructions for use. Also provided is a kit containing the article of manufacture according to any of the provided embodiments and instructions for use.

[0052] Also provided is a method of modulating an immune response, such as increasing or decreasing an immune response, in a subject, including administering the pharmaceutical composition according to any of the provided embodiments to the subject. In some embodiments, the method of modulating an immune response in a subject, includes administering the engineered cells according to any of the provided embodiments to the subject. In some cases, the engineered cells are autologous to the subject. In some instances, the engineered cells are allogenic to the subject. In some embodiments, the method that modulates the immune response treats a disease or condition in the subject. In some embodiments, the method comprises administering to the subject a soluble variant PD-L1 polypeptide according to any one of the embodiments described herein, an immunomodulatory protein according to any one of the embodiments described herein or a conjugate according to any one of the embodiments described herein. In some embodiments, the method comprises administering to the subject an infectious

agent encoding a variant PD-L1 polypeptide according to any one of the embodiments described herein.

[0053] In some of any such embodiments, the immune response is increased. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein that is soluble is administered to the subject. In some embodiments, the variant PD-L1 polypeptide or immunomodulatory protein is an Fc fusion protein. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein that is soluble, optionally that lacks a PD-L1 transmembane and intracellular signaling domain, is administered to the subject. In some cases, the soluble immunomodulatory protein is an immunomodulatory Fc fusion protein. In some embodiments, a variant PD-L1 polypeptide according to any of the provided embodiments, the immunomodulatory protein according to any of the provided embodiments, or the conjugate according to any of the provided embodiments is administered to the subject. In some embodiments, an engineered cell containing a secretable variant PD-L1 polypeptide is administered to the subject. In some of any such embodiments, an engineered cell according to any of the provided embodiments is administered to the subject. In some aspects, an infectious agent encoding a variant PD-L1 polypeptide that is a secretable immunomodulatory protein is administered to the subject, optionally under conditions in which the infectious agent infects a tumor cell or immune cell and the secretable immunomodulatory protein is secreted from the infected cell.

[0054] In some embodiment, the disease or condition is a tumor or cancer. In some examples, the disease or condition is selected from melanoma, lung cancer, bladder cancer, a hematological malignancy, liver cancer, brain cancer, renal cancer, breast cancer, pancreatic cancer, colorectal cancer, spleen cancer, prostate cancer, testicular cancer, ovarian cancer, uterine cancer, gastric carcinoma, a musculoskeletal cancer, a head and neck cancer, a gastrointestinal cancer, a germ cell cancer, or an endocrine and neuroendocrine cancer.

[0055] In some of any such embodiments, the immune response is decreased. In some embodiments, an immunomodulatory protein or conjugate containing a variant PD-L1 polypeptide linked to an IgSF domain or a moiety that localizes to a cell or tissue of an inflammatory environment is administered to the subject. In some cases, the binding molecule comprises an antibody or an antigen-binding fragment thereof or contains a wild-type IgSF domain or variant thereof. In some embodiments, the immunomodulatory protein according to

any of the provided embodiments or the conjugate according to any of the provided embodiments is administered to the subject.

[0056] In some embodiments, a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein is administered to the subject. In some embodiments, the engineered cell containing a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein according to any of the provided embodiments is administered to the subject. In some cases, an infectious agent encoding a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein is administered to the subject, optionally under conditions in which the infectious agent infects a tumor cell or immune cell and the transmembrane immunomodulatory protein is expressed on the surface of the infected cell.

[0057] In some embodiments, the disease or condition is an inflammatory or autoimmune disease or condition. In some of any such embodiments, the disease or condition is an antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis, a vasculitis, an autoimmune skin disease, transplantation, a Rheumatic disease, an inflammatory gastrointestinal disease, an inflammatory eye disease, an inflammatory neurological disease, an inflammatory pulmonary disease, an inflammatory endocrine disease, or an autoimmune hematological disease. In some examples, the disease or condition is selected from inflammatory bowel disease, transplant, Crohn's disease, ulcerative colitis, multiple sclerosis, asthma, rheumatoid arthritis, or psoriasis. In some of any such embodiments, the variant PD-L1 is administered in a format that decreases an immune response in the subject.

Brief Description of the Drawings

[0058] **FIG. 1A-1C** depicts various formats of the provided variant IgSF domain molecules. **FIG. 1A** depicts soluble molecules, including: (1) a variant IgSF domain (vIgD) fused to an Fc chain; (2) a stack molecule containing a first variant IgSF domain (first vIgD) and a second IgSF domain, such as a second variant IgSF domain (second vIgD); (3) a tumor targeting IgSF molecule containing a first variant IgSF domain (vIgD) and an IgSF domain that targets to a tumor antigen, such as an NKp30 IgSF domain; and (4) a variant IgSF domain (vIgD) linked to an antibody (V-mAb). **FIG. 1B** depicts a transmembrane immunomodulatory protein (TIP) containing a variant IgSF domain (vIgD) expressed on the surface of a cell. In an exemplary embodiment, the cognate binding partner of the transmembrane bound vIgD is an inhibitory receptor (e.g. PD-L1), and the TIP containing the vIgD (e.g. PD-L1 vIgD) antagonizes or blocks

the negative signaling of the inhibitory receptor, thereby resulting in an activated T cell or effector T cell. In some cases, if clustering of the inhibitory receptor (PD-1) is proximal to an activating receptor (e.g. CD28) then agonizing activity by the TIP may be realized. **FIG. 1C** depicts a secreted immunomodulatory protein (SIP) in which a variant IgSF domain (vIgD) is secreted from a cell, such as a first T cell (e.g. CAR T cell). In an exemplary embodiment, the cognate binding partner of the secreted vIgD is an inhibitory receptor (e.g., PD-1), which can be expressed by the first cell (e.g., T cell, such as a CAR T cell) and/or on a second cell (e.g. T cell; either endogenous or engineered, such as a CAR T cell). Upon binding of the SIP with its cognate binding partner, the SIP antagonizes or blocks the negative signaling via the inhibitory receptor, thereby resulting in an activated T cell or effector T cell. In all cases, the vIgD can be a V-domain (IgV) only, the combination of the V-domain (IgV) and C-domain (IgC), including the entire extracellular domain (ECD), or any combination of Ig domains of the IgSF superfamily member.

[0059] **FIG. 2** depicts an exemplary schematic of the activity of a variant IgSF domain (vIgD) fused to an Fc (vIgD-Fc) in which the vIgD is a variant of an IgSF domain of PD-L1. As shown, a soluble vIgD of PD-L1 interacts with its cognate binding partners to block interactions of PD-L1 or PD-L2 with PD-1, thereby blocking the PD-1 inhibitory receptor, and, in some cases, allowing the T cell to differentiate into an effector phenotype.

[0060] **FIG. 3** depicts an exemplary schematic of a stack molecule that is a multi-target checkpoint antagonist containing a first variant IgSF domain (first vIgD) that is a PD-L1 or PD-L2 vIgD and a second IgSF domain (e.g. a second vIgD) that binds to a second inhibitory receptor. In the exemplary schematic, the second IgSF domain (e.g. second vIgD) is a CD112 or CD155 vIgD. As shown, the first vIgD and second vIgD interact with their cognate binding partners to block interactions of PD-L1 or PD-L2 with PD-1 and block interactions of CD155 or CD112 with TIGIT and/or CD112R, respectively, thereby blocking multiple inhibitory receptors.

[0061] **FIG. 4** depicts an exemplary schematic of a stack molecule for localizing the variant IgSF (vIgD) to a tumor cell. In this format, the stack molecule contains a first variant IgSF domain (first vIgD) and a second IgSF domain (e.g. a second vIgD) in which the second IgSF domain (e.g a second vIgD) is a tumor-targeted IgSF domain that binds to a tumor antigen. An exemplary tumor-targeted IgSF domain is an IgSF domain of NKp30, which binds to the tumor antigen B7-H6. In this depiction, the variant IgSF domain (vIgD) is a variant of an IgSF domain of PD-L1. As shown, binding of tumor-targeted IgSF domain to the surface of the tumor cell

localizes the first variant IgSF domain on the tumor cell surface where it can interact with one or more of its cognate binding partners expressed on the surface of an adjacent immune cell (e.g. T cell) to antagonize PD-1 inhibitory activity and facilitate T cell activation.

[0062] **FIG. 5A** depicts various exemplary configurations of a stack molecule containing a first variant IgSF domain (first vIgD) and a second IgSF domain, such as a second variant IgSF domain (second vIgD). As shown, the first vIgD and second IgSF domain are independently linked, directly or indirectly, to the N- or C-terminus of an Fc region. For generating a homodimeric Fc molecule, the Fc region is one that is capable of forming a homodimer with a matched Fc region by co-expression of the individual Fc region in a cell. For generating a heterodimeric Fc molecule, the individual Fc region contain mutations (e.g. "knob-into-hole" mutations in the CH3 domain), such that formation of the heterodimer is favored compared to homodimers when the individual Fc region are co-expressed in a cell.

[0063] **FIG. 5B** depicts various exemplary configurations of a stack molecule containing a first variant IgSF domain (first vIgD), a second IgSF domain, such as a second variant IgSF domain (second vIgD), and a third IgSF domain, such as a third variant IgSF domain (third vIgD). As shown, the first vIgD, second IgSF, and third IgSF domains are independently linked, directly or indirectly, to the N- or C-terminus of an Fc region. For generating a homodimeric Fc molecule, the Fc region is one that is capable of forming a homodimer with a matched Fc region by co-expression of the individual Fc region in a cell.

[0064] **FIG. 6** depicts an exemplary schematic of the activity of a variant IgSF domain (vIgD) –conjugated to an antibody (V-Mab) in which the antibody (e.g. anti-HER2 antibody) binds to an antigen on the surface of the tumor cell to localize the vIgD to the cell. As shown, binding of the antibody to the surface of the tumor cell localizes the vIgD on the tumor cell surface where it can interact with one or more of its cognate binding partners expressed on the surface of an adjacent immune cell (e.g. T cell) to agonize or antagonize receptor signaling. In an exemplary embodiment as shown, the variant IgSF domain (vIgD) is a variant of an IgSF domain of PD-L1 that binds, such as has increased affinity for, the inhibitory receptor PD-1. Binding of the PD-L1 vIgD to the PD-1 inhibitory receptor antagonizes or blocks the negative signaling of the inhibitory receptor, thereby resulting in an activated T cell or effector T cell. In some cases, if clustering of the inhibitory receptor (PD-1) is proximal to an activating receptor (e.g. CD28) then agonizing of the inhibitory receptor activity by the TIP may be realized.

[0065] **FIG. 7A-7C** depicts various exemplary configurations of a variant IgSF-antibody conjugate (V-Mab). **FIG. 7A** shows various configurations in which a variant IgSF domain is linked, directly or indirectly, to the N- and/or C-terminus of the light chain of an antibody. **FIG. 7B** shows various configurations in which a variant IgSF domain is linked, directly or indirectly, to the N- and/or C-terminus of the heavy chain of an antibody. **FIG. 7C** depicts the results V-Mab configurations when a light chain of **FIG. 7A** and a heavy chain of **FIG. 7B** are co-expressed in a cell.

[0066] **FIG. 8** and **FIG. 9** depict the results for soluble variant PD-L1 IgV-Fc bioactivity tested in a human Mixed Lymphocyte Reaction (MLR). Approximately, 10,000 matured DC and 100,000 purified allogeneic CD3+ T cells were co-cultured with various increasing concentrations of variant PD-L1 IgV-Fc fusion proteins. Irrelevant human IgG or media only (designated "No Add") were used as negative controls. Control proteins, PDL1-Fc (full wild-type PD-L1 extracellular domain), wildtype PD-L1 IgV-Fc and positive control anti-PD-1 monoclonal antibody (nivolumab) were assessed. **FIG. 8** and **FIG. 9** sets forth the calculated levels of IFN-gamma in culture supernatants (pg/mL) at the indicated concentration of variant IgV-Fc fusion molecule.

[0067] **FIG. 10** depicts proliferation studies for T cells transduced with exemplary tested variant PD-L1 SIP.

[0068] **FIG. 11** depicts dose response for binding of the indicated variant IgV-Fc fusion molecules, PD-L1/CD155 stack Fc fusion molecule, or PD-L1/CD155/CD112 stack Fc fusion molecule to exhausted T cells.

[0069] **FIG. 12** sets forth the calculated levels of IFN-gamma in culture supernatants (pg/mL) of exhausted T cells at the indicated concentration of variant IgV-Fc fusion molecule, PD-L1/CD155 stack Fc fusion molecule, or antibody controls.

Detailed Description

[0070] Provided herein are immunomodulatory proteins that are or comprise variants or mutants of Programmed cell death 1 ligand 1 or PD-L1 (also known as cluster of differentiation 274, CD274. B7 homolog 1 or B7-H1) or specific binding fragments thereof that exhibit activity to bind to at least one target ligand cognate binding partner (also called counter-structure protein). In some embodiments, the variant PD-L1 polypeptides contain one or more amino acid modifications (e.g. amino acid substitutions, deletions or additions) compared to an unmodified

or wild-type PD-L1 polypeptide. In some embodiments, the one or more amino acid modifications (e.g. substitutions) are in an IgSF domain (e.g. IgV or ECD) of an unmodified or wild-type PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide and immunomodulatory proteins exhibits altered, such as increased or decreased, binding activity or affinity for at least one cognate binding partner, such as at least one of PD-1 or CD80. In some embodiments, the immunomodulatory proteins are soluble. In some embodiments, the immunomodulatory proteins are transmembrane immunomodulatory proteins capable of being expressed on the surface of cells. In some embodiments, also provided herein are one or more other immunomodulatory proteins that are conjugates or fusions containing a variant PD-L1 polypeptide provided herein and one or more other moiety or polypeptide.

[0071] In some embodiments, the variant PD-L1 polypeptides and immunomodulatory proteins modulate an immunological immune response, such an increase or decrease an immune response. In some embodiments, the variant PD-L1 polypeptides and immunomodulatory proteins provided herein can be used for the treatment of diseases or conditions that are associated with a dysregulated immune response.

[0072] In some embodiments, the provided variant PD-L1 polypeptides modulate T cell activation via interactions with costimulatory and/or coinhibitory signaling molecules. In general, antigen specific T-cell activation generally requires two distinct signals. The first signal is provided by the interaction of the T-cell receptor (TCR) with major histocompatibility complex (MHC) associated antigens present on antigen presenting cells (APCs). The second signal is costimulatory to TCR engagement and is necessary for T cell proliferation, differentiation and/or survival, including, in some cases, to avoid T-cell apoptosis or anergy.

[0073] In some embodiments, under normal physiological conditions, the T cell-mediated immune response is initiated by antigen recognition by the T cell receptor (TCR) and is regulated by a balance of co-stimulatory and inhibitory signals (e.g., immune checkpoint proteins). The immune system relies on immune checkpoints to prevent autoimmunity (i.e., self- tolerance) and to protect tissues from excessive damage during an immune response, for example during an attack against a pathogenic infection. In some cases, however, these immunomodulatory proteins can be dysregulated in diseases and conditions, including tumors, as a mechanism for evading the immune system.

[0074] In some embodiments, among known T-cell costimulatory receptors is Programmed cell death protein 1 or PD-1, which is the T-cell costimulatory receptor for the ligands PD-L1

(also known as cluster of differentiation 274, CD274. B7 homolog 1 or B7-H1) and Programmed cell death 1 ligand 2 or PD-L2 (also known as PDCD1L2, PDCD1LG2, cluster of differentiation 273, CD273. or B7-DC). PD-L1 and PD-L2 are normally expressed on the surface of T cells, B cells, and myeloid cells. PD-L1 and PD-L2 are negative regulators of immune activation and are capable of down-modulating the immune response via interactions with programmed death 1 (PD-1) receptor. In some aspects, PD-1 is expressed on NK cells and T cells, including CD4+ and CD8+ T cells, whereby engagement of PD-1 can inhibit activation cell activation, proliferation, and/or expansion.

[0075] However, PD-L1 ligands can also bind to Cluster of differentiation 80 (also known as CD80 or B7-1). The binding of PD-L1 to CD80 can block the interaction between PD-L1 and PD-1, and thereby potentiate or enhance the immune response. Thus, in some cases, interaction of PD-L1 with CD80 and PD-L1 with PD-1 yields opposing effects in modulating immune responses. Thus, PD-1 and CD80 may play opposing roles in immune responses to modulate pro-inflammatory or anti-inflammatory response, which, in some cases, are associated with a number of diseases and conditions.

[0076] In some embodiments, PD-1 and CD80 may play complementary roles in modeling an immune response. In some embodiments, enhancement or suppression of the activity of PD-1 receptor has clinical significance for treatment of inflammatory and autoimmune disorders, cancer, and viral infections. In some cases, however, therapies to intervene and alter the immunomodulatory effects of such receptors are constrained by the spatial orientation requirements as well as size limitations imposed by the confines of the immunological synapse. In some aspects, existing therapeutic drugs, including antibody drugs, may not be able to interact simultaneously with the multiple target proteins involved in modulating these interactions. In addition, in some cases, existing therapeutic drugs may only have the ability to antagonize but not agonize an immune response. Additionally, pharmacokinetic differences between drugs that independently target one of these receptors can create difficulties in properly maintaining a desired blood concentration of such drug combinations throughout the course of treatment.

[0077] In some embodiments, the provided variant PD-L1 polypeptides or immunomodulatory proteins modulate (e.g. increase or decrease) immunological activity associated PD-1. Thus, in some embodiments, the provided polypeptides overcome these constraints by providing variant PD-L1 with altered (e.g. increased or decreased) binding affinities to PD-1, thereby agonizing or antagonizing the effects of the receptor. In some

embodiments, the provided polypeptides overcome these constraints by providing variant PD-L1 with altered (e.g. increased or decreased) binding affinities to CD80, thereby modulating the effects of the interaction between PD-1 and PD-L1. Methods of making and using these variant PD-L1 are also provided.

[0078] All publications, including patents, patent applications scientific articles and databases, mentioned in this specification are herein incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, including patent, patent application, scientific article or database, were specifically and individually indicated to be incorporated by reference. If a definition set forth herein is contrary to or otherwise inconsistent with a definition set forth in the patents, applications, published applications and other publications that are herein incorporated by reference, the definition set forth herein prevails over the definition that is incorporated herein by reference.

[0079] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

I. DEFINITIONS

[0080] Unless defined otherwise, all terms of art, notations and other technical and scientific terms or terminology used herein are intended to have the same meaning as is commonly understood by one of ordinary skill in the art to which the claimed subject matter pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art.

[0081] The terms used throughout this specification are defined as follows unless otherwise limited in specific instances. As used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms, acronyms, and abbreviations used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Unless indicated otherwise, abbreviations and symbols for chemical and biochemical names is per IUPAC-IUB nomenclature. Unless indicated otherwise, all numerical ranges are inclusive of the values defining the range as well as all integer values in-between.

[0082] The term "affinity modified" as used in the context of an immunoglobulin superfamily domain, means a mammalian immunoglobulin superfamily (IgSF) domain having an

altered amino acid sequence (relative to the corresponding wild-type parental or unmodified IgSF domain) such that it has an increased or decreased binding affinity or avidity to at least one of its cognate binding partners (alternatively "counter-structures") compared to the parental wild-type or unmodified (i.e., non-affinity modified) IgSF control domain. Included in this context is an affinity modified PD-L1 IgSF domain. In some embodiments, the affinity-modified IgSF domain can contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more amino acid differences, such as amino acid substitutions, in a wildtype or unmodified IgSF domain. An increase or decrease in binding affinity or avidity can be determined using well known binding assays such as flow cytometry. Larsen et al., American Journal of Transplantation, Vol 5: 443-453 (2005). See also, Linsley et al., Immunity, Vol 1(9): 793-801 (1994). An increase in a protein's binding affinity or avidity to its cognate binding partner(s) is to a value at least 10% greater than that of the wild-type IgSF domain control and in some embodiments, at least 20%, 30%, 40%, 50%, 100%, 200%, 300%, 500%, 1000%, 5000%, or 10000% greater than that of the wild-type IgSF domain control value. A decrease in a protein's binding affinity or avidity to at least one of its cognate binding partner is to a value no greater than 90% of the control but no less than 10% of the wild-type IgSF domain control value, and in some embodiments no greater than 80%, 70% 60%, 50%, 40%, 30%, or 20% but no less than 10% of the wild-type IgSF domain control value. An affinity-modified protein is altered in primary amino acid sequence by substitution, addition, or deletion of amino acid residues. The term "affinity modified IgSF domain" is not to be construed as imposing any condition for any particular starting composition or method by which the affinity-modified IgSF domain was created. Thus, the affinity modified IgSF domains of the present invention are not limited to wild type IgSF domains that are then transformed to an affinity modified IgSF domain by any particular process of affinity modification. An affinity modified IgSF domain polypeptide can, for example, be generated starting from wild type mammalian IgSF domain sequence information, then modeled in silico for binding to its cognate binding partner, and finally recombinantly or chemically synthesized to yield the affinity modified IgSF domain composition of matter. In but one alternative example, an affinity modified IgSF domain can be created by site-directed mutagenesis of a wild-type IgSF domain. Thus, affinity modified IgSF domain denotes a product and not necessarily a product produced by any given process. A variety of techniques including recombinant methods, chemical synthesis, or combinations thereof, may be employed.

[0083] The term "allogeneic" as used herein means a cell or tissue that is removed from one organism and then infused or adoptively transferred into a genetically dissimilar organism of the same species. In some embodiments of the invention, the species is murine or human.

[0084] The term "autologous" as used herein means a cell or tissue that is removed from the same organism to which it is later infused or adoptively transferred. An autologous cell or tissue can be altered by, for example, recombinant DNA methodologies, such that it is no longer genetically identical to the native cell or native tissue which is removed from the organism. For example, a native autologous T-cell can be genetically engineered by recombinant DNA techniques to become an autologous engineered cell expressing a transmembrane immunomodulatory protein and/or chimeric antigen receptor (CAR), which in some cases involves engineering a T-cell or TIL (tumor infiltrating lymphocyte). The engineered cells are then infused into a patient from which the native T-cell was isolated. In some embodiments, the organism is human or murine.

[0085] The terms "binding affinity," and "binding avidity" as used herein means the specific binding affinity and specific binding avidity, respectively, of a protein for its counter-structure under specific binding conditions. In biochemical kinetics avidity refers to the accumulated strength of multiple affinities of individual non-covalent binding interactions, such as between PD-L1 and its counter-structures PD-1 and/or CD80. As such, avidity is distinct from affinity, which describes the strength of a single interaction. An increase or attenuation in binding affinity of a variant PD-L1 containing an affinity modified PD-L1 IgSF domain to its counter-structure is determined relative to the binding affinity of the unmodified PD-L1, such as an unmodified PD-L1 containing the native or wild-type IgSF domain, such as IgV domain. Methods for determining binding affinity or avidity are known in art. See, for example, Larsen et al., American Journal of Transplantation, Vol 5: 443-453 (2005). In some embodiments, a variant PD-L1 of the invention (i.e. a PD-L1 protein containing an affinity modified IgSF domain) specifically binds to PD-1 and/or CD80 measured by flow cytometry with a binding affinity that yields a Mean Fluorescence Intensity (MFI) value at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% greater than a wild-type PD-L1 control in a binding assay.

[0086] The term "biological half-life" refers to the amount of time it takes for a substance, such as an immunomodulatory polypeptide comprising a variant PD-L1 of the present invention, to lose half of its pharmacologic or physiologic activity or concentration. Biological half-life can be affected by elimination, excretion, degradation (e.g., enzymatic) of the substance, or

absorption and concentration in certain organs or tissues of the body. In some embodiments, biological half-life can be assessed by determining the time it takes for the blood plasma concentration of the substance to reach half its steady state level ("plasma half-life"). Conjugates that can be used to derivatize and increase the biological half-life of polypeptides of the invention are known in the art and include, but are not limited to, polyethylene glycol (PEG), hydroxyethyl starch (HES), XTEN (extended recombinant peptides; see, WO2013130683), human serum albumin (HSA), bovine serum albumin (BSA), lipids (acylation), and poly-Pro-Ala-Ser (PAS), polyglutamic acid (glutamylation).

[0087] The term "chimeric antigen receptor" or "CAR" as used herein refers to an artificial (i.e., man-made) transmembrane protein expressed on a mammalian cell comprising at least an ectodomain, a transmembrane, and an endodomain. Optionally, the CAR protein includes a "spacer" which covalently links the ectodomain to the transmembrane domain. A spacer is often a polypeptide linking the ectodomain to the transmembrane domain via peptide bonds. The CAR is typically expressed on a mammalian lymphocyte. In some embodiments, the CAR is expressed on a mammalian cell such as a T-cell or a tumor infiltrating lymphocyte (TIL). A CAR expressed on a T-cell is referred to herein as a "CAR T-cell" or "CAR-T." In some embodiments the CAR-T is a T helper cell, a cytotoxic T-cell, a natural killer T-cell, a memory T-cell, a regulatory T-cell, or a gamma delta T-cell. When used clinically in, e.g. adoptive cell transfer, a CAR-T with antigen binding specificity to the patient's tumor is typically engineered to express on a T-cell obtained from the patient. The engineered T-cell expressing the CAR is then infused back into the patient. The CAR-T is thus often an autologous CAR-T although allogeneic CAR-T are included within the scope of the invention. The ectodomain of a CAR comprises an antigen binding region, such as an antibody or antigen binding fragment thereof (e.g. scFv), that specifically binds under physiological conditions with a target antigen, such as a tumor specific antigen. Upon specific binding a biochemical chain of events (i.e., signal transduction) results in modulation of the immunological activity of the CAR-T. Thus, for example, upon specific binding by the antigen binding region of the CAR-T to its target antigen can lead to changes in the immunological activity of the T-cell activity as reflected by changes in cytotoxicity, proliferation or cytokine production. Signal transduction upon CAR-T activation is achieved in some embodiments by the CD3-zeta chain ("CD3-z") which is involved in signal transduction in native mammalian T-cells. CAR-Ts can further comprise multiple signaling domains such as CD28, 41BB or OX40, to further modulate immunomodulatory response of the

T-cell. CD3-z comprises a conserved motif known as an immunoreceptor tyrosine-based activation motif (ITAM) which is involved in T-cell receptor signal transduction.

[0088] The term "collectively" or "collective" when used in reference to cytokine production induced by the presence of two or more variant PD-L1 of the invention in an in vitro assay, means the overall cytokine expression level irrespective of the cytokine production induced by individual variant PD-L1. In some embodiments, the cytokine being assayed is IFN-gamma, such as in an in vitro primary T-cell assay.

[0089] The term "cognate binding partner" (used interchangeably with "counter-structure") in reference to a polypeptide, such as in reference to an IgSF domain of a variant PD-L1, refers to at least one molecule (typically a native mammalian protein) to which the referenced polypeptide specifically binds under specific binding conditions. In some aspects, a variant PD-L1 containing an affinity modified IgSF domain specifically binds to the counter-structure of the corresponding native or wildtype PD-L1 but with increased or attenuated affinity. A species of ligand recognized and specifically binding to its cognate receptor under specific binding conditions is an example of a counter-structure or cognate binding partner of that receptor. A "cognate cell surface binding partner" is a cognate binding partner expressed on a mammalian cell surface. A "cell surface molecular species" is a cognate binding partner of ligands of the immunological synapse (IS), expressed on and by cells, such as mammalian cells, forming the immunological synapse.

[0090] As used herein, "conjugate," "conjugation" or grammatical variations thereof refers the joining or linking together of two or more compounds resulting in the formation of another compound, by any joining or linking methods known in the art. It can also refer to a compound which is generated by the joining or linking together two or more compounds. For example, a variant PD-L1 polypeptide linked directly or indirectly to one or more chemical moieties or polypeptide is an exemplary conjugate. Such conjugates include fusion proteins, those produced by chemical conjugates and those produced by any other methods.

[0091] The term "competitive binding" as used herein means that a protein is capable of specifically binding to at least two cognate binding partners but that specific binding of one cognate binding partner inhibits, such as prevents or precludes, simultaneous binding of the second cognate binding partner. Thus, in some cases, it is not possible for a protein to bind the two cognate binding partners at the same time. Generally, competitive binders contain the same or overlapping binding site for specific binding but this is not a requirement. In some

embodiments, competitive binding causes a measurable inhibition (partial or complete) of specific binding of a protein to one of its cognate binding partner due to specific binding of a second cognate binding partner. A variety of methods are known to quantify competitive binding such as ELISA (enzyme linked immunosorbent assay) assays.

[0092] The term "conservative amino acid substitution" as used herein means an amino acid substitution in which an amino acid residue is substituted by another amino acid residue having a side chain R group with similar chemical properties (e.g., charge or hydrophobicity). Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine, and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartic acid and glutamic acid; and 7) sulfur-containing side chains: cysteine and methionine. Conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine.

[0093] The term, "corresponding to" with reference to positions of a protein, such as recitation that nucleotides or amino acid positions "correspond to" nucleotides or amino acid positions in a disclosed sequence, such as set forth in the Sequence listing, refers to nucleotides or amino acid positions identified upon alignment with the disclosed sequence based on structural sequence alignment or using a standard alignment algorithm, such as the GAP algorithm. For example, corresponding residues can be determined by alignment of a reference sequence with the sequence of wild-type PD-L1 set forth in SEQ ID NO:30 or 1728 (ECD domain) or set forth in SEQ ID NO: 55 or 309 (IgV domain) by structural alignment methods as described herein. By aligning the sequences, one skilled in the art can identify corresponding residues, for example, using conserved and identical amino acid residues as guides.

[0094] The terms "decrease" or "attenuate" "or suppress" as used herein means to decrease by a statistically significant amount. A decrease can be at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%.

[0095] The terms "derivatives" or "derivatized" refer to modification of a protein by covalently linking it, directly or indirectly, to a composition so as to alter such characteristics as biological half-life, bioavailability, immunogenicity, solubility, toxicity, potency, or efficacy while retaining or enhancing its therapeutic benefit. Derivatives of immunomodulatory

polypeptides of the invention are within the scope of the invention and can be made by, for example, glycosylation, pegylation, lipidation, or Fc-fusion.

[0096] As used herein, "domain" (typically a sequence of three or more, generally 5 or 7 or more amino acids, such as 10 to 200 amino acid residues) refers to a portion of a molecule, such as a protein or encoding nucleic acid,that is structurally and/or functionally distinct from other portions of the molecule and is identifiable. For example, domains include those portions of a polypeptide chain that can form an independently folded structure within a protein made up of one or more structural motifs and/or that is recognized by virtue of a functional activity, such as binding activity. A protein can have one, or more than one, distinct domains. For example, a domain can be identified, defined or distinguished by homology of the primary sequence or structure to related family members, such as homology to motifs. In another example, a domain can be distinguished by its function, such as an ability to interact with a biomolecule, such as a cognate binding partner. A domain independently can exhibit a biological function or activity such that the domain independently or fused to another molecule can perform an activity, such as, for example binding. A domain can be a linear sequence of amino acids or a non-linear sequence of amino acids. Many polypeptides contain a plurality of domains. Such domains are known, and can be identified by those of skill in the art. For exemplification herein, definitions are provided, but it is understood that it is well within the skill in the art to recognize particular domains by name. If needed appropriate software can be employed to identify domains.

[0097] The term "ectodomain" as used herein refers to the region of a membrane protein, such as a transmembrane protein, that lies outside the vesicular membrane. Ectodomains often comprise binding domains that specifically bind to ligands or cell surface receptors, such as via a binding domain that specifically binds to the ligand or cell surface receptor. The ectodomain of a cellular transmembrane protein is alternately referred to as an extracellular domain.

[0098] The terms "effective amount" or "therapeutically effective amount" refer to a quantity and/or concentration of a therapeutic composition of the invention, including a protein composition or cell composition, that when administered ex vivo (by contact with a cell from a patient) or in vivo (by administration into a patient) either alone (i.e., as a monotherapy) or in combination with additional therapeutic agents, yields a statistically significant decrease in disease progression as, for example, by ameliorating or eliminating symptoms and/or the cause of the disease. An effective amount may be an amount that relieves, lessens, or alleviates at least one symptom or biological response or effect associated with a disease or disorder, prevents

progression of the disease or disorder, or improves physical functioning of the patient. In the case of cell therapy, the effective amount is an effective dose or number of cells administered to a patient by adoptive cell therapy. In some embodiments the patient is a mammal such as a non-human primate or human patient.

[0099] The term "endodomain" as used herein refers to the region found in some membrane proteins, such as transmembrane proteins,that extends into the interior space defined by the cell surface membrane. In mammalian cells, the endodomain is the cytoplasmic region of the membrane protein. In cells, the endodomain interacts with intracellular constituents and can be play a role in signal transduction and thus, in some cases, can be an intracellular signaling domain. The endodomain of a cellular transmembrane protein is alternately referred to as a cytoplasmic domain, which, in some cases, can be a cytoplasmic signaling domain.

[0100] The terms "enhanced" or "increased" as used herein in the context of increasing immunological activity of a mammalian lymphocyte means to increase one or more activities the lymphocyte. An increased activity can be one or more of increase cell survival, cell proliferation, cytokine production, or T-cell cytotoxicity, such as by a statistically significant amount. In some embodiments, reference to increased immunological activity means to increase interferon gamma (IFN-gamma) production, such as by a statistically significant amount. In some embodiments, the immunological activity can be assessed in a mixed lymphocyte reaction (MLR) assay. Methods of conducting MLR assays are known in the art. Wang et al., Cancer Immunol Res. 2014 Sep: 2(9):846-56. Other methods of assessing activities of lymphocytes are known in the art, including any assay as described herein. In some embodiments an enhancement can be an increase of at least 10%, 20%, 30%, 40%, 50%, 75%,100%, 200%, 300%, 400%, or 500% greater than a non-zero control value.

[0101] The term "engineered cell" as used herein refers to a mammalian cell that has been genetically modified by human intervention such as by recombinant DNA methods or viral transduction. In some embodiments, the cell is an immune cell, such as a lymphocyte (e.g. T cell, B cell, NK cell) or an antigen presenting cell (e.g. dendritic cell). The cell can be a primary cell from a patient or can be a cell line. In some embodiments, an engineered cell of the invention comprises a variant PD-L1 of the invention engineered to modulate immunological activity of a T-cell expressing PD-1 and/or CD80 to which the variant PD-L1 specifically binds. In some embodiments, the variant PD-L1 is a transmembrane immunomodulatory protein (hereinafter referred to as "TIP") containing the extracellular domain or a portion thereof

containing the IgV or ECD domain linked to a transmembrane domain (e.g. a PD-L1 transmembrane domain) and, optionally, an intracellular signaling domain. In some cases, the TIP is formatted as a chimeric receptor containing a heterologous cytoplasmic signaling domain or endodomain. In some embodiments, an engineered cell is capable of expressing and secreting an immunomodulatory protein as described herein. Among provided engineered cells also are cells further containing an engineered T-cell receptor (TCR) or chimeric antigen receptor (CAR).

[0102] The term "engineered T-cell" as used herein refers to a T-cell such as a T helper cell, cytotoxic T-cell (alternatively, cytotoxic T lymphocyte or CTL), natural killer T-cell, regulatory T-cell, memory T-cell, or gamma delta T-cell, that has been genetically modified by human intervention such as by recombinant DNA methods or viral transduction methods. An engineered T-cell comprises a variant PD-L1 transmembrane immunomodulatory protein (TIP) or secreted immunomodulatory protein (SIP) of the present invention that is expressed on the T-cell and is engineered to modulate immunological activity of the engineered T-cell itself, or a mammalian cell to which the variant PD-L1 expressed on the T-cell specifically binds.

[0103] The term "engineered T-cell receptor" or "engineered TCR" refers to a T-cell receptor (TCR) engineered to specifically bind with a desired affinity to a major histocompatibility complex (MHC)/peptide target antigen that is selected, cloned, and/or subsequently introduced into a population of T-cells, often used for adoptive immunotherapy. In contrast to engineered TCRs, CARs are engineered to bind target antigens in a MHC independent manner.

[0104] The term "expressed on" as used herein is used in reference to a protein expressed on the surface of a cell, such as a mammalian cell. Thus, the protein is expressed as a membrane protein. In some embodiments, the expressed protein is a transmembrane protein. In some embodiments, the protein is conjugated to a small molecule moiety such as a drug or detectable label. Proteins expressed on the surface of a cell can include cell-surface proteins such as cell surface receptors that are expressed on mammalian cells.

[0105] The term "half-life extending moiety" refers to a moiety of a polypeptide fusion or chemical conjugate that extends the half-life of a protein circulating in mammalian blood serum compared to the half-life of the protein that is not so conjugated to the moiety. In some embodiments, half-life is extended by greater than or greater than about 1.2-fold, 1.5-fold, 2.0-fold, 3.0-fold, 4.0-fold, 5.0-fold, or 6.0-fold. In some embodiments, half-life is extended by more than 6 hours, more than 12 hours, more than 24 hours, more than 48 hours, more than 72 hours,

more than 96 hours or more than 1 week after *in vivo* administration compared to the protein without the half-life extending moiety. The half-life refers to the amount of time it takes for the protein to lose half of its concentration, amount, or activity. Half-life can be determined for example, by using an ELISA assay or an activity assay. Exemplary half-life extending moieties include an Fc domain, a multimerization domain, polyethylene glycol (PEG), hydroxyethyl starch (HES), XTEN (extended recombinant peptides; see, WO2013130683), human serum albumin (HSA), bovine serum albumin (BSA), lipids (acylation), and poly-Pro-Ala-Ser (PAS), and polyglutamic acid (glutamylation).

[0106] The term "immunological synapse" or "immune synapse" as used herein means the interface between a mammalian cell that expresses MHC I (major histocompatibility complex) or MHC II, such as an antigen-presenting cell or tumor cell, and a mammalian lymphocyte such as an effector T cell or Natural Killer (NK) cell.

[0107] An Fc (fragment crystallizable) region or domain of an immunoglobulin molecule (also termed an Fc polypeptide) corresponds largely to the constant region of the immunoglobulin heavy chain, and is responsible for various functions, including the antibody's effector function(s). The Fc domain contains part or all of a hinge domain of an immunoglobulin molecule plus a CH2 and a CH3 domain. The Fc domain can form a dimer of two polypeptide chains joined by one or more disulfide bonds. In some embodiments, the Fc is a variant Fc that exhibits reduced (e.g. reduced greater than 30%, 40%, 50%, 60%, 70%, 80%, 90% or more) activity to facilitate an effector function. In some embodiments, reference to amino acid substitutions in an Fc region is by EU numbering system unless described with reference to a specific SEQ ID NO. EU numbering is known and is according to the most recently updated IMGT Scientific Chart (IMGT®, the international ImMunoGeneTics information system®, http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IGHGnber.html (created: 17 May 2001 , last updated: 10 Jan 2013) and the EU index as reported in Kabat, E.A. et al. Sequences of Proteins of Immunological interest. 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991).

[0108] An immunoglobulin Fc fusion ("Fc-fusion"), such as an immunomodulatory Fc fusion protein, is a molecule comprising one or more polypeptides (or one or more small molecules) operably linked to an Fc region of an immunoglobulin. An Fc-fusion may comprise, for example, the Fc region of an antibody (which facilitates effector functions and

pharmacokinetics) and a variant PD-L1. An immunoglobulin Fc region may be linked indirectly or directly to one or more variant PD-L1 or small molecules (fusion partners). Various linkers are known in the art and can optionally be used to link an Fc to a fusion partner to generate an Fc-fusion. Fc-fusions of identical species can be dimerized to form Fc-fusion homodimers, or using non-identical species to form Fc-fusion heterodimers. In some embodiments, the Fc is a mammalian Fc such as a murine or human Fc.

[0109] The term "host cell" refers to a cell that can be used to express a protein encoded by a recombinant expression vector. A host cell can be a prokaryote, for example, E. coli, or it can be a eukaryote, for example, a single-celled eukaryote (e.g., a yeast or other fungus), a plant cell (e.g., a tobacco or tomato plant cell), an animal cell (e.g., a human cell, a monkey cell, a hamster cell, a rat cell, a mouse cell, or an insect cell) or a hybridoma. Examples of host cells include Chinese hamster ovary (CHO) cells or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media or CHO strain DX-B11, which is deficient in DHFR. Another example is Human Endothelial Kidney 293 cells or their derivatives. In some embodiments, a host cell is a mammalian cell (e.g., a human cell, a monkey cell, a hamster cell, a rat cell, a mouse cell, or an insect cell).

[0110] The term "immunoglobulin" (abbreviated "Ig") as used herein refers to a mammalian immunoglobulin protein including any of the five human classes of antibody: IgA (which includes subclasses IgA1 and IgA2), IgD, IgE, IgG (which includes subclasses IgG1, IgG2, IgG3, and IgG4), and IgM. The term is also inclusive of immunoglobulins that are less than full-length, whether wholly or partially synthetic (e.g., recombinant or chemical synthesis) or naturally produced, such as antigen binding fragment (Fab), variable fragment (Fv) containing V_H and V_L, the single chain variable fragment (scFv) containing V_H and V_L linked together in one chain, as well as other antibody V region fragments, such as Fab′, $F(ab)_2$, $F(ab')_2$, dsFv diabody, Fc, and Fd polypeptide fragments. Bispecific antibodies, homobispecific and heterobispecific, are included within the meaning of the term.

[0111] The term "immunoglobulin superfamily" or "IgSF" as used herein means the group of cell surface and soluble proteins that are involved in the recognition, binding, or adhesion processes of cells. Molecules are categorized as members of this superfamily based on shared structural features with immunoglobulins (i.e., antibodies); they all possess a domain known as an immunoglobulin domain or fold. Members of the IgSF include cell surface antigen receptors, co-receptors and co-stimulatory molecules of the immune system, molecules involved in antigen

presentation to lymphocytes, cell adhesion molecules, certain cytokine receptors and intracellular muscle proteins. They are commonly associated with roles in the immune system. Proteins in the immunological synapse are often members of the IgSF. IgSF can also be classified into "subfamilies" based on shared properties such as function. Such subfamilies typically consist of from 4 to 30 IgSF members.

[0112] The terms "IgSF domain" or "immunoglobulin domain" or "Ig domain" as used herein refers to a structural domain of IgSF proteins. Ig domains are named after the immunoglobulin molecules. They contain about 70-110 amino acids and are categorized according to their size and function. Ig-domains possess a characteristic Ig-fold, which has a sandwich-like structure formed by two sheets of antiparallel beta strands. Interactions between hydrophobic amino acids on the inner side of the sandwich and highly conserved disulfide bonds formed between cysteine residues in the B and F strands, stabilize the Ig-fold. One end of the Ig domain has a section called the complementarity determining region that is important for the specificity of antibodies for their ligands. The Ig like domains can be classified (into classes) as: IgV, IgC (which either can be an IgC1 or IgC2), or IgI. Most Ig domains are either variable (IgV) or constant (IgC). IgV domains with 9 beta strands are generally longer than IgC domains with 7 beta strands. Ig domains of some members of the IgSF resemble IgV domains in the amino acid sequence, yet are similar in size to IgC domains. These are called IgC2 domains, while standard IgC domains are called IgC1 domains. T-cell receptor (TCR) chains contain two Ig domains in the extracellular portion; one IgV domain at the N-terminus and one IgC1 domain adjacent to the cell membrane. PD-L1 contains two Ig domains: one IgV and one IgC domain.

[0113] The term "IgSF species" as used herein means an ensemble of IgSF member proteins with identical or substantially identical primary amino acid sequence. Each mammalian immunoglobulin superfamily (IgSF) member defines a unique identity of all IgSF species that belong to that IgSF member. Thus, each IgSF family member is unique from other IgSF family members and, accordingly, each species of a particular IgSF family member is unique from the species of another IgSF family member. Nevertheless, variation between molecules that are of the same IgSF species may occur owing to differences in post-translational modification such as glycosylation, phosphorylation, ubiquitination, nitrosylation, methylation, acetylation, and lipidation. Additionally, minor sequence differences within a single IgSF species owing to gene polymorphisms constitute another form of variation within a single IgSF species as do wild type

truncated forms of IgSF species owing to, for example, proteolytic cleavage. A "cell surface IgSF species" is an IgSF species expressed on the surface of a cell, generally a mammalian cell.

[0114] The term "immunological activity" as used herein in the context of mammalian lymphocytes such as T-cells refers to one or more cell survival, cell proliferation, cytokine production (e.g. interferon-gamma), or T-cell cytotoxicity activities. In some cases, an immunological activity can mean the cell expression of cytokines, such as chemokines or interleukins. Assays for determining enhancement or suppression of immunological activity include the MLR (mixed lymphocyte reaction) assays measuring interferon-gamma cytokine levels in culture supernatants (Wang et al., Cancer Immunol Res. 2014 Sep: 2(9):846-56), SEB (staphylococcal enterotoxin B) T cell stimulation assay (Wang et al., Cancer Immunol Res. 2014 Sep: 2(9):846-56), and anti-CD3 T cell stimulation assays (Li and Kurlander, J Transl Med. 2010: 8: 104). Since T cell activation is associated with secretion of IFN-gamma cytokine, detecting IFN-gamma levels in culture supernatants from these in vitro human T cell assays can be assayed using commercial ELISA kits (Wu et al, Immunol Lett 2008 Apr 15; 117(1): 57-62). Induction of an immune response results in an increase in immunological activity relative to quiescent lymphocytes. An immunomodulatory protein, such as a variant PD-L1 polypeptide containing an affinity modified IgSF domain, as provided herein can in some embodiments increase or, in alternative embodiments, decrease IFN-gamma (interferon-gamma) expression in a primary T-cell assay relative to a wild-type IgSF member or IgSF domain control. Those of skill will recognize that the format of the primary T-cell assay used to determine an increase in IFN-gamma expression can differ from that employed to assay for a decrease in IFN-gamma expression. In assaying for the ability of an immunomodulatory protein or affinity modified IgSF domain of the invention to alter IFN-gamma expression in a primary T-cell assay, a Mixed Lymphocyte Reaction (MLR) assay can be used. Conveniently, in some cases, a soluble form of an affinity modified IgSF domain of the invention can be employed to determine its ability to increase or decrease the IFN-gamma expression in a MLR. Alternatively, a co-immobilization assay can be used. In a co-immobilization assay, a T-cell receptor signal, provided in some embodiments by anti-CD3 antibody, is used in conjunction with a co-immobilized affinity modified IgSF domain, such as variant PD-L1, to determine the ability to increase or decrease IFN-gamma expression relative to a wild-type IgSF domain control. Methods to assay the immunological activity of engineered cells, including to evaluate the activity of a variant PD-L1 transmembrane immunomodulatory protein, are known in the art and include, but are not limited

to, the ability to expand T cells following antigen stimulation, sustain T cell expansion in the absence of re- stimulation, and anti-cancer activities in appropriate animal models. Assays also include assays to assess cytotoxicity, including a standard ^{51}Cr-release assay (see e.g. Milone et al., (2009) Molecular Therapy 17: 1453-1464) or flow based cytotoxicity assays, or an impedance based cytotoxicity assay (Peper et al. (2014) Journal of Immunological Methods, 405:192-198).

[0115] An "immunomodulatory polypeptide" or "immunomodulatory protein" is a polypeptide or protein molecule that modulates immunological activity. By "modulation" or "modulating" an immune response is meant that immunological activity is either increased or decreased. An immunomodulatory protein can be a single polypeptide chain or a multimer (dimers or higher order multimers) of at least two polypeptide chains covalently bonded to each other by, for example, interchain disulfide bonds. Thus, monomeric, dimeric, and higher order multimeric polypeptides are within the scope of the defined term. Multimeric polypeptides can be homomultimeric (of identical polypeptide chains) or heteromultimeric (of non-identical polypeptide chains). An immunomodulatory protein of the invention comprises a variant PD-L1.

[0116] The term "increase" as used herein means to increase by a statistically significant amount. An increase can be at least 5%, 10%, 20%, 30%, 40%, 50%, 75%, 100%, or greater than a non-zero control value.

[0117] An "isoform" of PD-L1 is one of a plurality naturally occurring PD-L1 polypeptides that differ in amino acid sequence. Isoforms can be the product of splice variants of an RNA transcript expressed by a single gene, or the expression product of highly similar but different genes yielding a functionally similar protein such as may occur from gene duplication. As used herein, the term "isoform" of PD-L1 also refers to the product of different alleles of a PD-L1 gene.

[0118] The term "lymphocyte" as used herein means any of three subtypes of white blood cell in a mammalian immune system. They include natural killer cells (NK cells) (which function in cell-mediated, cytotoxic innate immunity), T cells (for cell-mediated, cytotoxic adaptive immunity), and B cells (for humoral, antibody-driven adaptive immunity). T cells include: T helper cells, cytotoxic T-cells, natural killer T-cells, memory T-cells, regulatory T-cells, or gamma delta T-cells. Innate lymphoid cells (ILC) are also included within the definition of lymphocyte.

[0119] The terms "mammal," or "patient" specifically includes reference to at least one of a: human, chimpanzee, rhesus monkey, cynomolgus monkey, dog, cat, mouse, or rat.

[0120] The term "membrane protein" as used herein means a protein that, under physiological conditions, is attached directly or indirectly to a lipid bilayer. A lipid bilayer that forms a membrane can be a biological membrane such as a eukaryotic (e.g., mammalian) cell membrane or an artificial (i.e., man-made) membrane such as that found on a liposome. Attachment of a membrane protein to the lipid bilayer can be by way of covalent attachment, or by way of non-covalent interactions such as hydrophobic or electrostatic interactions. A membrane protein can be an integral membrane protein or a peripheral membrane protein. Membrane proteins that are peripheral membrane proteins are non-covalently attached to the lipid bilayer or non-covalently attached to an integral membrane protein. A peripheral membrane protein forms a temporary attachment to the lipid bilayer such that under the range of conditions that are physiological in a mammal, peripheral membrane protein can associate and/or disassociate from the lipid bilayer. In contrast to peripheral membrane proteins, integral membrane proteins form a substantially permanent attachment to the membrane's lipid bilayer such that under the range of conditions that are physiological in a mammal, integral membrane proteins do not disassociate from their attachment to the lipid bilayer. A membrane protein can form an attachment to the membrane by way of one layer of the lipid bilayer (monotopic), or attached by way of both layers of the membrane (polytopic). An integral membrane protein that interacts with only one lipid bilayer is an "integral monotopic protein". An integral membrane protein that interacts with both lipid bilayers is an "integral polytopic protein" alternatively referred to herein as a "transmembrane protein".

[0121] The terms "modulating" or "modulate" as used herein in the context of an immune response, such as a mammalian immune response, refer to any alteration, such as an increase or a decrease, of existing or potential immune responses that occurs as a result of administration of an immunomodulatory polypeptide comprising a variant PD-L1 of the present invention or as a result of administration of engineered cells expresses an immunomodulatory protein, such as a variant PD-L1 transmembrane immunomodulatory protein of the present invention. Thus, it refers to an alteration, such as an increase or decrease, of an immune response as compared to the immune response that occurs or is present in the absence of the administration of the immunomodulatory protein comprising the variant PD-L1 or cells expressing such an immunomodulatory polypeptide. Such modulation includes any induction, activation,

suppression or alteration in degree or extent of immunological activity of an immune cell. Immune cells include B cells, T cells, NK (natural killer) cells, NK T cells, professional antigen-presenting cells (APCs), and non-professional antigen-presenting cells, and inflammatory cells (neutrophils, macrophages, monocytes, eosinophils, and basophils). Modulation includes any change imparted on an existing immune response, a developing immune response, a potential immune response, or the capacity to induce, regulate, influence, or respond to an immune response. Modulation includes any alteration in the expression and/or function of genes, proteins and/or other molecules in immune cells as part of an immune response. Modulation of an immune response or modulation of immunological activity includes, for example, the following: elimination, deletion, or sequestration of immune cells; induction or generation of immune cells that can modulate the functional capacity of other cells such as autoreactive lymphocytes, antigen presenting cells, or inflammatory cells; induction of an unresponsive state in immune cells (i.e., anergy); enhancing or suppressing the activity or function of immune cells, including but not limited to altering the pattern of proteins expressed by these cells. Examples include altered production and/or secretion of certain classes of molecules such as cytokines, chemokines, growth factors, transcription factors, kinases, costimulatory molecules, or other cell surface receptors or any combination of these modulatory events. Modulation can be assessed, for example, by an alteration in IFN-gamma (interferon gamma) expression relative to the wild-type PD-L1 control in a primary T cell assay (see, Zhao and Ji, Exp Cell Res. 2016 Jan1; 340(1): 132-138). Modulation can be assessed, for example, by an alteration of an immunological activity of engineered cells, such as an alteration in in cytotoxic activity of engineered cells or an alteration in cytokine secretion of engineered cells relative to cells engineered with a wild-type PD-L1 transmembrane protein

[0122] The term "molecular species" as used herein means an ensemble of proteins with identical or substantially identical primary amino acid sequence. Each mammalian immunoglobulin superfamily (IgSF) member defines a collection of identical or substantially identical molecular species. Thus, for example, human PD-L1 is an IgSF member and each human PD-L1 molecule is a molecular species of PD-L1. Variation between molecules that are of the same molecular species may occur owing to differences in post-translational modification such as glycosylation, phosphorylation, ubiquitination, nitrosylation, methylation, acetylation, and lipidation. Additionally, minor sequence differences within a single molecular species owing to gene polymorphisms constitute another form of variation within a single molecular species as

do wild type truncated forms of a single molecular species owing to, for example, proteolytic cleavage. A "cell surface molecular species" is a molecular species expressed on the surface of a mammalian cell. Two or more different species of protein, each of which is present exclusively on one or exclusively the other (but not both) of the two mammalian cells forming the IS, are said to be in "cis" or "cis configuration" with each other. Two different species of protein, the first of which is exclusively present on one of the two mammalian cells forming the IS and the second of which is present exclusively on the second of the two mammalian cells forming the IS, are said to be in "trans" or "trans configuration." Two different species of protein each of which is present on both of the two mammalian cells forming the IS are in both cis and trans configurations on these cells.

[0123] The term, a "multimerization domain" refers to a sequence of amino acids that promotes stable interaction of a polypeptide molecule with one or more additional polypeptide molecules, each containing a complementary multimerization domain (e.g. a first multimerization domain and a second multimerization domain), which can be the same or a different multimerization domain. The interactions between complementary multimerization domains, e.g. interaction between a first multimerization domain and a second multimerization domain, form a stable protein-protein interaction to produce a multimer of the polypeptide molecule with the additional polypeptide molecule. In some cases, the multimerization domain is the same and interacts with itself to form a stable protein-protein interaction between two polypeptide chains.. Generally, a polypeptide is joined directly or indirectly to the multimerization domain. Exemplary multimerization domains include the immunoglobulin sequences or portions thereof, leucine zippers, hydrophobic regions, hydrophilic regions, and compatible protein-protein interaction domains. The multimerization domain, for example, can be an immunoglobulin constant region or domain, such as, for example, the Fc domain or portions thereof from IgG, including IgG1, IgG2, IgG3 or IgG4 subtypes, IgA, IgE, IgD and IgM and modified forms thereof.

[0124] The terms "nucleic acid" and "polynucleotide" are used interchangeably to refer to a polymer of nucleic acid residues (e.g., deoxyribonucleotides or ribonucleotides) in either single- or double-stranded form. Unless specifically limited, the terms encompass nucleic acids containing known analogues of natural nucleotides and that have similar binding properties to it and are metabolized in a manner similar to naturally-occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified

variants thereof (e.g., degenerate codon substitutions) and complementary nucleotide sequences as well as the sequence explicitly indicated (a "reference sequence"). Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues. The term nucleic acid or polynucleotide encompasses cDNA or mRNA encoded by a gene.

[0125] The term "non-competitive binding" as used herein means the ability of a protein to specifically bind simultaneously to at least two cognate binding partners. Thus, the protein is able to bind to at least two different cognate binding partners at the same time, although the binding interaction need not be for the same duration such that, in some cases, the protein is specifically bound to only one of the cognate binding partners. In some embodiments, the binding occurs under specific binding conditions. In some embodiments, the simultaneous binding is such that binding of one cognate binding partner does not substantially inhibit simultaneous binding to a second cognate binding partner. In some embodiments, non-competitive binding means that binding a second cognate binding partner to its binding site on the protein does not displace the binding of a first cognate binding partner to its binding site on the protein. Methods of assessing non-competitive binding are well known in the art such as the method described in Perez de La Lastra et al., Immunology, 1999 Apr: 96(4): 663–670. In some cases, in non-competitive interactions, the first cognate binding partner specifically binds at an interaction site that does not overlap with the interaction site of the second cognate binding partner such that binding of the second cognate binding partner does not directly interfere with the binding of the first cognate binding partner. Thus, any effect on binding of the cognate binding partner by the binding of the second cognate binding partner is through a mechanism other than direct interference with the binding of the first cognate binding partner. For example, in the context of enzyme-substrate interactions, a non-competitive inhibitor binds to a site other than the active site of the enzyme. Non-competitive binding encompasses uncompetitive binding interactions in which a second cognate binding partner specifically binds at an interaction site that does not overlap with the binding of the first cognate binding partner but binds to the second interaction site only when the first interaction site is occupied by the first cognate binding partner.

[0126] The term "pharmaceutical composition" refers to a composition suitable for pharmaceutical use in a mammalian subject, often a human. A pharmaceutical composition typically comprises an effective amount of an active agent (e.g., an immunomodulatory

polypeptide comprising a variant PD-L1 or engineered cells expressing a variant PD-L1 transmembrane immunomodulatory protein) and a carrier, excipient, or diluent. The carrier, excipient, or diluent is typically a pharmaceutically acceptable carrier, excipient or diluent, respectively.

[0127] The terms "polypeptide" and "protein" are used interchangeably herein and refer to a molecular chain of two or more amino acids linked through peptide bonds. The terms do not refer to a specific length of the product. Thus, "peptides," and "oligopeptides," are included within the definition of polypeptide. The terms include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. The terms also include molecules in which one or more amino acid analogs or non-canonical or unnatural amino acids are included as can be synthesized, or expressed recombinantly using known protein engineering techniques. In addition, proteins can be derivatized.

[0128] The term "primary T-cell assay" as used herein refers to an in vitro assay to measure interferon-gamma ("IFN-gamma") expression. A variety of such primary T-cell assays are known in the art. In a preferred embodiment, the assay used is an anti-CD3 coimmobilizaton assay. In this assay, primary T cells are stimulated by anti-CD3 immobilized with or without additional recombinant proteins. Culture supernatants are harvested at timepoints, usually 24-72 hours. In another embodiment, the assay used is the MLR. In this assay, primary T cells are stimulated with allogeneic APC. Culture supernatants are harvested at timepoints, usually 24-72 hours. Human IFN-gamma levels are measured in culture supernatants by standard ELISA techniques. Commercial kits are available from vendors and the assay is performed according to manufacturer's recommendation.

[0129] The term "purified" as applied to nucleic acids, such as encoding immunomodulatory proteins of the invention, generally denotes a nucleic acid or polypeptide that is substantially free from other components as determined by analytical techniques well known in the art (e.g., a purified polypeptide or polynucleotide forms a discrete band in an electrophoretic gel, chromatographic eluate, and/or a media subjected to density gradient centrifugation). For example, a nucleic acid or polypeptide that gives rise to essentially one band in an electrophoretic gel is "purified." A purified nucleic acid or protein of the invention is at least about 50% pure, usually at least about 75%, 80%, 85%, 90%, 95%, 96%, 99% or more pure (e.g., percent by weight or on a molar basis).

[0130] The term "recombinant" indicates that the material (e.g., a nucleic acid or a polypeptide) has been artificially (i.e., non-naturally) altered by human intervention. The alteration can be performed on the material within,or removed from, its natural environment or state. For example, a "recombinant nucleic acid" is one that is made by recombining nucleic acids, e.g., during cloning, affinity modification, DNA shuffling or other well-known molecular biological procedures. A "recombinant DNA molecule," is comprised of segments of DNA joined together by means of such molecular biological techniques. The term "recombinant protein" or "recombinant polypeptide" as used herein refers to a protein molecule which is expressed using a recombinant DNA molecule. A "recombinant host cell" is a cell that contains and/or expresses a recombinant nucleic acid or that is otherwise altered by genetic engineering, such as by introducing into the cell a nucleic acid molecule encoding a recombinant protein, such as a transmembrane immunomodulatory protein provided herein. Transcriptional control signals in eukaryotes comprise "promoter" and "enhancer" elements. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription. Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect and mammalian cells and viruses (analogous control elements, i.e., promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the protein of interest. The terms "in operable combination," "in operable order" and "operably linked" as used herein refer to the linkage of nucleic acid sequences in such a manner or orientation that a nucleic acid molecule capable of directing the transcription of a given gene and/or the synthesis of a desired protein molecule is produced.

[0131] The term "recombinant expression vector" as used herein refers to a DNA molecule containing a desired coding sequence and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular host cell. Nucleic acid sequences necessary for expression in prokaryotes include a promoter, optionally an operator sequence, a ribosome binding site and possibly other sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals. A secretory signal peptide sequence can also, optionally, be encoded by the recombinant expression vector, operably linked to the coding sequence for the recombinant protein, such as a recombinant fusion protein, so that the expressed fusion protein can be secreted by the recombinant host cell, for easier isolation of the fusion protein from the cell, if desired. The term includes the vector as a

self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Among the vectors are viral vectors, such as lentiviral vectors.

[0132] The term "selectivity" refers to the preference of a subject protein, or polypeptide, for specific binding of one substrate, such as one cognate binding partner, compared to specific binding for another substrate, such as a different cognate binding partner of the subject protein. Selectivity can be reflected as a ratio of the binding activity (e.g. binding affinity) of a subject protein and a first substrate, such as a first cognate binding partner, (e.g., K_{d1}) and the binding activity (e.g. binding affinity) of the same subject protein with a second cognate binding partner (e.g., K_{d2}).

[0133] The term "sequence identity" as used herein refers to the sequence identity between genes or proteins at the nucleotide or amino acid level, respectively. "Sequence identity" is a measure of identity between proteins at the amino acid level and a measure of identity between nucleic acids at nucleotide level. The protein sequence identity may be determined by comparing the amino acid sequence in a given position in each sequence when the sequences are aligned. Similarly, the nucleic acid sequence identity may be determined by comparing the nucleotide sequence in a given position in each sequence when the sequences are aligned. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Center for Biotechnology Information (NCBI) website.

[0134] The term "soluble" as used herein in reference to proteins, means that the protein is not a membrane protein. In general, a soluble protein contains only the extracellular domain of an IgSF family member receptor, or a portion thereof containing an IgSF domain or domains or specific-binding fragments thereof, but does not contain the transmembrane domain. In some cases, solubility of a protein can be improved by linkage or attachment, directly or indirectly via a linker, to an Fc domain, which, in some cases, also can improve the stability and/or half-life of the protein. In some aspects, a soluble protein is an Fc fusion protein.

[0135] The term "species" as used herein with respect to polypeptides or nucleic acids means an ensemble of molecules with identical or substantially identical sequences. Variation between polypeptides that are of the same species may occur owing to differences in post-

translational modification such as glycosylation, phosphorylation, ubiquitination, nitrosylation, methylation, acetylation, and lipidation. Slightly truncated sequences of polypeptides that differ (or encode a difference) from the full length species at the amino-terminus or carboxy-terminus by no more than 1, 2, or 3 amino acid residues are considered to be of a single species. Such microheterogeneities are a common feature of manufactured proteins.

[0136] The term "specific binding fragment" as used herein in reference to a full-length wild-type mammalian PD-L1 polypeptide or an IgV or an IgC (e.g. IgC2) domain thereof, means a polypeptide having a subsequence of the full-length polypeptide or an IgV and/or IgC domain and that specifically binds in vitro and/or in vivo to a mammalian PD-1 and/or mammalian CD80 such as a human or murine PD-1 or CD80. In some embodiments, the specific binding fragment comprises an PD-L1 IgV or a PD-L1 IgC2 subsequence that is at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% the sequence length of the full-length wild-type sequence or an IgV or an IgC (e.g. IgC2) sequence thereof. The specific binding fragment can be altered in sequence to form a variant PD-L1 of the invention.

[0137] The term "specifically binds" as used herein means the ability of a protein, under specific binding conditions, to bind to a target protein such that its affinity or avidity is at least 5 times as great, but optionally at least 10, 20, 30, 40, 50, 100, 250 or 500 times as great, or even at least 1000 times as great as the average affinity or avidity of the same protein to a collection of random peptides or polypeptides of sufficient statistical size. A specifically binding protein need not bind exclusively to a single target molecule but may specifically bind to a non-target molecule due to similarity in structural conformation between the target and non-target (e.g., paralogs or orthologs). Those of skill will recognize that specific binding to a molecule having the same function in a different species of animal (i.e., ortholog) or to a non-target molecule having a substantially similar epitope as the target molecule (e.g., paralog) is possible and does not detract from the specificity of binding which is determined relative to a statistically valid collection of unique non-targets (e.g., random polypeptides). Thus, a polypeptide of the invention may specifically bind to more than one distinct species of target molecule due to cross-reactivity. Solid-phase ELISA immunoassays, ForteBio Octet, or Biacore measurements can be used to determine specific binding between two proteins. Generally, interactions between two binding proteins have dissociation constants (K_d) less than $1x10^{-5}$ M, and often as low as 1×10^{-12} M. In certain embodiments of the present disclosure, interactions between two binding proteins have

dissociation constants of less than or less than about $1x10^{-6}$ M, $1x10^{-7}$ M, $1x10^{-8}$ M, $1x10^{-9}$ M, $1x10^{-10}$ M or $1x10^{-11}$ M or less.

[0138] The terms "surface expresses" or "surface expression" in reference to a mammalian cell expressing a polypeptide means that the polypeptide is expressed as a membrane protein. In some embodiments, the membrane protein is a transmembrane protein.

[0139] As used herein, "synthetic," with reference to, for example, a synthetic nucleic acid molecule or a synthetic gene or a synthetic peptide refers to a nucleic acid molecule or polypeptide molecule that is produced by recombinant methods and/or by chemical synthesis methods.

[0140] The term "targeting moiety" as used herein refers to a composition that is covalently or non-covalently attached to, or physically encapsulates, a polypeptide comprising a variant PD-L1 of the present invention. The targeting moiety has specific binding affinity for a desired counter-structure such as a cell surface receptor (e.g., PD-1), or a tumor antigen such as tumor specific antigen (TSA) or a tumor associated antigen (TAA) such as B7-H6. Typically, the desired counter-structure is localized on a specific tissue or cell-type. Targeting moieties include: antibodies, antigen binding fragment (Fab), variable fragment (Fv) containing V_H and V_L, the single chain variable fragment (scFv) containing V_H and V_L linked together in one chain, as well as other antibody V region fragments, such as Fab', $F(ab)_2$, $F(ab')_2$, dsFv diabody, nanobodies, soluble receptors, receptor ligands, affinity matured receptors or ligands, as well as small molecule (<500 dalton) compositions (e.g., specific binding receptor compositions). Targeting moieties can also be attached covalently or non-covalently to the lipid membrane of liposomes that encapsulate a polypeptide of the present invention.

[0141] The term "transmembrane protein" as used herein means a membrane protein that substantially or completely spans a lipid bilayer such as those lipid bilayers found in a biological membrane such as a mammalian cell, or in an artificial construct such as a liposome. The transmembrane protein comprises a transmembrane domain ("transmembrane domain") by which it is integrated into the lipid bilayer and by which the integration is thermodynamically stable under physiological conditions. Transmembrane domains are generally predictable from their amino acid sequence via any number of commercially available bioinformatics software applications on the basis of their elevated hydrophobicity relative to regions of the protein that interact with aqueous environments (e.g., cytosol, extracellular fluid). A transmembrane domain is often a hydrophobic alpha helix that spans the membrane. A transmembrane protein can pass

through the both layers of the lipid bilayer once or multiple times. A transmembrane protein includes the provided transmembrane immunomodulatory proteins described herein. In addition to the transmembrane domain, a transmembrane immunomodulatory protein of the invention further comprises an ectodomain and, in some embodiments, an endodomain.

[0142] The terms "treating," "treatment," or "therapy" of a disease or disorder as used herein mean slowing, stopping or reversing the disease or disorders progression, as evidenced by decreasing, cessation or elimination of either clinical or diagnostic symptoms, by administration of a therapeutic composition (e.g. containing an immunomodulatory protein or engineered cells) of the invention either alone or in combination with another compound as described herein. "Treating," "treatment," or "therapy" also means a decrease in the severity of symptoms in an acute or chronic disease or disorder or a decrease in the relapse rate as for example in the case of a relapsing or remitting autoimmune disease course or a decrease in inflammation in the case of an inflammatory aspect of an autoimmune disease. As used herein in the context of cancer, the terms "treatment" or, "inhibit," "inhibiting" or "inhibition" of cancer refers to at least one of: a statistically significant decrease in the rate of tumor growth, a cessation of tumor growth, or a reduction in the size, mass, metabolic activity, or volume of the tumor, as measured by standard criteria such as, but not limited to, the Response Evaluation Criteria for Solid Tumors (RECIST), or a statistically significant increase in progression free survival (PFS) or overall survival (OS). "Preventing," "prophylaxis," or "prevention" of a disease or disorder as used in the context of this invention refers to the administration of an immunomodulatory polypeptide or engineered cells of the invention, either alone or in combination with another compound, to prevent the occurrence or onset of a disease or disorder or some or all of the symptoms of a disease or disorder or to lessen the likelihood of the onset of a disease or disorder.

[0143] The term "tumor specific antigen" or "TSA" as used herein refers to a counter-structure that is present primarily on tumor cells of a mammalian subject but generally not found on normal cells of the mammalian subject. A tumor specific antigen need not be exclusive to tumor cells but the percentage of cells of a particular mammal that have the tumor specific antigen is sufficiently high or the levels of the tumor specific antigen on the surface of the tumor are sufficiently high such that it can be targeted by anti-tumor therapeutics, such as immunomodulatory polypeptides of the invention, and provide prevention or treatment of the mammal from the effects of the tumor. In some embodiments, in a random statistical sample of cells from a mammal with a tumor, at least 50% of the cells displaying a TSA are cancerous. In

other embodiments, at least 60%, 70%, 80%, 85%, 90%, 95%, or 99% of the cells displaying a TSA are cancerous.

[0144] The term "variant" (also "modified" or mutant") as used in reference to a variant PD-L1 means a PD-L1, such as a mammalian (e.g., human or murine) PD-L1 created by human intervention. The variant PD-L1 is a polypeptide having an altered amino acid sequence, relative to an unmodified or wild-type PD-L1. The variant PD-L1 is a polypeptide which differs from a wild-type PD-L1 isoform sequence by one or more amino acid substitutions, deletions, additions, or combinations thereof. For purposes herein, the variant PD-L1 contains at least one affinity modified domain, whereby one or more of the amino acid differences occurs in an IgSF domain (e.g. IgV domain or ECD). A variant PD-L1 can contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more amino acid differences, such as amino acid substitutions. A variant PD-L1 polypeptide generally exhibits at least 50%, 60%, 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a corresponding wild-type or unmodified PD-L1, such as to the sequence of SEQ ID NO:3, a mature sequence thereof (lacking the signal sequence) or a portion thereof containing the extracellular domain or an IgSF domain thereof. In some embodiments, a variant PD-L1 polypeptide exhibits at least 50%, 60%, 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a corresponding wild-type or unmodified PD-L1 comprising the sequence set forth in SEQ ID NO:30 or 1728 or SEQ ID NO: 55 or 309. Non-naturally occurring amino acids as well as naturally occurring amino acids are included within the scope of permissible substitutions or additions. A variant PD-L1 is not limited to any particular method of making and includes, for example, de novo chemical synthesis, de novo recombinant DNA techniques, or combinations thereof. A variant PD-L1 of the invention specifically binds to at least one or more of PD-1 or CD80 of a mammalian species. In some embodiments, the altered amino acid sequence results in an altered (i.e., increased or decreased) binding affinity or avidity to PD-1 and/or CD80 compared to the wild-type or unmodified PD-L1 protein. An increase or decrease in binding affinity or avidity can be determined using well known binding assays such as flow cytometry. Larsen et al., American Journal of Transplantation, Vol 5: 443-453 (2005). See also, Linsley et al., Immunity, Vol 1(9): 793-801 (1994). An increase in variant PD-L1 binding affinity or avidity to PD-1 and/or CD80 is to a value at least 5% greater than that of the wild-type or unmodified PD-L1 and in some embodiments, at least 10%, 15%, 20%, 30%, 40%, 50%, 100%

greater than that of the wild-type or unmodified PD-L1 control value. A decrease in PD-L1 binding affinity or avidity to PD-1 and/or CD80 is to a value no greater than 95% of the wild-type or unmodified control values, and in some embodiments no greater than 80%, 70% 60%, 50%, 40%, 30%, 20%, 10%, 5%, or no detectable binding affinity or avidity of the wild-type or unmodified control values. A variant PD-L1 is altered in primary amino acid sequence by substitution, addition, or deletion of amino acid residues. The term "variant" in the context of variant PD-L1 is not to be construed as imposing any condition for any particular starting composition or method by which the variant PD-L1 is created. A variant PD-L1 can, for example, be generated starting from wild type mammalian PD-L1 sequence information, then modeled in silico for binding to PD-1 and/or CD80, and finally recombinantly or chemically synthesized to yield a variant PD-L1 of the present invention. In but one alternative example, a variant PD-L1 can be created by site-directed mutagenesis of a wild-type PD-L1. Thus, variant PD-L1 denotes a composition and not necessarily a product produced by any given process. A variety of techniques including recombinant methods, chemical synthesis, or combinations thereof, may be employed.

[0145] The term "wild-type" or "natural" or "native" as used herein is used in connection with biological materials such as nucleic acid molecules, proteins (e.g., PD-L1), IgSF members, host cells, and the like, refers to those which are found in nature and not modified by human intervention.

II. VARIANT PD-L1 POLYPEPTIDES

[0146] Provided herein are variant PD-L1 polypeptides that exhibit altered (increased or decreased) binding activity or affinity for one or more of a PD-L1 cognate binding partner. In some embodiments, the PD-L1 cognate binding partner is PD-1 or CD80. In some embodiments, the PD-L1 cognate binding partner is PD-1. In some embodiments, the variant PD-L1 polypeptide contains one or more amino acids modifications, such as one or more substitutions (alternatively, "mutations" or "replacements"), deletions or addition, in an immunoglobulin superfamily (IgSF) domain (IgD) relative to a wild-type or unmodified PD-L1 polypeptide or a portion of a wild-type or unmodified PD-L1 containing the IgD or a specific binding fragment thereof . Thus, a provided variant PD-L1 polypeptide is or comprises a variant IgD (hereinafter called "vIgD") in which the one or more amino acid modifications (e.g. substitutions) is in an IgD.

[0147] In some embodiments, the IgD comprises an IgV domain or an IgC (e.g. IgC2) domain or specific binding fragment of the IgV domain or the IgC (e.g. IgC2) domain, or combinations thereof. In some embodiments, the IgD can be an IgV only, the combination of the IgV and IgC, including the entire extracellular domain (ECD), or any combination of Ig domains of PD-L1. Table 2 provides exemplary residues that correspond to IgV or IgC regions of PD-L1. In some embodiments, the variant PD-L1 polypeptide contains an IgV domain or an IgC domain or specific binding fragments thereof in which the at least one amino acid modifications (e.g. substitutions) is in the IgV domain or IgC domain or a specific binding fragment thereof. In some embodiments, the variant PD-L1 polypeptide contains an IgV domain or specific binding fragments thereof in which the at least one of the amino acid modifications (e.g. substitutions) is in the IgV domain or a specific binding fragment thereof. In some embodiments, by virtue of the altered binding activity or affinity, the altered IgV domain or IgC (e.g. IgC2) domain is an affinity-modified IgSF domain.

[0148] In some embodiments, the variant is modified in one more IgSF domains relative to the sequence of an unmodified PD-L1 sequence. In some embodiments, the unmodified PD-L1 sequence is a wild-type PD-L1. In some embodiments, the unmodified or wild-type PD-L1 has the sequence of a native PD-L1 or an ortholog thereof. In some embodiments, the unmodified PD-L1 is or comprises the extracellular domain (ECD) of PD-L1 or a portion thereof containing one or more IgSF domain (see Table 2). In some embodiments, the extracellular domain of an unmodified or wild-type PD-L1 polypeptide comprises an IgV domain and an IgC (e.g. IgC2) domain or domains. However, the variant PD-L1 polypeptide need not comprise both the IgV domain and the IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide comprises or consists essentially of the IgV domain or a specific binding fragment thereof. In some embodiments, the variant PD-L1 polypeptide comprises or consists essentially of one or both of the IgC (e.g. IgC2) domain or specific binding fragments thereof. In some embodiments, the variant PD-L1 polypeptide comprises or consists essentially of only one of the IgC (e.g. IgC2) domain or a specific binding fragment thereof. In some embodiments, the variant PD-L1 polypeptide comprises the IgV domain or a specific binding fragment thereof, and the first and second IgC (e.g. IgC2) domains or specific binding fragment thereof. In some embodiments, the variant PD-L1 is soluble and lacks a transmembrane domain. In some embodiments, the variant PD-L1 further comprises a transmembrane domain and, in some cases, also a cytoplasmic domain.

[0149] In some embodiments, the wild-type or unmodified PD-L1 sequence is a mammalian PD-L1 sequence. In some embodiments, the wild-type or unmodified PD-L1 sequence can be a mammalian PD-L1 that includes, but is not limited to, human, mouse, cynomolgus monkey, or rat. In some embodiments, the wild-type or unmodified PD-L1 sequence is human.

[0150] In some embodiments, the wild-type or unmodified PD-L1 sequence has (i) the sequence of amino acids set forth in SEQ ID NO:3 or a mature form thereof lacking the signal sequence, (ii) a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO:3 or the mature form thereof, or (iii) is a portion of (i) or (ii) containing an IgV domain or IgC (e.g. IgC2) domain or specific binding fragments thereof.

[0151] In some embodiments, the wild-type or unmodified PD-L1 sequence is or comprises an extracellular domain of the PD-L1 or a portion thereof. In some embodiments, the unmodified or wild-type PD-L1 polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 30 or 1728, or an ortholog thereof. In some cases, the unmodified or wild-type PD-L1 polypeptide can comprise (i) the sequence of amino acids set forth in SEQ ID NO: 30 or 1728, (ii) a sequence of amino acids that has at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO: 30 or 1728, or (iii) is a specific binding fragment of the sequence of (i) or (ii) comprising an IgV domain or an IgC (e.g. IgC2) domain.

[0152] In some embodiments, the wild-type or unmodified PD-L1 polypeptide comprises an IgV domain or an IgC (e.g. IgC2) domain or domains, or a specific binding fragment thereof. In some embodiments, the IgV domain of the wild-type or unmodified PD-L1 polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 55 or 309(corresponding to amino acid residues24-130 of SEQ ID NO: 3), or an ortholog thereof. For example, the IgV domain of the unmodified or wild-type PD-L1 polypeptide can contain (i) the sequence of amino acids set forth in SEQ ID NO: 55 or 309, (ii) a sequence of amino acids that has at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO: 55 or 309, or (iii) a specific binding fragment of the sequence of (i) or (ii). In some embodiments, the wild-type or unmodified IgV domain is capable of binding one or more PD-L1 cognate binding proteins, such as one or more of PD-1 or CD80.

[0153] In some embodiments, a first IgC2 domain of the wild-type or unmodified PD-L1 polypeptide comprises the amino acid sequence set forth as residues 133-225 of SEQ ID NO: 3,

or an ortholog thereof. For example, an IgC2 domain of the unmodified or wild-type PD-L1 polypeptide can contain (i) the sequence of amino acids set forth as residues 133-225 of SEQ ID NO: 3, (ii) a sequence of amino acids that has at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to residues 133-225 of SEQ ID NO: 3, or (iii) a specific binding fragment of (i) or (ii). In some embodiments, the wild-type or unmodified IgC domain is capable of binding one or more PD-L1 cognate binding proteins.

[0154] In some embodiments, the wild-type or unmodified PD-L1 polypeptide contains a specific binding fragment of PD-L1, such as a specific binding fragment of the IgV domain or the IgC (e.g. IgC2) domain. In some embodiments the specific binding fragment can bind PD-1 and/or CD80. The specific binding fragment can have an amino acid length of at least 50 amino acids, such as at least 60, 70, 80, 90, 100, or 110 amino acids. In some embodiments, a specific binding fragment of the IgV domain contains an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% of the length of the IgV domain set forth as amino acids 24-130 of SEQ ID NO: 3. In some embodiments, a specific binding fragment of an IgC (e.g. IgC2) domain comprises an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% of the length of the IgC domain set forth as amino acids 133-225 of SEQ ID NO: 3.

[0155] In some embodiments, the variant PD-L1 polypeptide comprises the ECD domain or a portion thereof comprising one or more affinity modified IgSF domains. In some embodiments, the variant PD-L1 polypeptides can comprise an IgV domain or an IgC (e.g. IgC2) domain or domains, or a specific binding fragment of the IgV domain or a specific binding fragment of the IgC (e.g. IgC2) domain or domains in which one or more of the IgSF domains (IgV or IgC) contains the one or more amino acid modifications (e.g. substitutions). In some embodiments, the variant PD-L1 polypeptides can comprise an IgV domain and an IgC (e.g. IgC2) domain or domains, or a specific binding fragment of the IgV domain and a specific binding fragment of the IgC (e.g. IgC2) domain or domains, in which at least one of the IgV or IgC domain contains the amino acid modification(s) (e.g. substitution(s)). In some embodiments, the variant PD-L1 polypeptide comprises a full-length IgV domain. In some embodiments, the variant PD-L1 polypeptide comprises a full-length IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide comprises a specific binding fragment of the IgV domain. In some embodiments, the variant PD-L1 polypeptide comprises a specific binding fragment of the IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1

polypeptide comprises a full-length IgV domain and a full-length IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide comprises a full-length IgV domain and a specific binding fragment of an IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide comprises a specific binding fragment of an IgV domain and a full-length IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide comprises a specific binding fragment of an IgV domain and a specific binding fragment of an IgC (e.g. IgC2) domain or domains.

[0156] In any of such embodiments, the one or more amino acid modifications (e.g. substitutions) of the variant PD-L1 polypeptides can be located in any one or more of the PD-L1 polypeptide IgSF domains. For example, in some embodiments, one or more amino acid modifications (e.g. substitutions) are located in the extracellular domain of the variant PD-L1 polypeptide. In some embodiments, one or more amino acid modifications (e.g. substitutions) are located in the IgV domain or specific binding fragment of the IgV domain. In some embodiments, one or more amino acid modifications (e.g. substitutions) are located in an IgC (e.g. IgC2) domain or specific binding fragment of an IgC (e.g. IgC2) domain.

[0157] Generally, each of the various attributes of polypeptides are separately disclosed below (e.g., soluble and membrane bound polypeptides, affinity of PD-L1 for PD-1 and CD80, number of variations per polypeptide chain, number of linked polypeptide chains, the number and nature of amino acid alterations per variant PD-L1, etc.). However, as will be clear to the skilled artisan, any particular polypeptide can comprise a combination of these independent attributes. It is understood that reference to amino acids, including to a specific sequence set forth as a SEQ ID NO used to describe domain organization of an IgSF domain are for illustrative purposes and are not meant to limit the scope of the embodiments provided. It is understood that polypeptides and the description of domains thereof are theoretically derived based on homology analysis and alignments with similar molecules. Thus, the exact locus can vary, and is not necessarily the same for each protein. Hence, the specific IgSF domain, such as specific IgV domain or IgC domain, can be several amino acids (such as one, two, three or four) longer or shorter.

[0158] Further, various embodiments of the invention as discussed below are frequently provided within the meaning of a defined term as disclosed above. The embodiments described in a particular definition are therefore to be interpreted as being incorporated by reference when the defined term is utilized in discussing the various aspects and attributes described herein.

Thus, the headings, the order of presentation of the various aspects and embodiments, and the separate disclosure of each independent attribute is not meant to be a limitation to the scope of the present disclosure.

A. Exemplary Modifications

[0159] Provided herein are variant PD-L1 polypeptides containing at least one affinity-modified IgSF domain (e.g., ECD, IgV, or IgC) or a specific binding fragment thereof relative to an IgSF domain contained in a wild-type or unmodified PD-L1 polypeptide such that the variant PD-L1 polypeptide exhibits altered (increased or decreased) binding activity or affinity for one or more ligands PD-1 or CD80 compared to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, a variant PD-L1 polypeptide has a binding affinity for PD-1 and/or CD80 that differs from that of a wild-type or unmodified PD-L1 polypeptide control sequence as determined by, for example, solid-phase ELISA immunoassays, flow cytometry, ForteBio Octet or Biacore assays. In some embodiments, the variant PD-L1 polypeptide has an increased binding affinity for PD-1 and/or CD80. In some embodiments, the variant PD-L1 polypeptide has a decreased binding affinity for PD-1 and/or CD80, relative to a wild-type or unmodified PD-L1 polypeptide. The PD-1 and/or the CD80 can be a mammalian protein, such as a human protein or a murine protein.

[0160] Binding affinities for each of the cognate binding partners are independent; that is, in some embodiments, a variant PD-L1 polypeptide has an increased binding affinity for one or both of PD-1 and/or CD80, and a decreased binding affinity for one or both of PD-1 and CD80, relative to a wild-type or unmodified PD-L1 polypeptide.

[0161] In some embodiments, the variant PD-L1 polypeptide has an increased binding affinity for PD-1, relative to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide has an increased binding affinity for CD80, relative to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide has a decreased binding affinity for PD-1, relative to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide has a decreased binding affinity for CD80, relative to a wild-type or unmodified PD-L1polypeptide.

[0162] In some embodiments, the variant PD-L1 polypeptide has an increased binding affinity for PD-1 and CD80, relative to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide has an increased binding affinity for PD-1 and a decreased binding affinity for CD80, relative to a wild-type or unmodified PD-L1 polypeptide.

In some embodiments, the variant PD-L1 polypeptide has a decreased binding affinity for PD-1 and CD80, relative to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide has a decreased binding affinity for PD-1 and an increased binding affinity for CD80, relative to a wild-type or unmodified PD-L1 polypeptide.

[0163] In some embodiments, a variant PD-L1 polypeptide with increased or greater binding affinity to PD-1 and/or CD80 will have an increase in binding affinity relative to the wild-type or unmodified PD-L1 polypeptide control of at least about 5%, such as at least about 10%, 15%, 20%, 25%, 35%, or 50% for the PD-1 and/or CD80. In some embodiments, the increase in binding affinity relative to the wild-type or unmodified PD-L1 polypeptide is more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold. In such examples, the wild-type or unmodified PD-L1 polypeptide has the same sequence as the variant PD-L1 polypeptide except that it does not contain the one or more amino acid modifications (e.g. substitutions).

[0164] In some embodiments, a variant PD-L1 polypeptide with reduced or decreased binding affinity to PD-1 and/or CD80 will have decrease in binding affinity relative to the wild-type or unmodified PD-L1 polypeptide control of at least 5%, such as at least about 10%, 15%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more for the PD-1 and/or CD80. In some embodiments, the decrease in binding affinity relative to the wild-type or unmodified PD-L1 polypeptide is more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold. In such examples, the wild-type or unmodified PD-L1 polypeptide has the same sequence as the variant PD-L1 polypeptide except that it does not contain the one or more amino acid modifications (e.g. substitutions).

[0165] In some embodiments, the equilibrium dissociation constant (K_d) of any of the foregoing embodiments to PD-1 and/or CD80 can be less than $1x10^{-5}$ M, $1x10^{-6}$ M, $1x10^{-7}$ M, $1x10^{-8}$ M, $1x10^{-9}$ M, $1x10^{-10}$ M or $1x10^{-11}$M, or $1x10^{-12}$ M or less.

[0166] The wild-type or unmodified PD-L1 sequence does not necessarily have to be used as a starting composition to generate variant PD-L1 polypeptides described herein. Therefore, use of the term "modification", such as "substitution", does not imply that the present embodiments are limited to a particular method of making variant PD-L1 polypeptides. Variant PD-L1 polypeptides can be made, for example, by *de novo* peptide synthesis and thus does not necessarily require a modification, such as a "substitution", in the sense of altering a codon to encode for the modification, e.g. substitution. This principle also extends to the terms "addition"

and "deletion" of an amino acid residue which likewise do not imply a particular method of making. The means by which the variant PD-L1 polypeptides are designed or created is not limited to any particular method. In some embodiments, however, a wild-type or unmodified PD-L1 encoding nucleic acid is mutagenized from wild-type or unmodified PD-L1 genetic material and screened for desired specific binding affinity and/or induction of IFN-gamma expression or other functional activity. In some embodiments, a variant PD-L1 polypeptide is synthesized *de novo* utilizing protein or nucleic acid sequences available at any number of publicly available databases and then subsequently screened. The National Center for Biotechnology Information provides such information and its website is publicly accessible via the internet as is the UniProtKB database as discussed previously.

[0167] Unless stated otherwise, as indicated throughout the present disclosure, the amino acid modification(s) are designated by amino acid position number corresponding to the numbering of positions of the unmodified ECD sequence set forth in SEQ ID NO:30 or 1728 or also, where applicable, the unmodified IgV sequence set forth in SEQ ID NO: 309 (containing residues 1-114, respectively, of SEQ ID NO:30) as follows:

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEED
LKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRIT
VKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTT
NSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNER
(SEQ ID NO:30)

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEED
LKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRIT
VKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTT
NSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERT
(SEQ ID NO:1728)

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFV
HGEEDLKVQHSSYRQRARLL KDQLSLGNAALQITDVKLQDAGVYRCMISY
GGADYKRITVKVNA (SEQ ID NO:309)

[0168] Modifications provided herein can be in an unmodified PD-L1 polypeptide set forth in SEQ ID NO:30, 309 or 1728. In some cases, modifications also can be in an unmodified IgV set forth in SEQ ID NO:55. In some embodiments, the unmodified PD-L1 polypeptide has 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO: 30, 55, 309 or 1728.

PKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSS YRQRARLL KDQLSLGNAALQITDVKLQDAGVYRCMISY GGADYKRITVKV (SEQ ID NO:55)

[0169] It is within the level of a skilled artisan to identify the corresponding position of a modification, e.g. amino acid substitution, in a PD-L1 polypeptide, including portion thereof containing an IgSF domain (e.g. ECD or IgV) thereof, such as by alignment of a reference sequence with SEQ ID NO:30, or SEQ ID NO:309. In the listing of modifications throughout this disclosure, the amino acid position is indicated in the middle, with the corresponding unmodified (e.g. wild-type) amino acid listed before the number and the identified variant amino acid substitution listed after the number. If the modification is a deletion of the position a "del" is indicated and if the modification is an insertion at the position an "ins" is indicated. In some cases, an insertion is listed with the amino acid position indicated in the middle, with the corresponding unmodified (e.g. wild-type) amino acid listed before and after the number and the identified variant amino acid insertion listed after the unmodified (e.g. wild-type) amino acid.

[0170] In some embodiments, the variant PD-L1 polypeptide has one or more amino acid modifications, e.g. substitutions, in a wild-type or unmodified PD-L1 sequence. The one or more amino acid modifications, e.g. substitutions, can be in the ectodomain (extracellular domain) of the wild-type or unmodified PD-L1 sequence. In some embodiments, the one or more amino acid modifications, e.g. substitutions, are in the IgV domain or specific binding fragment thereof. In some embodiments, the one or more amino acid modifications, e.g. substitutions, are in the ECD domain or specific binding fragment thereof. In some embodiments, the one or more amino acid modifications, e.g. substitutions, are in an IgC (e.g. IgC2) domain or specific binding fragment thereof. In some embodiments of the variant PD-L1 polypeptide, some of the one or more amino acid modifications, e.g. substitutions, are in the IgV domain or a specific binding

fragment thereof, and some of the one or more amino acid modifications, e.g. substitutions, are in an IgC domain or domains (e.g. IgC2) or a specific binding fragment thereof.

[0171] In some embodiments, the variant PD-L1 polypeptide has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid modifications, e.g. substitutions. The modifications (e.g. substitutions) can be in the IgV domain or the IgC (e.g. IgC2) domain or domains. In some embodiments, the variant PD-L1 polypeptide has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid modifications, e.g. substitutions, in the IgV domain or specific binding fragment thereof. In some embodiments, the variant PD-L1 polypeptide has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid modifications, e.g. substitutions, in the IgC (e.g. IgC2) domain or domains or specific binding fragment thereof. In some embodiments, the variant PD-L1 polypeptide has at least about 85%, 86%, 86%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with the wild-type or unmodified PD-L1 polypeptide or specific binding fragment thereof, such as with the amino acid sequence of SEQ ID NO: 30, 1728, 55 or 309.

[0172] In some embodiments, the variant PD-L1 polypeptide has one or more amino acid modifications, e.g. substitutions, in an unmodified PD-L1 or specific binding fragment thereof corresponding to position(s) 6, 10, 11, 14, 15, 16, 17, 18, 19, 20, 22, 23, 26, 27, 28, 33, 35, 36, 40, 41, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 60, 64, 65, 68, 71, 72, 73, 74, 75, 78, 79, 83, 85, 89, 90, 93, 97, 98, 99, 101, 102, 103, 104, 106, 110, 111, 112, 113, 117, 119, 120, 121, 124, 129, 130, 131, 134, 137, 138, 144, 148, 149, 150, 155, 158, 160, 163, 165, 167, 170, 171, 173, 175, 176, 177, 179, 180, 183, 185, 188, 189, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 207, 213, or 221, with reference to positions set forth in SEQ ID NO: 30 or 1728. In some embodiments, such variant PD-L1 polypeptides exhibit altered binding affinity to one or more of PD-1 and/or CD80 compared to the wild-type or unmodified PD-L1 polypeptide. For example, in some embodiments, the variant PD-L1 polypeptide exhibits increased binding affinity to PD-1 and/or CD80 compared to a wild-type or unmodified PD-L1 polypeptide. In some embodiments, the variant PD-L1 polypeptide exhibits decreased binding affinity to PD-1 or CD80 compared to a wild-type or unmodified PD-L1 polypeptide.

[0173] In some embodiments, the variant PD-L1 polypeptide has one or more amino acid modification, e.g. amino acid substitution, selected from P6S, Y10F, V11A, V11E, Y14S, G15A, S16G, N17D, M18I, M18T, M18V, T19A, T19I, I20L, C22R, K23E, K23N, K23R, E26A, E27D, E27G, K28E, K28I, K28N, K28R, A33D, L35P, I36S, I36T, E40G, M41K, M41V, D43G,

D43V, K44E, N45D, N45I, N45T, I46V, I47T, F49S, V50A, H51N, H51R, H51Y, G52R, G52V, E53G, E53V, E54G, D55G, D55N, D55S, D55V, L56Q, K57E, K57R, V58A, V58D, H60R, R64S, Q65L, R68L, K71E, D72G, Q73R, L74P, S75P, N78I, N78S, A79T, I83T, D85E, Q89R, D90G, V93E, M97I, M97K, M97L, I98L, I98T, I98V, S99G, G101D, G101G-ins (G101GG), G102D, A103V, D104G, K106E, K106R, V110M, , K111E, K111T, V112A, N113Y, N117S, I119T, N120S, Q121L, L124S, V129A, V129D, T130A, S131F, E134G, C137R, Q138R, K144E, K144Q, I148V, W149R, T150A, Q155H, S158G, K160M, T163I, K163N, N165Y, K167R, K167T, E170G, K171R, F173I, F173L, K173Y, V175A, T176N, S177C, L179P, R180S, T183A, T183I, T185A, I188V, F189L, F189S, T192S, F193S, R194G, R194W, R195G, R195S, R195T, L196S, D197G, P198S, P198T, E199G, E200K, E200N, N201D, N201Y, H202Q, T203A, A204T, L206F, V207A, L213P, OR T221L or a conservative amino acid substitution thereof. A conservative amino acid substitution is any amino acid that falls in the same class of amino acids as the substituted amino acids, other than the wild-type or unmodified amino acid. The classes of amino acids are aliphatic (glycine, alanine, valine, leucine, and isoleucine), hydroxyl or sulfur-containing (serine, cysteine, threonine, and methionine), cyclic (proline), aromatic (phenylalanine, tyrosine, tryptophan), basic (histidine, lysine, and arginine), and acidic/amide (aspartate, glutamate, asparagine, and glutamine).

[0174] In some embodiments, the variant PD-L1 polypeptide has two or more amino acid modifications, e.g. amino acid substitutions, selected from P6S, Y10F, V11A, V11E, Y14S, G15A, S16G, N17D, M18I, M18T, M18V, T19A, T19I, I20L, C22R, K23E, K23N, K23R, E26A, E27D, E27G, K28E, K28I, K28N, K28R, A33D, L35P, I36S, I36T, E40G, M41K, M41V, D43G, D43V, K44E, N45D, N45I, N45T, I46V, I47T, F49S, V50A, H51N, H51R, H51Y, G52R, G52V, E53G, E53V, E54G, D55G, D55N, D55S, D55V, L56Q, K57E, K57R, V58A, V58D, H60R, R64S, Q65L, R68L, K71E, D72G, Q73R, L74P, S75P, N78I, N78S, A79T, I83T, D85E, Q89R, D90G, V93E, M97I, M97K, M97L, I98L, I98T, I98V, S99G, G101D, G101G-ins (G101GG), G102D, A103V, D104G, K106E, K106R, V110M, K111E, K111T, V112A, N113Y, N117S, I119T, N120S, Q121L, L124S, V129A, V129D, T130A, S131F, E134G, C137R, Q138R, K144E, K144Q, I148V, W149R, T150A, Q155H, S158G, K160M, T163I, K163N, N165Y, K167R, K167T, E170G, K171R, F173I, F173L, K173Y, V175A, S177C, L179P, R180S, T183A, T183I, T185A, I188V, F189L, F189S, T192S, F193S, R194G, R194W, R195G, R195S, R195T, L196S, D197G, P198S, P198T, E199G, E200K, E200N, N201D, N201Y, H202Q, T203A, A204T, L206F, V207A, L213P, or T221L.

[0175] In some embodiments, the amino acid modifications, e.g. amino acid substitutions, include K28N/M41V/N45T/H51N/K57E, I20L/I36T/N45D/I47T, I20L/M41K/K44E, P6S/N45T/N78I/I83T, N78I , M41K/N78I, N45T/N78I, I20L/N45T, N45T, M41K, I20L/I36T/N45D, N17D/N45T/V50A/D72G, I20L/F49S, N45T/V50A, I20L/N45T/N78I, I20L/N45T/V50A, M41V/N45T, M41K/N45T, A33D/S75P/D85E, M18I/M41K/D43G/H51R/N78I, V11E/I20L/I36T/N45D/H60R/S75P, A33D/V50A, S16G/A33D/K71E/S75P, E27G/N45T/M97I, E27G/N45T/K57R, A33D/E53V, D43G/N45D/V58A, E40G/D43V/N45T/V50A, Y14S/K28E/N45T A33D/N78S, A33D/N78I, A33D/N45T, A33D/N45T/N78I, E27G/N45T/V50A, N45T/V50A/N78S, I20L/N45T/V110M, I20L/I36T/N45T/V50A, N45T/L74P/S75P, N45T/S75P, S75P/K106R, S75P, A33D/S75P, A33D/S75P/D104G, A33D/S75P, I20L/E27G/N45T/V50A, I20L/E27G/D43G/N45D/V58A/N78I, I20L/D43G/N45D/V58A/N78I, I20L/A33D/D43G/N45D/V58A/N78I , I20L/D43G/N45D/N78I, E27G/N45T/V50A/N78I, N45T/V50A/N78I, V11A/I20L/E27G/D43G/N45D/H51Y/S99G, I20L/E27G/D43G/N45T/V50A , I20L/K28E/D43G/N45D/V58A/Q89R , I20L/I36T/N45D , I20L/K28E/D43G/N45D/E53G/V58A/N78I, A33D/D43G/N45D/V58A/S75P, K23R/D43G/N45D, I20L/D43G/N45D/V58A/N78I/D90G/G101D, D43G/N45D/L56Q/V58A/G101GG, I20L/K23E/D43G/N45D/V58A/N78I, I20L/K23E/D43G/N45D/V50A/N78I, T19I/E27G/N45I/V50A/N78I/M97K, I20L/M41K/D43G/N45D, K23R/N45T/N78I, I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG), K57R/S99G, K57R/S99G/F189L, M18V/M97L/F193S/R195G/E200K/H202Q, I36S/M41K/M97L/K144Q/R195G/E200K/H202Q/L206F, C22R/Q65L/L124S/K144Q/R195G/E200N/H202Q/T221L, M18V/I98L/L124S/P198T/L206F, S99G/N117S/I148V/K171R/R180S, I36T/M97L/A103V/Q155H, K28I/S99G, R195S, A79T/S99G/T185A/R195G/E200K/H202Q/L206F, K57R/S99G/L124S/K144Q, K57R/S99G/R195G, D55V/M97L/S99G, E27G/I36T/D55N/M97L/K111E, E54G/M97L/S99G, G15A/I36T/M97L/K111E/H202Q, G15A/I36T/V129D, G15A/I36T/V129D/R195G, G15A/V129D, I36S/M97L, I36T/D55N/M97L/K111E/A204T, I36T/D55N/M97L/K111E/V129A/F173L, I36T/D55S/M97L/K111E/I148V/R180S, I36T/G52R/M97L/V112A/K144E/V175A/P198T, I36T/I46V/D55G/M97L/K106E/K144E/T185A/R195G, I36T/I83T/M97L/K144E/P198T, I36T/M97L/K111E, I36T/M97L/K144E/P198T, I36T/M97L/Q155H/F193S/N201Y,

I36T/M97L/V129D, L35P/I36S/M97L/K111E, M18I/I36T/E53G/M97L/K144E/E199G/V207A, M18T/I36T/D55N/M97L/K111E, M18V/M97L/T176N/R195G, M97L/S99G, N17D/M97L/S99G, S99G/T185A/R195G/P198T, V129D/H202Q, V129D/P198T, V129D/T150A, V93E/V129D, Y10F/M18V/S99G/Q138R/T203A, N45D, K160M/R195G, N45D/K144E, N45D/P198S, N45D/P198T, N45D/R195G, N45D/R195S, N45D/S131F, N45D/V58D, V129D/R195S, I98T/F173Y/L196S, N45D/E134G/L213P, N45D/F173I/S177C, N45D/I148V/R195G, N45D/K111T/R195G, N45D/N113Y/R195S, N45D/N165Y/E170G, N45D/Q89R/I98V, N45D/S131F/P198S, N45D/S75P/P198S, N45D/V50A/R195T, E27D/N45D/T183A/I188V, F173Y/T183I/L196S/T203A, K23N/N45D/S75P/N120S, N45D/G102D/R194W/R195G, N45D/G52V/Q121L/P198S, N45D/I148V/R195G/N201D, N45D/K111T/T183A/I188V, N45D/Q89R/F189S/P198S, N45D/S99G/C137R/V207A, N45D/T163I/K167R/R195G, N45D/T183A/T192S/R194G, N45D/V50A/I119T/K144E, T19A/N45D/K144E/R195G, V11E/N45D/T130A/P198T, V26A/N45D/T163I/T185A, K23N/N45D/L124S/K167T/R195G, K23N/N45D/Q73R/T163I, K28E/N45D/W149R/S158G/P198T, K28R/N45D/K57E/I98V/R195S, K28R/N45D/V129D/T163N/R195T, M41K/D43G/N45D/R64S/R195G, M41K/D43G/N45D/R64S/S99G, N45D/R68L/F173L/D197G/P198S, N45D/V50A/I148V/R195G/N201D, M41K/D43G/K44E/N45D/R195G/N201D, or N45D/V50A/L124S/K144E/L179P/R195G.

[0176] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 20, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution I20L or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 27, 33, 36, 43, 45, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/E27G, I20L/A33D, I20L/I36T, I20L/D43G, I20L/N45D, I20L/N45T, I20L/V50A, I20L/V58A, I20L/S75P, I20L/N78I, I20L/M97L, I20L/S99G, I20L/R195G, I20L/P198S or I20L/R198T.

[0177] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 27, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution E27G or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 33, 36, 43, 45, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/E27G, E27G/A33D, E27G/I36T, E27G/D43G, E27G/N45D, E27G/N45T, E27G/V50A, E27G/V58A, E27G/S75P, E27G/N78I, E27G/M97L, E27G/S99G, E27G/R195G, E27G/P198S or E27G/R198T.

[0178] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 33, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution A33D or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 36, 43, 45, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/A33D, E27G/A33D, A33D/I36T, A33D/D43G, A33D/N45D, A33D/N45T, A33D/V50A, A33D/V58A, A33D/S75P, A33D/N78I, A33D/M97L, A33D/S99G, A33D/R195G, A33D/P198S or A33D/R198T.

[0179] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 36, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution I36T or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions,

at one or more positions 20, 27, 33, 43, 45, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/I36T, E27G/I36T, A33D/I36T, I36T/D43G, I36T/N45D, I36T/N45T, A33D/V50A, I36T/V58A, I36T/S75P, I36T/N78I, I36T/M97L, I36T/S99G, I36T/R195G, I36T/P198S or I36T/R198T.

[0180] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 43, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution D43G or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 45, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/D43G, E27G/D43G, A33D/D43G, I36T/D43G, D43G/N45D, D43G/N45T, D43G/V50A, D43G/V58A, D43G/S75P, D43G/N78I, D43G/M97L, D43G/S99G, D43G/R195G, D43G/P198S or D43G/R198T. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications D43G/N45D/V58A.

[0181] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 45, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution N45D or N45T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 50, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, V50A, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the

variant PD-L1 polypeptide comprises the amino acid modifications I20L/N45D, E27G/N45D, A33D/N45D, I36T/N45D, D43G/N45D, N45D/V50A, N45D/V58A, N45D/S75P, N45D/S75P, N45D/N78I, N45D/M97L, N45D/S99G, N45D/R195G, N45D/P198S or N45D/R198T. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/N45T, E27G/N45T, A33D/N45T, I36T/N45T, D43G/N45T, N45T/V50A, N45T/V58A, N45T/S75P, N45T/N78I, N45T/M97L, N45T/S99G, N45T/R195G, N45T/P198S or N45T/R198T. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications D43G/N45D/V58A.

[0182] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 50, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution V50A, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 58, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V58A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/V50A, E27G/V50A, A33D/V50A, I36T/V50A, D43G/V50A, N45D/V50A, V50A/V58A, V50A/S75P, V50A/N78I, V50A/M97L, V50A/S99G, V50A/R195G, V50A/P198S or V50A/R198T.

[0183] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 58, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution V58A, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 75, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, S75P, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/V58A, E27G/V58A,

A33D/V58A, I36T/V58A, D43G/V58A, N45D/V58A, V50A/V58A, V58A/S75P, V58A/N78I, V58A/M97L, V58A/S99G, V58A/R195G, V58A/P198S or V58A/R198T. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications D43G/N45D/V58A.

[0184] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 75, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution S75P, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 78, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, N78I, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/S75P, E27G/S75P, A33D/S75P, I36T/S75P, D43G/S75P, N45D/S75P, V50A/S75P, V58A/S75P, S75P/N78I, S75P/M97L, S75P/S99G, S75P/R195G, S75P/P198S or S75P/R198T.

[0185] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 78, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution N78I, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 75, 97, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, M97L, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/N78I, E27G/N78I, A33D/N78I, I36T/N78I, D43G/N78I, N45D/N78I, V50A/N78I, V58A/N78I, S75P/N78I, N78I/M97L, N78I/S99G, N78I/R195G, N78I/P198S or N78I/R198T.

[0186] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 97, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution M97L, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 75, 78, 99, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, S99G, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/M97L, E27G/M97L, A33D/M97L, I36T/M97L, D43G/M97L, N45D/M97L, V50A/M97L, V58A/M97L, S75P/M97L, N78I/M97L, M97L/S99G, M97L/R195G, M97L/P198S or M97L/R198T.

[0187] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 99, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution S99G, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 75, 78, 97, 195 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, R195G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/S99G, E27G/S99G, A33D/S99G, I36T/S99G, D43G/S99G, N45D/S99G, V50A/S99G, V58A/S99G, S75P/S99G, N78I/S99G, M97L/S99G, S99G/R195G, S99G/P198S or S99G/R198T.

[0188] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 195, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution R195G, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid

substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 75, 78, 97, 99 or 198. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/R195G, E27G/R195G, A33D/R195G, I36T/R195G, D43G/R195G, N45D/R195G, V50A/R195G, V58A/R195G, S75P/R195G, N78I/R195G, M97L/R195G, S99G/R195G, R195G/P198S or R195G/R198T.

[0189] In some embodiments, the variant PD-L1 polypeptide comprises amino acid modifications in an unmodified PD-L1 or specific binding fragment thereof at a position corresponding to position 198, with reference to numbering of positions set forth in SEQ ID NO:30. In some embodiments, the amino acid modification is the amino acid substitution P198S or P198T, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide further contains one or more amino acid modifications, e.g. amino acid substitutions, at one or more positions 20, 27, 33, 36, 43, 45, 50, 58, 75, 78, 97, 99 or 195. In some embodiments, the one or more amino acid modification is one or more amino acid substitutions I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, M97L, S99G, or R195G, or a conservative amino acid substitution thereof. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/P198S, E27G/P198S, A33D/P198S, I36T/P198S, D43G/P198S, N45D/P198S, V50A/P198S, V58A/P198S, S75P/P198S, N78I/P198S, M97L/P198S, S99G/P198S, or R195G/P198S. In some embodiments, the variant PD-L1 polypeptide comprises the amino acid modifications I20L/P198T, E27G/P198T, A33D/P198T, I36T/P198T, D43G/P198T, N45D/P198T, V50A/P198T, V58A/P198T, S75P/P198T, N78I/P198T, M97L/P198T, S99G/P198T, or R195G/P198T.

[0190] In some embodiments, the variant PD-L1 polypeptide comprises any of the substitutions (mutations) listed in Table 1. Table 1 also provides exemplary sequences by reference to SEQ ID NO for the extracellular domain (ECD) or IgV domain of wild-type PD-L1 or exemplary variant PD-L1 polypeptides. As indicated, the exact locus or residues corresponding to a given domain can vary, such as depending on the methods used to identify or classify the domain. Also, in some cases, adjacent N- and/or C-terminal amino acids of a given domain (e.g. ECD or IgV) also can be included in a sequence of a variant IgSF polypeptide, such

as to ensure proper folding of the domain when expressed. Thus, it is understood that the exemplification of the SEQ ID NOSs in Table 1 is not to be construed as limiting. For example, the particular domain, such as the ECD or IgV domain, of a variant PD-L1 polypeptide can be several amino acids longer or shorter, such as 1-10, e.g. 1, 2, 3, 4, 5, 6 or 7 amino acids longer or shorter, than the sequence of amino acids set forth in the respective SEQ ID NO.

[0191] In some embodiments, the variant PD-L1 polypeptide comprises or consists of any of the extracellular domain (ECD) sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008). In some embodiments, the variant PD-L1 polypeptide comprises or consists of a polypeptide sequence that exhibits at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, such as at least 96% identity, 97% identity, 98% identity, or 99% identity to any of the extracellular domain (ECD) sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008) and contains the amino acid modification(s), e.g. substitution(s), not present in the wild-type or unmodified PD-L1. In some embodiments, the variant PD-L1 polypeptide comprises or consists of a specific binding fragment of any of the extracellular domain (ECD) sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008) and contains the amino acid modification(s), e.g. substitution(s), not present in the wild-type or unmodified PD-L1.

[0192] In some embodiments, the variant PD-L1 polypeptide comprises or consists of any of the IgV sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937). In some embodiments, the variant PD-L1 polypeptide comprises or consists of a polypeptide sequence that exhibits at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, such as at least 96% identity, 97% identity, 98% identity, or 99% identity to any of the IgV sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937) and contains the amino acid modification(s), e.g. substitution(s), not present in the wild-type or unmodified PD-L1. In some embodiments, the variant PD-L1 polypeptide comprises or consists of a specific binding fragment of any of the IgV sequences listed in Table 1 (i.e., any one of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937) and contains the amino acid modification(s), e.g. substitution(s), not present in the wild-type or unmodified PD-L1.

TABLE 1: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	30, 1728	55, 309
K28N/M41V/N45T/H51N/K57E	56, 1943	121, 244
I20L/I36T/N45D/I47T	57, 1944	122, 245
I20L/M41K/K44E	58, 1945	123, 246
P6S/N45T/N78I/I83T	59, 1946	124, 247
N78I	60, 1947	125, 248
M41K/N78I	61, 1948	126, 249
N45T/N78I	62, 1949	127, 250
I20L/N45T	63, 1950	128, 251
N45T	64, 1951	129, 252
M41K	65, 1952	130, 253
I20L/I36T/N45D	66, 1953	131, 254
N17D/N45T/V50A/D72G	67, 1954	132, 255
I20L/F49S	68, 1955	133, 256
N45T/V50A	69, 1956	134, 257
I20L/N45T/N78I	70, 1957	135, 258
I20L/N45T/V50A	71, 1958	136, 259
M41V/N45T	72, 1959	137, 260
M41K/N45T	73, 1960	138, 261
A33D/S75P/D85E	74, 1961	139, 262
M18I/M41K/D43G/H51R/N78I	75, 1962	140, 263
V11E/I20L/I36T/N45D/H60R/S75P	76, 1963	141, 264
A33D/V50A	77, 1964	142, 265
S16G/A33D/K71E/S75P	78, 1965	143, 266
E27G/N45T/M97I	79, 1966	144, 267
E27G/N45T/K57R	80, 1967	145, 268
A33D/E53V	81, 1968	146, 269
D43G/N45D/V58A	82, 1969	147, 270
E40G/D43V/N45T/V50A	83, 1970	148, 271
Y14S/K28E/N45T	84, 1971	149, 272
A33D/N78S	85, 1972	150, 272
A33D/N78I	86, 1973	151, 274
A33D/N45T	87, 1974	152, 275
A33D/N45T/N78I	88, 1975	153, 276
E27G/N45T/V50A	89, 1976	154, 277
N45T/V50A/N78S	90, 1977	155, 278
I20L/N45T/V110M	91, 1978	156, 279
I20L/I36T/N45T/V50A	92, 1979	157, 280
N45T/L74P/S75P	93, 1980	158, 281
N45T/S75P	94, 1981	159, 282
S75P/K106R	95, 1982	160, 283
S75P	96, 1983	161, 284

TABLE 1: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
A33D/S75P	97, 1984	162, 285
A33D/S75P/D104G	98, 1985	163, 286
A33D/S75P	99, 1986	164, 287
I20L/E27G/N45T/V50A	100, 1987	165, 288
I20L/E27G/D43G/N45D/V58A/N78I	101, 1988	166, 289
I20L/D43G/N45D/V58A/N78I	102, 1989	167, 290
I20L/A33D/D43G/N45D/V58A/N78I	103, 1990	168, 291
I20L/D43G/N45D/N78I	104, 1991	169, 292
E27G/N45T/V50A/N78I	105, 1992	170, 293
N45T/V50A/N78I	106, 1993	171, 294
V11A/I20L/E27G/D43G/N45D/H51Y/S99G	107, 1994	172, 295
I20L/E27G/D43G/N45T/V50A	108, 1995	173, 296
I20L/K28E/D43G/N45D/V58A/Q89R	109, 1996	174, 297
I20L/I36T/N45D	110, 1997	175, 298
I20L/K28E/D43G/N45D/E53G/V58A/N78I	111, 1998	176, 299
A33D/D43G/N45D/V58A/S75P	112, 1999	177, 300
K23R/D43G/N45D	113, 2000	178, 301
I20L/D43G/N45D/V58A/N78I/D90G/G101D	114, 2001	179, 302
D43G/N45D/L56Q/V58A/ G101G-ins (G101GG)	115, 2002	180, 303
I20L/K23E/D43G/N45D/V58A/N78I	116, 2003	181, 304
I20L/K23E/D43G/N45D/V50A/N78I	117, 2004	182, 305
T19I/E27G/N45I/V50A/N78I/M97K	118, 2005	183, 306
I20L/M41K/D43G/N45D	119, 2006	184, 307
K23R/N45T/N78I	120, 2007	185, 308
I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG)	1725, 2008	1726, 1727
K57R/S99G	1729, 1819	1908, 1923
K57R/S99G/F189L	1730, 1820	
M18V/M97L/F193S/R195G/E200K/H202Q	1731, 1821	
I36S/M41K/M97L/K144Q/R195G/E200K/H202Q/L206F	1732, 1822	
C22R/Q65L/L124S/K144Q/R195G/E200N/H202Q/T221L	1733	
M18V/I98L/L124S/P198T/L206F	1734, 1823	
S99G/N117S/I148V/K171R/R180S	1735, 1824	
I36T/M97L/A103V/Q155H	1736, 1825	
K28I/S99G	1737, 1826	1909, 1924
R195S	1738, 1827	
A79T/S99G/T185A/R195G/E200K/H202Q/L206F	1739, 1828	
K57R/S99G/L124S/K144Q	1740, 1829	
K57R/S99G/R195G	1741, 1830	
D55V/M97L/S99G	1742, 1831	1910, 1925

TABLE 1: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
E27G/I36T/D55N/M97L/K111E	1743, 1832	1911, 1926
E54G/M97L/S99G	1744, 1833	1912, 1927
G15A/I36T/M97L/K111E/H202Q	1745, 1834	
G15A/I36T/V129D	1746, 1835	
G15A/I36T/V129D/R195G	1747, 1836	
G15A/V129D	1748, 1837	
I36S/M97L	1749, 1838	1913, 1928
I36T/D55N/M97L/K111E/A204T	1750, 1839	
I36T/D55N/M97L/K111E/V129A/F173L	1751, 1840	
I36T/D55S/M97L/K111E/I148V/R180S	1752, 1841	
I36T/G52R/M97L/V112A/K144E/V175A/P198T	1753, 1842	
I36T/I46V/D55G/M97L/K106E/K144E/T185A/R195G	1754, 1843	
I36T/I83T/M97L/K144E/P198T	1755, 1844	
I36T/M97L/K111E	1756, 1845	1914, 1929
I36T/M97L/K144E/P198T	1757, 1846	
I36T/M97L/Q155H/F193S/N201Y	1758, 1847	
I36T/M97L/V129D	1759, 1848	
L35P/I36S/M97L/K111E	1760, 1849	1915, 1930
M18I/I36T/E53G/M97L/K144E/E199G/V207A	1761, 1850	
M18T/I36T/D55N/M97L/K111E	1762, 1851	1916, 1931
M18V/M97L/T176N/R195G	1763, 1852	
M97L/S99G	1764, 1853	1917, 1932
N17D/M97L/S99G	1765, 1854	1918, 1933
S99G/T185A/R195G/P198T	1766, 1855	
V129D/H202Q	1767, 1856	
V129D/P198T	1768, 1857	
V129D/T150A	1769, 1858	
V93E/V129D	1770, 1859	
Y10F/M18V/S99G/Q138R/T203A	1771, 1860	
N45D	1772, 1861	1919, 1934
K160M/R195G	1773, 1862	
N45D/K144E	1774, 1863	
N45D/P198S	1775, 1864	
N45D/P198T	1776, 1865	
N45D/R195G	1777, 1866	
N45D/R195S	1778, 1867	
N45D/S131F	1779, 1868	
N45D/V58D	1780, 1869	1920, 1935
V129D/R195S	1781, 1870	
I98T/F173Y/L196S	1782, 1871	
N45D/E134G/L213P	1783, 1872	
N45D/F173I/S177C	1784, 1873	

TABLE 1: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
N45D/I148V/R195G	1785, 1874	
N45D/K111T/R195G	1786, 1875	
N45D/N113Y/R195S	1787, 1876	
N45D/N165Y/E170G	1788, 1877	
N45D/Q89R/I98V	1789, 1878	1921, 1936
N45D/S131F/P198S	1790, 1879	
N45D/S75P/P198S	1791, 1880	
N45D/V50A/R195T	1792, 1881	
E27D/N45D/T183A/I188V	1793, 1882	
F173Y/T183I/L196S/T203A	1794, 1883	
K23N/N45D/S75P/N120S	1795, 1884	
N45D/G102D/R194W/R195G	1796, 1885	
N45D/G52V/Q121L/P198S	1797, 1886	
N45D/I148V/R195G/N201D	1798, 1887	
N45D/K111T/T183A/I188V	1799, 1888	
N45D/Q89R/F189S/P198S	1800, 1889	
N45D/S99G/C137R/V207A	1801, 1890	
N45D/T163I/K167R/R195G	1802, 1891	
N45D/T183A/T192S/R194G	1803, 1892	
N45D/V50A/I119T/K144E	1804, 1893	
T19A/N45D/K144E/R195G	1805, 1894	
V11E/N45D/T130A/P198T	1806, 1895	
V26A/N45D/T163I/T185A	1807, 1896	
K23N/N45D/L124S/K167T/R195G	1808, 1897	
K23N/N45D/Q73R/T163I	1809, 1898	
K28E/N45D/W149R/S158G/P198T	1810, 1899	
K28R/N45D/K57E/I98V/R195S	1811, 1900	
K28R/N45D/V129D/T163N/R195T	1812, 1901	
M41K/D43G/N45D/R64S/R195G	1813, 1902	
M41K/D43G/N45D/R64S/S99G	1814, 1903	1922, 1937
N45D/R68L/F173L/D197G/P198S	1815, 1904	
N45D/V50A/I148V/R195G/N201D	1816, 1905	
M41K/D43G/K44E/N45D/R195G/N201D	1817, 1906	
N45D/V50A/L124S/K144E/L179P/R195G	1818, 1907	

[0193] In some embodiments, the variant PD-L1 polypeptide exhibits increased affinity for the ectodomain of PD-1 compared to the wild-type or unmodified PD-L1 polypeptide, such as comprising the sequence set forth in SEQ ID NO: 30, 1728, 55 or 309. In some embodiments, the PD-L1 polypeptide exhibits increased affinity for the ectodomain of CD80 compared to the wild-type or unmodified PD-L1, such as comprising the sequence set forth in SEQ ID NO: 30,

1728, 55 or 309. In some embodiments, the PD-L1 polypeptide exhibits increased affinity for the ectodomain of PD-1 and the ectodomain of CD80 compared to the wild-type or unmodified PD-L1, such as comprising the sequence set forth in SEQ ID NO: 30, 1728, 55 or 309.

[0194] In some embodiments, the variant PD-L1 polypeptide exhibits increased binding affinity for binding one of the ectodomains of PD-1 or CD80 and exhibits decreased binding affinity for binding to the other of the ectodomains of PD-1 or CD80 compared to the wild-type or unmodified PD-L1 polypeptide, such as comprising the sequence set forth in SEQ ID NO: 30, 1728, 55 or 309. In some embodiments, the variant PD-L1 polypeptide exhibits increased affinity for the ectodomain of PD-1, and decreased affinity for the ectodomain of CD80, compared to wild-type or unmodified PD-L1 polypeptide, such as comprising the sequence set forth in SEQ ID NO: 30, 1728, 55 or 309. In some embodiments, the variant PD-L1 polypeptide exhibits increased affinity for the ectodomain of CD80 and decreased affinity for the ectodomain of PD-1, compared to wild-type or unmodified PD-L1 polypeptide, such as comprising the sequence set forth in SEQ ID NO: 30, 1728, 55 or 309.

[0195] In some embodiments, a variant PD-L1 polypeptide exhibits increased selectivity for PD-1 versus CD80 compared to the ratio of binding of the unmodified PD-L1 polypeptide (e.g. set forth in SEQ ID NO: 30, 55 or 309) for binding PD-1 versus CD80, such as indicated by a ratio of PD-1binding to CD80 binding (PD-1:CD80 binding ratio) that is greater than 1. In some embodiments, the variant PD-L1 polypeptide exhibits a ratio of binding PD-1 versus CD80 that is greater than or greater than about or 1.1, 1.2, 1.3, 1.4, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, or more.

III. FORMAT OF VARIANT POLYPEPTIDES

[0196] The immunomodulatory polypeptide comprising a variant PD-L1 provided herein in which is contained a vIgD can be formatted in a variety of ways, including as a soluble protein, membrane bound protein or secreted protein. In some embodiments, the particular format can be chosen for the desired therapeutic application. In some cases, an immunomodulatory polypeptide comprising a variant PD-L1 polypeptide is provided in a format to antagonize or block activity of its cognate binding partner, e.g. PD-1. In some embodiments, antagonism of PD-1 may be useful to promote immunity in oncology. In some cases, an immunomodulatory polypeptide comprising a variant PD-L1 polypeptide is provided in a format to agonize or stimulate activity of its cognate binding partner, e.g. PD-1. In some embodiments, agonism of PD-1 may be useful

for treating inflammation or autoimmunity. A skilled artisan can readily determine the activity of a particular format, such as for antagonizing or agonizing one or more specific cognate binding partner. Exemplary methods for assessing such activities are provided herein, including in the examples.

[0197] In some aspects, provided are immunomodulatory proteins comprising a vIgD of PD-L1 in which such proteins are soluble, e.g. fused to an Fc chain. In some aspects, one or more additional IgSF domain, such as one or more additional vIgD, may be linked to a vIgD of PD-L1 as provided herein (hereinafter called a "stack" or "stacked" immunomodulatory protein). In some embodiments, the modular format of the provided immunomodulatory proteins provides flexibility for engineering or generating immunomodulatory proteins for modulating activity of multiple counterstrucutres (multiple cognate binding partners). In some embodiments, such "stack" molecules can be provided in a soluble format or, in some cases, may be provided as membrane bound or secreted proteins. In some embodiments, a variant PD-L1 immunomodulatory protein is provided as a conjugate in which is contained a vIgD of PD-L1 linked, directly or indirectly, to a targeting agent or moiety, e.g. to an antibody or other binding molecules that specifically binds to a ligand, e.g. an antigen, for example, for targeting or localizing the vIgD to a specific environment or cell, such as when administered to a subject. In some embodiments, the targeting agent, e.g. antibody or other binding molecule, binds to a tumor antigen, thereby localizing the variant PD-L1 containing the vIgD to the tumor microenvironment, for example, to modulate activity of tumor infiltrating lymphocytes (TILs) specific to the tumor microenvironment. In some embodiments, the targeting agent, e.g. antibody or other binding molecule, binds to an antigen expressed on antigen presenting cells or normal tissue in an inflammatory environment, thereby localizing the variant PD-L1 containing the vIgD to areas of unwanted autoimmune inflammation, for example, to modulate activity of T cells targeting self antigen.

[0198] In some embodiments, provided immunomodulatory proteins are expressed in cells and provided as part of an engineered cellular therapy (ECT). In some embodiments, the variant PD-L1 polypeptide is expressed in a cell, such as an immune cell (e.g. T cell or antigen presenting cell), in membrane-bound form, thereby providing a transmembrane immunomodulatory protein (hereinafter also called a "TIP"). In some embodiments, depending on the cognate binding partner recognized by the TIP, engineered cells expressing a TIP can agonize a cognate binding partner by providing a costimulatory signal, either positive to

negative, to other engineered cells and/or to endogenous T cells. In some aspects, the variant PD-L1 polypeptide is expressed in a cell, such as an immune cell (e.g. T cell or antigen presenting cell), in secretable form to thereby produce a secreted or soluble form of the variant PD-L1 polypeptide (hereinafter also called a "SIP"), such as when the cells are administered to a subject. In some aspects, a SIP can antagonize a cognate binding partner in the environment (e.g. tumor microenvironment) in which it is secreted. In some embodiments, a variant PD-L1 polypeptide is expressed in an infectious agent (e.g. viral or bacterial agent) which, upon administration to a subject, is able to infect a cell in vivo, such as an immune cell (e.g. T cell or antigen presenting cell), for delivery or expression of the variant polypeptide as a TIP or a SIP in the cell.

[0199] In some embodiments, a soluble immunomodulatory polypeptide, such as a variant PD-L1 containing a vIgD, can be encapsulated within a liposome which itself can be conjugated to any one of or any combination of the provided conjugates (e.g., a targeting moiety). In some embodiments, the soluble or membrane bound immunomodulatory polypeptides of the invention are deglycosylated. In more specific embodiments, the variant PD-L1 sequence is deglycosylated. In even more specific embodiments, the IgV and/or IgC (e.g. IgC2) domain or domains of the variant PD-L1 is deglycosylated.

[0200] Non-limiting examples of provided formats are described in FIGS. 1A-1C and further described below.

A. Soluble Protein

[0201] In some embodiments, the immunomodulatory protein containing a variant PD-L1 polypeptide is a soluble protein. Those of skill will appreciate that cell surface proteins typically have an intracellular, transmembrane, and extracellular domain (ECD) and that a soluble form of such proteins can be made using the extracellular domain or an immunologically active subsequence thereof. Thus, in some embodiments, the immunomodulatory protein containing a variant PD-L1 polypeptide lacks a transmembrane domain or a portion of the transmembrane domain. In some embodiments, the immunomodulatory protein containing a variant PD-L1 lacks the intracellular (cytoplasmic) domain or a portion of the intracellular domain. In some embodiments, the immunomodulatory protein containing the variant PD-L1 polypeptide only contains the vIgD portion containing the ECD domain or a portion thereof containing an IgV domain and/or IgC (e.g. IgC2) domain or domains or specific binding fragments thereof containing the amino acid modification(s).

[0202] In some embodiments, the immunomodulatory protein is or contains a variant PD-L1 polypeptide that is in monomer form and/or that exhibits monovalent binding to its binding partner. In some aspects, a variant PD-L1 polypeptide as described, such as a variant PD-L1 that is soluble and/or that lacks a transmembrane domain and intracellular signaling domain, is linked, directly or indirectly, to a further moiety. In some embodiments, the further moiety is a protein, peptide, small molecule or nucleic acid. In some embodiments, the monovalent immunomodulatory protein is a fusion protein. In some embodiments, the moiety is a half-life extending molecule. Exemplary of such half-life extending molecules include, but are not limited to, albumin, an albumin-binding polypeptide, Pro/Ala/Ser (PAS), a C-terminal peptide (CTP) of the beta subunit of human chorionic gonadotropin, polyethylene glycol (PEG), long unstructured hydrophilic sequences of amino acids (XTEN), hydroxyethyl starch (HES), an albumin-binding small molecule, or a combination thereof.

[0203] In some embodiments, the immunomodulatory polypeptide comprising a variant PD-L1 can be linked to a moiety that includes conformationally disordered polypeptide sequences composed of the amino acids Pro, Ala, and Ser (See e.g., WO2008/155134, SEQ ID NO: 2025). In some cases, the amino acid repeat is at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more amino acid residues, wherein each repeat comprises (an) Ala, Ser, and Pro residue(s). Thus, provided herein is an immunomodulatory protein is a PASylated protein wherein the variant PD-L1 polypeptide is linked, directly or indirectly via a linker, to Pro/Ala/Ser (PAS). In some embodiments, one or more additional linker structures may be used.

[0204] In some embodiments, the moiety facilitates detection or purification of the variant PD-L1 polypeptide. In some cases, the immunomodulatory polypeptide comprises a tag or fusion domain, e.g. affinity or purification tag, linked, directly or indirectly, to the N- and/or c-terminus of the PD-L1 polypeptide. Various suitable polypeptide tags and/or fusion domains are known, and include but are not limited to, a poly-histidine (His) tag, a FLAG-tag (SEQ ID NO: 2010), a Myc-tag, and fluorescent protein-tags (e.g., EGFP, set forth in SEQ ID NOs: 2027-2029). In some cases, the immunomodulatory polypeptide comprising a variant PD-L1 comprises at least six histidine residues (set forth in SEQ ID NO: 2011). In some cases, the immunomodulatory polypeptide comprising a variant PD-L1 further comprises various combinations of moieties. For example, the immunomodulatory polypeptide comprising a variant PD-L1 further comprises one or more polyhistidine-tag and FLAG tag.

[0205] In some embodiments, the PD-L1 polypeptide is linked to a modified immunoglobulin heavy chain constant region (Fc) that remains in monovalent form such as set forth in SEQ ID NO: 1187.

[0206] In some embodiments, the immunomodulatory protein contains a variant PD-L1 polypeptide that is linked, directly or indirectly via a linker to a multimerization domain. In some aspects, the multimerization domain inreases half-life of the molecule. Interaction of two or more variant PD-L1 polypeptides can be facilitated by their linkage, either directly or indirectly, to any moiety or other polypeptide that are themselves able to interact to form a stable structure. For example, separate encoded variant PD-L1 polypeptide chains can be joined by multimerization, whereby multimerization of the polypeptides is mediated by a multimerization domain. Typically, the multimerization domain provides for the formation of a stable protein-protein interaction between a first variant PD-L1 polypeptide and a second variant PD-L1 polypeptide.

[0207] Homo- or heteromultimeric polypeptides can be generated from co-expression of separate variant PD-L1 polypeptides. The first and second variant PD-L1 polypeptides can be the same or different. In particular embodiments, the first and second variant PD-L1 polypeptide are the same in a homodimer, and each are linked to a multimerization domain that is the same. In other embodiments, heterodimers can be formed by linking first and second variant PD-L1 polypeptides that are different. In such embodiments, in some aspects the first and second variant PD-L1 polypeptide are linked to different multimerization domains capable of promoting heterodimer formation.

[0208] In some embodiments, a multimerization domain includes any capable of forming a stable protein-protein interaction. The multimerization domains can interact via an immunoglobulin sequence (e.g. Fc domain; see e.g., International Patent Pub. Nos. WO 93/10151 and WO 2005/063816 US; U.S. Pub. No. 2006/0024298; U.S. Pat. No. 5,457,035); leucine zipper (e.g. from nuclear transforming proteins fos and jun or the proto-oncogene c-myc or from General Control of Nitrogen (GCN4)) (ee e.g., Busch and Sassone-Corsi (1990) Trends Genetics, 6:36-40; Gentz et al., (1989) Science, 243:1695-1699); a hydrophobic region; a hydrophilic region; or a free thiol which forms an intermolecular disulfide bond between the chimeric molecules of a homo- or heteromultimer. In addition, a multimerization domain can include an amino acid sequence comprising a protuberance complementary to an amino acid sequence comprising a hole, such as is described, for example, in U.S. Pat. No. 5,731,168;

International Patent Pub. Nos. WO 98/50431 and WO 2005/063816; Ridgway et al. (1996) Protein Engineering, 9:617-621. Such a multimerization region can be engineered such that steric interactions not only promote stable interaction, but further promote the formation of heterodimers over homodimers from a mixture of chimeric monomers. Generally, protuberances are constructed by replacing small amino acid side chains from the interface of the first polypeptide with larger side chains (e.g., tyrosine or tryptophan). Compensatory cavities of identical or similar size to the protuberances are optionally created on the interface of the second polypeptide by replacing large amino acid side chains with smaller ones (e.g., alanine or threonine). Exemplary multimerization domains are described below.

[0209] The variant PD-L1 polypeptide can be joined anywhere, but typically via its N- or C-terminus, to the N- or C-terminus of a multimerization domain to form a chimeric polypeptide. The linkage can be direct or indirect via a linker. The chimeric polypeptide can be a fusion protein or can be formed by chemical linkage, such as through covalent or non-covalent interactions. For example, when preparing a chimeric polypeptide containing a multimerization domain, nucleic acid encoding all or part of a variant PD-L1 polypeptide can be operably linked to nucleic acid encoding the multimerization domain sequence, directly or indirectly or optionally via a linker domain. In some cases, the construct encodes a chimeric protein where the C-terminus of the variant PD-L1 polypeptide is joined to the N-terminus of the multimerization domain. In some instances, a construct can encode a chimeric protein where the N-terminus of the variant PD-L1 polypeptide is joined to the C-terminus of the multimerization domain.

[0210] A polypeptide multimer contains multiple, such as two, chimeric proteins created by linking, directly or indirectly, two of the same or different variant PD-L1 polypeptides directly or indirectly to a multimerization domain. In some examples, where the multimerization domain is a polypeptide, a gene fusion encoding the variant PD-L1 polypeptide and multimerization domain is inserted into an appropriate expression vector. The resulting chimeric or fusion protein can be expressed in host cells transformed with the recombinant expression vector, and allowed to assemble into multimers, where the multimerization domains interact to form multivalent polypeptides. Chemical linkage of multimerization domains to variant PD-L1 polypeptides can be effected using heterobifunctional linkers.

[0211] The resulting chimeric polypeptides, such as fusion proteins, and multimers formed therefrom, can be purified by any suitable method such as, for example, by affinity chromatography over Protein A or Protein G columns. Where two nucleic acid molecules

encoding different polypeptides are transformed into cells, formation of homo- and heterodimers will occur. Conditions for expression can be adjusted so that heterodimer formation is favored over homodimer formation.

[0212] In some embodiments, the multimerization domain is an Fc domain or portions thereof from an immunoglobulin. In some embodiments, the immunomodulatory protein comprises a variant PD-L1 polypeptide attached to an immunoglobulin Fc (yielding an "immunomodulatory Fc fusion," such as a "PD-L1-Fc variant fusion," also termed a PD-L1 vIgD-Fc fusion). In some embodiments, the attachment of the variant PD-L1 polypeptide is at the N-terminus of the Fc. In some embodiments, the attachment of the variant PD-L1 polypeptide is at the C-terminus of the Fc. In some embodiments, two or more PD-L1 variant polypeptides (the same or different) are independently attached at the N-terminus and at the C-terminus.

[0213] In some embodiments, the Fc is murine or human Fc. In some embodiments, the Fc is a mammalian or human IgGl, lgG2, lgG3, or lgG4 Fc regions. In some embodiments, the Fc is derived from IgG1, such as human IgG1. In some embodiments, the Fc comprises the amino acid sequence set forth in SEQ ID NO: 187 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 187.

[0214] In some embodiments, the Fc region contains one more modifications to alter (e.g. reduce) one or more of its normal functions. In general, the Fc region is responsible for effector functions, such as complement-dependent cytotoxicity (CDC) and antibody-dependent cell cytotoxicity (ADCC), in addition to the antigen-binding capacity, which is the main function of immunoglobulins. In some cases, effector functions of an Fc region can include programmed cell death and cellular phagocytosis. Additionally, the FcRn sequence present in the Fc region plays the role of regulating the IgG level in serum by increasing the in vivo half-life by conjugation to an in vivo FcRn receptor. In some embodiments, such functions can be reduced or altered in an Fc for use with the provided Fc fusion proteins.

[0215] In some embodiments, one or more amino acid modifications may be introduced into the Fc region of a PD-L1-Fc variant fusion provided herein, thereby generating an Fc region variant. In some embodiments, the Fc region variant has decreased effector function. There are many examples of changes or mutations to Fc sequences that can alter effector function. For example, WO 00/42072, WO2006019447, WO2012125850, WO2015/107026, US2016/0017041

and Shields *et al. J Biol. Chem.* 9(2): 6591-6604 (2001) describe exemplary Fc variants with improved or diminished binding to FcRs. The contents of those publications are specifically incorporated herein by reference.

[0216] In some embodiments, the provided variant PD-L1-Fc fusions comprise an Fc region that exhibits reduced effector functions, which makes it a desirable candidate for applications in which the half-life of the PD-L1-Fc variant fusion *in vivo* is important yet certain effector functions (such as CDC and ADCC) are unnecessary or deleterious. *In vitro* and/or *in vivo* cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the PD-L1-Fc variant fusion lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 2 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-492 (1991). Non-limiting examples of *in vitro* assays to assess ADCC activity of a molecule of interest is described in U.S. Pat. No. 5,500,362 (see, *e.g.* Hellstrom, I. *et al. Proc. Nat'l Acad. Sci. USA* 83:7059-7063 (1986)) and Hellstrom, I *et al.*, *Proc. Nat'l Acad. Sci. USA* 82:1499-1502 (1985); U.S. Pat. No. 5,821,337 (see Bruggemann, M. *et al.*, *J. Exp. Med.* 166:1351-1361 (1987)). Alternatively, non-radioactive assay methods may be employed (see, for example, ACTI™ non-radioactive cytotoxicity assay for flow cytometry (CellTechnology, Inc. Mountain View, Calif.; and CytoTox 96™ non-radioactive cytotoxicity assay (Promega, Madison, Wis.). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, *e.g.*, in an animal model such as that disclosed in Clynes *et al. Proc. Nat'l Acad. Sci. USA* 95:652-656 (1998). C1q binding assays may also be carried out to confirm that the PD-L1-Fc variant fusion is unable to bind C1q and hence lacks CDC activity. See, *e.g.*, C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, for example, Gazzano-Santoro *et al.*, *J. Immunol. Methods* 202:163 (1996); Cragg, M. S. *et al.*, *Blood* 101:1045-1052 (2003); and Cragg, M. S. and M. J. Glennie, *Blood* 103:2738-2743 (2004)). FcRn binding and *in vivo* clearance/half-life determinations can also be performed using methods known in the art (see, *e.g.*, Petkova, S. B. *et al.*, *Int'l. Immunol.* 18(12):1759-1769 (2006)).

[0217] PD-L1-Fc variant fusions with reduced effector function include those with substitution of one or more of Fc region residues 238, 265, 269, 270, 297, 327 and 329 by EU numbering (U.S. Pat. No. 6,737,056). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327 by EU numbering, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 to alanine (U.S. Pat. No. 7,332,581).

[0218] In some embodiments, the Fc region of PD-L1-Fc variant fusions has an Fc region in which any one or more of amino acids at positions 234, 235, 236, 237, 238, 239, 270, 297, 298, 325, and 329 (indicated by EU numbering) are substituted with different amino acids compared to the native Fc region. Such alterations of Fc region are not limited to the above-described alterations, and include, for example, alterations such as deglycosylated chains (N297A and N297Q), IgG1-N297G, IgG1-L234A/L235A, IgG1-L234A/L235E/G237A, IgG1-A325A/A330S/P331S, IgG1-C226S/C229S, IgG1-C226S/C229S/E233P/L234V/L235A, IgG1-E233P/L234V/L235A/G236del/ S267K, IgG1-L234F/L235E/P331S, IgG1-S267E/L328F, IgG2-V234A/G237A, IgG2-H268Q/V309L/A330S/A331S, IgG4-L235A/G237A/E318A, and IgG4-L236E described in Current Opinion in Biotechnology (2009) 20 (6), 685-691; alterations such as G236R/L328R, L235G/G236R, N325A/L328R, and N325LL328R described in WO 2008/092117; amino acid insertions at positions 233, 234, 235, and 237 (indicated by EU numbering); and alterations at the sites described in WO 2000/042072.

[0219] Certain Fc variants with improved or diminished binding to FcRs are described. (See, *e.g.*, U.S. Pat. No. 6,737,056; WO 2004/056312, WO2006019447 and Shields *et al.*, *J. Biol. Chem.* 9(2): 6591-6604 (2001).)

[0220] In some embodiments, there is provided a PD-L1-Fc variant fusion comprising a variant Fc region comprising one or more amino acid substitutions which increase half-life and/or improve binding to the neonatal Fc receptor (FcRn). Antibodies with increased half-lives and improved binding to FcRn are described in US2005/0014934A1 (Hinton *et al.*) or WO2015107026. Those antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Such Fc variants include those with substitutions at one or more of Fc region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434 by EU numbering, *e.g.*, substitution of Fc region residue 434 (U.S. Pat. No. 7,371,826).

[0221] In some embodiments, the Fc region of a PD-L1-Fc variant fusion comprises one or more amino acid substitution E356D and M358L by EU numbering. In some embodiments, the Fc region of a PD-L1-Fc variant fusion comprises one or more amino acid substitutions C220S, C226S and/or C229S by EU numbering. In some embodiments, the Fc region of a PD-L1 variant fusion comprises one or more amino acid substitutions R292C and V302C. *See* also Duncan & Winter, *Nature* 322:738-40 (1988); U.S. Pat. No. 5,648,260; U.S. Pat. No. 5,624,821; and WO 94/29351 concerning other examples of Fc region variants.

[0222] In some embodiments, alterations are made in the Fc region that result in diminished C1q binding and/or Complement Dependent Cytotoxicity (CDC), *e.g.*, as described in U.S. Pat. No. 6,194,551, WO 99/51642, and Idusogie *et al.*, *J. Immunol.* 164: 4178-4184 (2000).

[0223] In some embodiments, there is provided a PD-L1-Fc variant fusion comprising a variant Fc region comprising one or more amino acid modifications, wherein the variant Fc region is derived from IgG1, such as human IgG1. In some embodiments, the variant Fc region is derived from the amino acid sequence set forth in SEQ ID NO: 187. In some embodiments, the Fc contains at least one amino acid substitution that is N82G by numbering of SEQ ID NO: 187 (corresponding to N297G by EU numbering). In some embodiments, the Fc further contains at least one amino acid substitution that is R77C or V87C by numbering of SEQ ID NO: 187 (corresponding to R292C or V302C by EU numbering). In some embodiments, the variant Fc region further comprises a C5S amino acid modification by numbering of SEQ ID NO: 187 (corresponding to C220S by EU numbering). For example, in some embodiments, the variant Fc region comprises the following amino acid modifications: V297G and one or more of the following amino acid modifications C220S, R292C or V302C by EU numbering (corresponding to N82G and one or more of the following amino acid modifications C5S, R77C or V87C with reference to SEQ ID NO:187), e.g., the Fc region comprises the sequence set forth in SEQ ID NO:1157. In some embodiments, the variant Fc region comprises one or more of the amino acid modifications C220S, L234A, L235E or G237A, e.g. the Fc region comprises the sequence set forth in SEQ ID NO:1158. In some embodiments, the variant Fc region comprises one or more of the amino acid modifications C220S, L235P, L234V, L235A, G236del or S267K, e.g. the Fc region comprises the sequence set forth in SEQ ID NO:1159. In some embodiments, the variant Fc comprises one or more of the amino acid modifications C220S, L234A, L235E, G237A, E356D or M358L, e.g. the Fc region comprises the sequence set forth in SEQ ID NO:1155.

[0224] In some embodiments, the Fc region lacks the C-terminal lysine corresponding to position 232 of the wild-type or unmodified Fc set forth in SEQ ID NO: 187 (corresponding to K447del by EU numbering). In some aspects, such an Fc region can additionally include one or more additional modifications, e.g. amino acid substitutions, such as any as described. Exemplary of such an Fc region is set forth in SEQ ID NO: 1938, 1939, 1940, or 1715.

[0225] In some embodiments, there is provided a PD-L1-Fc variant fusion comprising a variant Fc region in which the variant Fc comprises the sequence of amino acids set forth in any of SEQ ID NOS:1155, 1157, 1158, 1159, 1715, 1938, 1939, or 1940 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to any of SEQ ID NOS: 1155, 1157, 1158, 1159, 1715, 1938, 1939, or 1940.

[0226] In some embodiments, the Fc is derived from IgG2, such as human IgG2. In some embodiments, the Fc comprises the amino acid sequence set forth in SEQ ID NO: 188 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 188.

[0227] In some embodiments, the Fc comprises the amino acid sequence set forth in SEQ ID NO: 1200 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 1200. In some embodiments, the IgG4 Fc is a stabilized Fc in which the CH3 domain of human IgG4 is substituted with the CH3 domain of human IgG1 and which exhibits inhibited aggregate formation, an antibody in which the CH3 and CH2 domains of human IgG4 are substituted with the CH3 and CH2 domains of human IgG1, respectively, or an antibody in which arginine at position 409 indicated in the EU index proposed by Kabat et al. of human IgG4 is substituted with lysine and which exhibits inhibited aggregate formation (see e.g. U.S. Patent No. 8,911,726. In some embodiments, the Fc is an IgG4 containing the S228P mutation, which has been shown to prevent recombination between a therapeutic antibody and an endogenous IgG4 by Fab-arm exchange (see e.g. Labrijin et al. (2009) Nat. Biotechnol., 27(8): 767-71.) In some embodiments, the Fc comprises the amino acid sequence set forth in SEQ ID NO: 1201 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 1201.

[0228] In some embodiments, the variant PD-L1 polypeptide is directly linked to the Fc sequence. In some embodiments, the variant PD-L1 polypeptide is indirectly linked to the Fc

sequence, such as via a linker. In some embodiments, one or more "peptide linkers" link the variant PD-L1 polypeptide and the Fc domain. In some embodiments, a peptide linker can be a single amino acid residue or greater in length. In some embodiments, the peptide linker has at least one amino acid residue but is no more than 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid residues in length. In some embodiments, the linker is three alanines (AAA). In some embodiments, the linker is a flexible linker. In some embodiments, the linker is (in one-letter amino acid code): GGGGS ("4GS" or "G_4S"; SEQ ID NO: 1942) or multimers of the 4GS linker, such as repeats of 2, 3, 4, or 5 4GS linkers, such as set forth in SEQ ID NO: 240 (2xGGGGS) or SEQ ID NO:239 (3xGGGGS). In some embodiments, the linker (in one-letter amino acid code) is GSGGGGS (SEQ ID NO:1941). In some embodiments, the linker also can include a series of alanine residues alone or in addition to another peptide linker (such as a 4GS linker or multimer thereof). In some embodiments, the number of alanine residues in each series is: 2, 3, 4, 5, or 6 alanines. In some embodiments, the linker is a rigid linker. For example, the linker is an α-helical linker. In some embodiments, the linker is (in one-letter amino acid code): EAAAK or multimers of the EAAAK linker, such as repeats of 2, 3, 4, or 5 EAAAK linkers, such as set forth in SEQ ID NO: 2022 (1xEAAAK), SEQ ID NO: 2023 (3xEAAAK) or SEQ ID NO: 2024 (5xEAAAK). In some embodiments, the linker can further include amino acids introduced by cloning and/or from a restriction site, for example the linker can include the amino acids GS (in one-letter amino acid code) as introduced by use of the restriction site BAMHI. For example, in some embodiments, the linker (in one-letter amino acid code) is GSGGGGS (SEQ ID NO:1941), $GS(G_4S)_3$ (SEQ ID NO: 2031), or $GS(G_4S)_5$ (SEQ ID NO: 2032). In some examples, the linker is a 2xGGGGS followed by three alanines (GGGGSGGGGSAAA; SEQ ID NO: 241). In some cases, the immunomodulatory polypeptide comprising a variant PD-L1 comprises various combinations of peptide linkers.

[0229] In some embodiments, the variant PD-L1-Fc fusion protein is a dimer formed by two variant PD-L1 Fc polypeptides linked to an Fc domain. In some embodiments, the dimer is a homodimer in which the two variant PD-L1 Fc polypeptides are the same. In some embodiments, the dimer is a heterodimer in which the two variant PD-L1 Fc polypeptides are different.

[0230] Also provided are nucleic acid molecules encoding the variant PD-L1-Fc fusion protein. In some embodiments, for production of an Fc fusion protein, a nucleic acid molecule encoding a variant PD-L1-Fc fusion protein is inserted into an appropriate expression vector.

The resulting variant PD-L1-Fc fusion protein can be expressed in host cells transformed with the expression where assembly between Fc domains occurs by interchain disulfide bonds formed between the Fc moieties to yield dimeric, such as divalent, variant PD-L1-Fc fusion proteins.

[0231] The resulting Fc fusion proteins can be easily purified by affinity chromatography over Protein A or Protein G columns. For the generation of heterodimers, additional steps for purification can be necessary. For example, where two nucleic acids encoding different variant PD-L1 polypeptides are transformed into cells, the formation of heterodimers must be biochemically achieved since variant PD-L1 molecules carrying the Fc-domain will be expressed as disulfide-linked homodimers as well. Thus, homodimers can be reduced under conditions that favor the disruption of interchain disulfides, but do no effect intra-chain disulfides. In some cases, different variant-PD-L1 Fc monomers are mixed in equimolar amounts and oxidized to form a mixture of homo- and heterodimers. The components of this mixture are separated by chromatographic techniques. Alternatively, the formation of this type of heterodimer can be biased by genetically engineering and expressing Fc fusion molecules that contain a variant PD-L1 polypeptide using knob-into-hole methods described below.

B. Stack Molecules with Additional IgSF Domains

[0232] In some embodiments, the immunomodulatory proteins can contain any of the variant PD-L1 polypeptides provided herein linked, directly or indirectly, to one or more other immunoglobulin superfamily (IgSF) domain ("stacked" immunomodulatory protein construct and also called a "Type II" immunomodulatory protein). In some aspects, this can create unique multi-domain immunomodulatory proteins that bind two or more, such as three or more, cognate binding partners, thereby providing a multi-targeting modulation of the immune synapse.

[0233] In some embodiments, an immunomodulatory protein comprises a combination (a "non-wild-type combination") and/or arrangement (a "non-wild type arrangement" or "non-wild-type permutation") of a variant PD-L1 domain with one or more other affinity modified and/or non-affinity modified IgSF domain sequences of another IgSF family member (e.g. a mammalian IgSF family member) that are not found in wild-type IgSF family members. In some embodiments, the immunomodulatory protein contains 2, 3, 4, 5 or 6 immunoglobulin superfamily (IgSF) domains, where at least one of the IgSF domain is a variant PD-L1 IgSF domain (vIgD of PD-L1) according to the provided description.

[0234] In some embodiments, the sequences of the additional IgSF domains can be a modified IgSF domain that contains one or more amino acid modifications, e.g. substitutions,

compared to a wildtype or unmodified IgSF domain. In some embodiments, the IgSF domain can be non-affinity modified (e.g., wild-type) or have been affinity modified. In some embodiments, the unmodified or wild-type IgSF domain can be from mouse, rat, cynomolgus monkey, or human origin, or combinations thereof. In some embodiments, the additional IgSF domains can be an IgSF domain of an IgSF family member set forth in Table 2. In some embodiments, the additional IgSF domain can be an affinity-modified IgSF domain containing one or more amino acid modifications, e.g. substitutions, compared to an IgSF domain contained in an IgSF family member set forth in Table 2.

[0235] In some embodiments, the additional IgSF domain is an affinity or non-affinity modified IgSF domain contained in an IgSF family member of a family selected from Signal-Regulatory Protein (SIRP) Family, Triggering Receptor Expressed On Myeloid Cells Like (TREML) Family, Carcinoembryonic Antigen-related Cell Adhesion Molecule (CEACAM) Family, Sialic Acid Binding Ig-Like Lectin (SIGLEC) Family, Butyrophilin Family, B7 family, CD28 family, V-set and Immunoglobulin Domain Containing (VSIG) family, V-set transmembrane Domain (VSTM) family, Major Histocompatibility Complex (MHC) family, Signaling lymphocytic activation molecule (SLAM) family, Leukocyte immunoglobulin-like receptor (LIR), Nectin (Nec) family, Nectin-like (NECL) family, Poliovirus receptor related (PVR) family, Natural cytotoxicity triggering receptor (NCR) family, T cell immunoglobulin and mucin (TIM) family or Killer-cell immunoglobulin-like receptors (KIR) family. In some embodiments, the additional IgSF domains are independently derived from an IgSF protein selected from the group consisting of CD80(B7-1), CD86(B7-2), CD274 (PD-L1, B7-H1), PDCD1LG2(PD-L2, CD273), ICOSLG(B7RP1, CD275, ICOSL, B7-H2), CD276(B7-H3), VTCN1(B7-H4), CD28, CTLA4, PDCD1(PD-1), ICOS, BTLA(CD272), CD4, CD8A(CD8-alpha), CD8B(CD8-beta), LAG3, HAVCR2(TIM-3), CEACAM1, TIGIT, PVR(CD155), PVRL2(CD112), CD226, CD2, CD160, CD200, CD200R1(CD200R), NCR3 (NKp30), and VSIG8.

[0236] The first column of Table 2 provides the name and, optionally, the name of some possible synonyms for that particular IgSF member. The second column provides the protein identifier of the UniProtKB database, a publicly available database accessible via the internet at uniprot.org or, in some cases, the GenBank Number. The Universal Protein Resource (UniProt) is a comprehensive resource for protein sequence and annotation data. The UniProt databases include the UniProt Knowledgebase (UniProtKB). UniProt is a collaboration between the

European Bioinformatics Institute (EMBL-EBI), the SIB Swiss Institute of Bioinformatics and the Protein Information Resource (PIR) and supported mainly by a grant from the U.S. National Institutes of Health (NIH). GenBank is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (Nucleic Acids Research, 2013 Jan;41(D1):D36-42). The third column provides the region where the indicated IgSF domain is located. The region is specified as a range where the domain is inclusive of the residues defining the range. Column 3 also indicates the IgSF domain class for the specified IgSF region. Column 4 provides the region where the indicated additional domains are located (signal peptide, S; extracellular domain, E; transmembrane domain, T; cytoplasmic domain, C). It is understood that description of domains can vary depending on the methods used to identify or classify the domain, and may be identified differently from different sources. The description of residues corresponding to a domain in Table 2 is for exemplification only and can be several amino acids (such as one, two, three or four) longer or shorter. Column 5 indicates for some of the listed IgSF members, some of its cognate cell surface binding partners.

TABLE 2. IgSF members according to the present disclosure.

IgSF Member (Synonyms)	NCBI Protein Accession Number/ UniProtKB Protein Identifier	IgSF Region & Domain Class	Other Domains	Cognate Cell Surface Binding Partners	IgSF Member Amino Acid Sequence (SEQ ID NO)		
					Precursor (mature residues)	Mature	ECD
CD80 (B7-1)	NP_005182.1 P33681	35-135, 35-138,37-138, or 35-141 IgV, 145-230 or 154-232 IgC	S: 1-34, E: 35-242, T: 243-263, C: 264-288	CD28, CTLA4, PD-L1	SEQ ID NO: 1 (35-288)	SEQ ID NO: 189	SEQ ID NO: 28
CD86 (B7-2)	P42081.2	33-131 IgV, 150-225 IgC2	S: 1-23, E: 24-247, T: 248-268, C: 269-329	CD28, CTLA4	SEQ ID NO: 2 (24-329)	SEQ ID NO: 190	SEQ ID NO: 29
CD274 (PD-L1, B7-H1)	Q9NZQ7.1 NP_054862.1	24-130 or 19-127 IgV, 133-225 IgC2	S: 1-18, E: 19-238, T: 239-259, C: 260-290	PD-1, B7-1	SEQ ID NO: 3 (19-290)	SEQ ID NO: 191	SEQ ID NO: 30

TABLE 2. IgSF members according to the present disclosure.

IgSF Member (Synonyms)	NCBI Protein Accession Number/ UniProtKB Protein Identifier	IgSF Region & Domain Class	Other Domains	Cognate Cell Surface Binding Partners	IgSF Member Amino Acid Sequence (SEQ ID NO)		
					Precursor (mature residues)	Mature	ECD
PDCD1LG2 (PD-L2, CD273)	Q9BQ51.2	21-118 IgV, 122-203 IgC2	S: 1-19, E: 20-220, T: 221-241, C: 242-273	PD-1, RGMb	SEQ ID NO: 4 (20-273)	SEQ ID NO: 192	SEQ ID NO: 31
ICOSLG (B7RP1, CD275, ICOSL, B7-H2)	O75144.2	19-129 IgV, 141-227 IgC2	S: 1-18, E: 19-256, T: 257-277, C: 278-302	ICOS, CD28, CTLA4	SEQ ID NO: 5 (19-302)	SEQ ID NO: 193	SEQ ID NO: 32
CD276 (B7-H3)	Q5ZPR3.1	29-139 IgV, 145-238 IgC2, 243-357 IgV2, 363-456, 367-453 IgC2	S: 1-28, E: 29-466, T: 467-487, C: 488-534		SEQ ID NO: 6 (29-534)	SEQ ID NO: 194	SEQ ID NO: 33
VTCN1 (B7-H4)	Q7Z7D3.1	35-146 IgV, 153-241 IgV	S: 1-24, E: 25-259, T: 260-280, C: 281-282		SEQ ID NO: 7 (25-282)	SEQ ID NO: 195	SEQ ID NO: 34
CD28	P10747.1	28-137 IgV	S: 1-18, E: 19-152, T: 153-179, C: 180-220	B7-1, B7-2, B7RP1	SEQ ID NO: 8 (19-220)	SEQ ID NO: 196	SEQ ID NO: 35
CTLA-4	P16410.3	39-140 IgV	S: 1-35, E: 36-161, T: 162-182, C: 183-223	B7-1, B7-2, B7RP1	SEQ ID NO: 9 (36-223)	SEQ ID NO: 197	SEQ ID NO: 36

TABLE 2. IgSF members according to the present disclosure.

IgSF Member (Synonyms)	NCBI Protein Accession Number/ UniProtKB Protein Identifier	IgSF Region & Domain Class	Other Domains	Cognate Cell Surface Binding Partners	IgSF Member Amino Acid Sequence (SEQ ID NO)		
					Precursor (mature residues)	Mature	ECD
PDCD1 (PD-1)	Q15116.3	35-145 IgV	S: 1-20, E: 21-170, T: 171-191, C: 192-288	PD-L1, PD-L2	SEQ ID NO: 10 (21-288)	SEQ ID NO: 198	SEQ ID NO: 37
ICOS	Q9Y6W8.1	30-132 IgV	S: 1-20, E: 21-140, T: 141-161, C: 162-199	B7RP1	SEQ ID NO: 11 (21-199)	SEQ ID NO: 199	SEQ ID NO: 38
BTLA (CD272)	Q7Z6A9.3	31-132 IgV	S: 1-30, E: 31-157, T: 158-178, C: 179-289	HVEM	SEQ ID NO: 12 (31-289)	SEQ ID NO: 200	SEQ ID NO: 39
CD4	P01730.1	26-125 IgV, 126-203 IgC2, 204-317 IgC2, 317-389, 318-374 IgC2	S: 1-25, E: 26-396, T: 397-418, C: 419-458	MHC class II	SEQ ID NO: 13 (26-458)	SEQ ID NO: 201	SEQ ID NO: 40
CD8A (CD8-alpha)	P01732.1	22-135 IgV	S: 1-21, E: 22-182, T: 183-203, C: 204-235	MHC class I	SEQ ID NO: 14 (22-235)	SEQ ID NO: 202	SEQ ID NO: 41
CD8B (CD8-beta)	P10966.1	22-132 IgV	S: 1-21, E: 22-170, T: 171-191, C: 192-210	MHC class I	SEQ ID NO: 15 (22-210)	SEQ ID NO: 203	SEQ ID NO: 42

TABLE 2. IgSF members according to the present disclosure.

IgSF Member (Synonyms)	NCBI Protein Accession Number/ UniProtKB Protein Identifier	IgSF Region & Domain Class	Other Domains	Cognate Cell Surface Binding Partners	IgSF Member Amino Acid Sequence (SEQ ID NO)		
					Precursor (mature residues)	Mature	ECD
LAG3	P18627.5	37-167 IgV, 168-252 IgC2, 265-343 IgC2, 349-419 IgC2	S: 1-28, E: 29-450, T: 451-471, C: 472-525	MHC class II	SEQ ID NO: 16 (29-525)	SEQ ID NO: 204	SEQ ID NO: 43
HAVCR2 (TIM-3)	Q8TDQ0.3	22-124 IgV	S: 1-21, E: 22-202, T: 203-223, C: 224-301	CEACAM-1, phosphatidylserine, Galectin-9, HMGB1	SEQ ID NO: 17 (22-301)	SEQ ID NO: 205	SEQ ID NO: 44
CEACAM1	P13688.2	35-142 IgV, 145-232 IgC2, 237-317 IgC2, 323-413 IgC2	S: 1-34, E: 35-428, T: 429-452, C: 453-526	TIM-3	SEQ ID NO: 18 (35-526)	SEQ ID NO: 206	SEQ ID NO: 45
TIGIT	Q495A1.1	22-124 IgV	S: 1-21, E: 22-141, T: 142-162, C: 163-244	CD155, CD112	SEQ ID NO: 19 (22-244)	SEQ ID NO: 207	SEQ ID NO: 46
PVR (CD155)	P15151.2	24-139 IgV, 145-237 IgC2, 244-328 IgC2	S: 1-20, E: 21-343, T: 344-367, C: 368-417	TIGIT, CD226, CD96, poliovirus	SEQ ID NO: 20 (21-417)	SEQ ID NO: 208	SEQ ID NO: 47
PVRL2 (CD112)	Q92692.1	32-156 IgV, 162-256 IgC2, 261-345 IgC2	S: 1-31, E: 32-360, T: 361-381, C: 382-538	TIGIT, CD226, CD112R	SEQ ID NO: 21 (32-538)	SEQ ID NO: 209	SEQ ID NO: 48

TABLE 2. IgSF members according to the present disclosure.

IgSF Member (Synonyms)	NCBI Protein Accession Number/ UniProtKB Protein Identifier	IgSF Region & Domain Class	Other Domains	Cognate Cell Surface Binding Partners	IgSF Member Amino Acid Sequence (SEQ ID NO)		
					Precursor (mature residues)	Mature	ECD
CD226	Q15762.2	19-126 IgC2, 135-239 IgC2	S: 1-18, E: 19-254, T: 255-275, C: 276-336	CD155, CD112	SEQ ID NO: 22 (19-336)	SEQ ID NO: 210	SEQ ID NO: 49
CD2	P06729.2	25-128 IgV, 129-209 IgC2	S: 1-24, E: 25-209, T: 210-235, C: 236-351	CD58	SEQ ID NO: 23 (25-351)	SEQ ID NO: 211	SEQ ID NO: 50
CD160	O95971.1	27-122 IgV	N/A	HVEM, MHC family of proteins	SEQ ID NO: 24 (27-159)	SEQ ID NO: 212	SEQ ID NO: 51
CD200	P41217.4	31-141 IgV, 142-232 IgC2	S: 1-30, E: 31-232, T: 233-259, C: 260-278	CD200R	SEQ ID NO: 25 (31-278)	SEQ ID NO: 213	SEQ ID NO: 52
CD200R1 (CD200R)	Q8TD46.2	53-139 IgV, 140-228 IgC2	S: 1-28, E: 29-243, T: 244-264, C: 265-325	CD200	SEQ ID NO: 26 (29-325)	SEQ ID NO: 214	SEQ ID NO: 53
NCR3 (NKp30)	O14931.1	19-126 IgC-like	S: 1-18, E: 19-135, T: 136-156, C: 157-201	B7-H6	SEQ ID NO:27 (19-201)	SEQ ID NO: 215	SEQ ID NO: 54
VSIG8	Q5VU13	22-141 IgV1, 146-257 IgV2	S: 1-21 E: 22-263 T: 264-284 C: 285-414	VISTA	SEQ ID NO: 216 (22-414)	SEQ ID NO: 217	SEQ ID NO: 218

[0237] In some embodiments, the provided immunomodulatory proteins, in addition to containing a variant PD-L1 polypeptide, also contains at least 1, 2, 3, 4, 5 or 6 additional immunoglobulin superfamily (IgSF) domains, such as an IgD domain of an IgSF family member set forth in Table 2. In some embodiments, the provided immunomodulatory protein contains at least one additional IgSF domain (e.g. second IgSF domain). In some embodiments, the provided immunomodulatory protein contains at least two additional IgSF domains (e.g. second and third IgSF domain). In some embodiments, the provided immunomodulatory protein contains at least three additional IgSF domains (e.g. second, third and fourth). In some embodiments, the provided immunomodulatory protein contains at least four additional IgSF domains (e.g. second, third, fourth and fifth). In some embodiments, the provided immunomodulatory protein contains at least five additional IgSF domains (e.g. second, third, fourth, fifth and sixth). In some embodiments, the provided immunomodulatory protein contains at least six additional IgSF domains (e.g. second, third, fourth, fifth, sixth and seventh). In some embodiments, each of the IgSF domains in the immunomodulatory protein are different. In some embodiments, at least one of the additional IgSF domain is the same as at least one other IgSF domain in the immunomodulatory protein. In some embodiments, each of the IgSF domains is from or derived from a different IgSF family member. In some embodiments, at least two of the IgSF domains is from or derived from the same IgSF family member.

[0238] In some embodiments, the additional IgSF domain comprises an IgV domain or an IgC (e.g., IgC2) domain or domains, or a specific binding fragment of the IgV domain or a specific binding fragment of the IgC (e.g., IgC2) domain or domains. In some embodiments, the additional IgSF domain is or comprises a full-length IgV domain. In some embodiments, the additional IgSF domain is or comprises a full-length IgC (e.g., IgC2) domain or domains. In some embodiments, the additional IgSF domain is or comprises a specific binding fragment of the IgV domain. In some embodiments, the additional IgSF domain is or comprises a specific binding fragment of the IgC (e.g., IgC2) domain or domains. In some embodiments, the immunomodulatory protein contains at least two additional IgSF domains from a single (same) IgSF member. For example, in some aspects, the immunomodulatory protein contains an ECD or portion thereof of an IgSF member containing a full-length IgV domain and a full-length IgC (e.g., IgC2) domain or domains or specific binding fragments thereof.

[0239] In some embodiments, the provided immunomodulatory proteins contains at least one additional IgSF domain (e.g. a second or, in some cases, also a third IgSF domain and so on) in

which at least one additional, e.g. a second or third IgSF domain, is an IgSF domain set forth in a wild-type or unmodified IgSF domain or a specific binding fragment thereof contained in the sequence of amino acids set forth in any of SEQ ID NOS: 1-27 and 216. In some embodiments, the wild-type or unmodified IgSF domain is an IgV domain or an IgC domain, such as an IgC1 or IgC2 domain.

[0240] In some embodiments, the provided immunomodulatory proteins, in addition to containing a variant PD-L1 polypeptide, also contains at least one additional affinity-modified IgSF domain (e.g. a second or, in some cases, also a third affinity-modified IgSF domain and so on) in which at least one additional IgSF domain is a vIgD that contains one or more amino acid modifications (e.g. substitution, deletion or mutation) compared to an IgSF domain in a wild-type or unmodified IgSF domain, such as an IgSF domain in an IgSF family member set forth in Table 2. In some embodiments, the additional, e.g., second or third, affinity-modified IgSF domain comprises at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a wild-type or unmodified IgSF domain or a specific binding fragment thereof contained in the sequence of amino acids set forth in any of SEQ ID NOS: 1-27 and 216. In some embodiments, the wild-type or unmodified IgSF domain is an IgV domain or an IgC domain, such as an IgC1 or IgC2 domain. In some embodiments, the additional, e.g., or second or third, IgSF domain is an affinity-modified IgV domain and/or IgC domain. In some embodiments, the one or more additional IgSF domain is an affinity-modified IgSF domain that contains an IgV domain and/or an IgC (e.g., IgC2) domain or domains, or a specific binding fragment of the IgV domain and/or a specific binding fragment of the IgC (e.g., IgC2) domain or domains, in which the IgV and/or IgC domain contains the amino acid modification(s) (e.g., substitution(s)). In some embodiments, the one or more additional affinity-modified IgSF domain contains an IgV domain containing the amino acid modification(s) (e.g. substitution(s)). In some embodiments, the one or more additional affinity-modified IgSF domain include IgSF domains present in the ECD or a portion of the ECD of the corresponding unmodified IgSF family member, such as a full-length IgV domain and a full-length IgC (e.g., IgC2) domain or domains, or specific binding fragments thereof, in which one or both of the IgV and IgC contain the amino acid modification(s) (e.g. substitution(s)).

[0241] In some embodiments, the immunomodulatory polypeptide comprising a variant PD-L1 can include one or more vIgD of PD-L1 provided herein. In some embodiments, a variant PD-L1 immunomodulatory protein provided herein will comprise exactly 1, 2, 3, 4, 5 or more

variant PD-L1 sequences. In some embodiments, at least two of variant PD-L1 sequences are identical variant IgSF domains.

[0242] In some embodiments, the provided immunomodulatory polypeptide comprises two or more vIgD sequences of PD-L1. Multiple variant PD-L1 within the polypeptide chain can be identical (i.e., the same species) to each other or be non-identical (i.e., different species) variant PD-L1 sequences. In addition to single polypeptide chain embodiments, in some embodiments two, three, four, or more of the polypeptides of the invention can be covalently or non-covalently attached to each other. Thus, monomeric, dimeric, and higher order (e.g., 3, 4, 5, or more) multimeric proteins are provided herein. For example, in some embodiments exactly two polypeptides of the invention can be covalently or non-covalently attached to each other to form a dimer. In some embodiments, attachment is made via interchain cysteine disulfide bonds. Compositions comprising two or more polypeptides of the invention can be of an identical species or substantially identical species of polypeptide (e.g., a homodimer) or of non-identical species of polypeptides (e.g., a heterodimer). A composition having a plurality of linked polypeptides of the invention can, as noted above, have one or more identical or non-identical variant PD-L1 of the invention in each polypeptide chain. In some specific embodiments, identical or substantially identical species (allowing for 3 or fewer N-terminus or C-terminus amino acid sequence differences) of PD-L1-Fc variant fusion polypeptides will be dimerized to create a homodimer. Alternatively, different species of PD-L1-Fc variant fusion polypeptides can be dimerized to yield a heterodimer.

[0243] In some embodiments, the provided immunomodulatory protein contains at least one additional (e.g. or second or, in some cases, also a third IgSF domain and so on)IgSF domain that is a vIgD that contains one or more amino acid substitutions compared to an IgSF domain (e.g. IgV) of a wild-type or unmodified IgSF domain other than PD-L1.

[0244] In some embodiments, the one or more additional IgSF domain (e.g. second or third IgSF) domain is an IgSF domain (e.g. ECD or IgV) of another IgSF family member that itself also binds to an inhibitory receptor. In some aspects, the one or more additional IgSF domain (e.g. second or third IgSF) domain is an affinity-modified IgSF domain that is a variant IgSF domain (vIgD) of an IgSF family member that bind to an inhibitory receptor and that contains one or more amino acid substitutions in an IgSF domain (e.g. ECD or IgV), in which, in some cases, the one or more amino acid modifications result in increased binding to the inhibitory receptor. In some embodiments, the vIgD contains one or more amino acid modifications (e.g.

substitutions, deletions or additions) in a wild-type or unmodified IgSF domain (e.g. ECD or IgV) of an IgSF family member that binds to an inhibitory receptor. In addition to PD-1, exemplary of such inhibitory receptors are CTLA-4, LAG3, TIGIT, TIM-3, or BTLA. In some embodiments, the one or more additional IgSF domain is from an IgSF family member selected from CD155, CD112, PD-L2, CD80 or CEACAM1. Thus, in some aspects, provided are multi-target checkpoint antagonists that target or block activity of more than one inhibitory receptor.

[0245] In some embodiments, the immunomodulatory protein in a multi-target checkpoint antagonist that targets or blocks activity of at least two, three, four or more inhibitory receptors. In some embodiments, there is provided an immunomodulatory protein containing any one of the variant PD-L1 polypeptides and one or more IgSF domain of an inhibitory receptor, such as a wild-type or unmodified inhibitory receptor. In some embodiments, there is provided an immunomodulatory protein containing any one of the variant PD-L1 polypeptides and one or more IgSF domain of CD80, e.g. wild-type or unmodified CD80, such as an IgV domain set forth in SEQ ID NO:1005, 1079 or 2030 or an ECD or a portion thereof (containing the IgV and IgC domain or specific binding fragments thereof) set forth in SEQ ID NO:28 or a portion thereof. In some embodiments, there is provided an immunomodulatory protein containing any one of the variant PD-L1 polypeptides and one or more IgSF domain of CD112, e.g. wild-type or unmodified CD112, such as an IgV domain set forth in SEQ ID NO:666 or 761 or an ECD or a portion thereof (containing the IgV and IgC domain or specific binding fragments thereof) set forth in SEQ ID NO:48 or a portion thereof. In some embodiments, there is provided an immunomodulatory protein containing any one of the variant PD-L1 polypeptides and one or more IgSF domain of PD-L2, e.g. wild-type or unmodified PD-L2, such as an IgV domain set forth in SEQ ID NO:1203 or 1263 or an ECD or a portion thereof (containing the IgV and IgC domain or specific binding fragments thereof) set forth in SEQ ID NO:31 or a portion thereof. In some embodiments, there is provided an an immunomodulatory protein containing any one of the variant PD-L1 polypeptides and one or more IgSF domain of CD155, e.g. wild-type or unmodified CD155, such as an IgV domain set forth in SEQ ID NO 310 or 353 or an ECD or a portion thereof (containing the IgV and IgC domain or specific binding fragments thereof) set forth in SEQ ID NO:47 or a portion thereof.

[0246] In some embodiments, there is provided an immunomodulatory protein containing one or more additional IgSF domain (e.g., second or third IgSF) that is a vIgD of an IgSF family member that binds to an inhibitory receptor in which the one or more amino acid modifications in

an IgSF domain (e.g. IgV) results in increased binding affinity of the vIgD, or a fusion or immunomodulatory protein containing the vIgD, for its inhibitory receptor cognate binding partner compared to the unmodified IgSF domain, such as binding affinity that is increased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold. In some embodiments, the one or more amino acid modifications in an IgSF domain (e.g. IgV) results in increased selectivity of the vIgD, or a fusion or immunomodulatory protein containing the vIgD for its inhibitory receptor compared to the unmodified IgSF domain. In some embodiments, the increased selectivity is a greater ratio of binding of the vIgD for the inhibitory receptor versus another cognate binding partner, such as a cognate binding partner that is not an inhibitory receptor, compared to the ratio of binding of the unmodified IgSF for the inhibitory receptor versus the another cognate binding partner. In some embodiments, the ratio is greater by at least or at least about 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold.

[0247] In some embodiments, the at least one additional (e.g. second or third) vIgD is an IgSF domain (e.g. IgV) of a variant CD80 polypeptide that contains one or more amino acid modifications (e.g. substitutions, deletions or additions) in the IgSF domain (e.g. IgV) of CD155 or CD112, which are IgSF family members that bind to the inhibitory receptor TIGIT. In some embodiments, the at least one additional (e.g. second) vIgD contains one or more amino acid modifications (e.g. substitutions, deletions or additions) in an IgSF domain (e.g. IgV) of CD80, which is an IgSF family member that bind to the inhibitory receptor CTLA-4. Exemplary amino acid modifications, such as substitutions, deletions or additions, in an IgSF domain (e.g. ECD or IgV containing IgV and IgC) of a variant CD80 polypeptide are set forth in Table 3. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD80 polypeptide containing an IgV domain including any of the amino acid modifications set forth in Table 3, such as the IgV domain set forth in any of SEQ ID NOS:1006-1078, 1080-1112, 1114-1152 or an IgV domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1006-1078, 1080-1112, 1114-1152 and contains the one or more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD80 polypeptide containing an ECD or a portion thereof containing the IgV and/or IgC domains, in which is contained any of the amino acid modifications set forth in Table 3, such as the ECD set forth in

any of SEQ ID NOS: 932-964, 966-1004 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 932-964, 966-1004 and contains the one or more amino acid modifications.

[0248] In some embodiments, the at least one additional (e.g., second or third) vIgD is an IgSF domain (e.g. IgV) of a variant CD155 polypeptide that contains one or more amino acid modifications (e.g., substitutions, deletions or additions) in the IgSF domain (e.g., IgV) compared to unmodified or wild-type CD155, which, in some aspects, result in increased binding to the inhibitory receptor TIGIT. Exemplary amino acid modifications, such as substitutions, deletions or additions, in an IgSF domain (e.g. IgV or ECD containing IgV and IgC) of a variant CD155 polypeptide are set forth in Table 5. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD155 polypeptide containing an IgV domain including any of the amino acid modifications set forth in Table 5, such as the IgV domain set forth in any of SEQ ID NOS: 332-352, 354-374, 472-665, 1505-1550, 1570-1714, or an IgV domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 332-352, 354-374, 472-665, 1505-1550, 1570-1714 and contains the one more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD155 polypeptide containing an ECD or a portion thereof containing the IgV and/or IgC domains, in which is contained any of the amino acid modifications set forth in Table 5, such as the ECD set forth in any of SEQ ID NOS: 311-331, 375-471, 1551-1622 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 311-331, 375-471, 1551-1622 and contains the one or more amino acid modifications.

[0249] In some embodiments, the at least one additional (e.g., second or third) vIgD is an IgSF domain (e.g. IgV) of a variant CD112 polypeptide that contains one or more amino acid modifications (e.g., substitutions, deletions or additions) in the IgSF domain (e.g., IgV) compared to unmodified or wild-type CD112, which, in some aspects, result in increased binding to the inhibitory receptor TIGIT. Exemplary amino acid modifications, such as substitutions, deletions or additions, in an IgSF domain (e.g. IgV or ECD containing IgV and IgC) of a variant CD112 polypeptide are set forth in Table 4. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD112 polypeptide containing an IgV domain including any of the amino acid

modifications set forth in Table 4, such as the IgV domain set forth in any of SEQ ID NOS: 714-760, 762-808, 850-931, or an IgV domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 714-760, 762-808, 850-931 and contains the one more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1polypeptides and a variant CD112 polypeptide containing an ECD or a portion thereof containing the IgV and/or IgC domains, in which is contained any of the amino acid modifications set forth in Table 4, such as the ECD set forth in any of SEQ ID NOS: 667-713, 809-849, 1433-1456 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 667-713, 809-849, 1433-1456 and contains the one or more amino acid modifications.

[0250] In some embodiments, the at least one additional (e.g., second or third) vIgD is an IgSF domain (e.g. IgV) of a variant PD-L2 polypeptide that contains one or more amino acid modifications (e.g., substitutions, deletions or additions) in the IgSF domain (e.g., ECD or IgV) compared to unmodified or wild-type PD-L2, which, in some aspects, result in increased binding to the inhibitory receptor PD-1. Exemplary amino acid modifications, such as substitutions, deletions or additions, in an IgSF domain (e.g. IgV or ECD containing IgV and IgC) of a variant PD-L2 polypeptide are set forth in Table 8. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant PD-L2 polypeptide containing an IgV domain including any of the amino acid modifications set forth in Table 8, such as the IgV domain set forth in any of SEQ ID NOS: 1281-1331, 1333-1407, 1409-1432 or an IgV domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1281-1331, 1333-1407, 1409-1432 and contains the one more more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant PD-L2 polypeptide containing an ECD or a portion thereof containing the IgV and/or IgC domains, in which is contained any of the amino acid modifications set forth in Table 8, such as the ECD set forth in any of SEQ ID NOS:1204-1254, 1256-1280 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1204-1254, 1256-1280 and contains the one or more amino acid modifications.

[0251] In some embodiments, the one or more additional IgSF domain (e.g. second IgSF) domain is an IgSF domain (e.g. IgV) of another IgSF family member that binds or recognizes a tumor antigen. In such embodiments, the IgSF family member serves as a tumor-localizing moiety, thereby bringing the vIgD of PD-L1 in close proximity to immune cells in the tumor microenvironment. In some embodiments, the additional IgSF domain (e.g. second IgSF) domain is an IgSF domain of NKp30, which binds or recognizes B7-H6 expressed on a tumor cell. In some embodiments, the at least one additional (e.g. second) IgSF domain, e.g. NKp30, is an affinity-modified IgSF domain or vIgD that contains one or more amino acid modifications (e.g. substitutions, deletions or additions). In some embodiments, the one or more amino acid modifications increase binding affinity and/or selectivity to B7-H6 compared to unmodified IgSF domain, e.g. NKp30, such as by at least or at least about 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold. Exemplary amino acid modifications, such as substitutions, deletions or additions, in an IgSF domain (e.g. IgC-like or full ECD) of a variant NKp30 polypeptide are set forth in Table 6. Among the exemplary polypeptides is an NKp30 variant that contains the mutations L30V/A60V/S64P/S86G with reference to positions in the NKp30 extracellular domain corresponding to positions set forth in SEQ ID NO: 54. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant NKp30 polypeptide containing an IgC-like domain including any of the amino acid modifications set forth in Table 6, such as the IgC-like domain set forth in any of SEQ ID NOS: 1184-1188 or an IgC-like domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1184-1188 and contains the one more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant NKp30 polypeptide containing an ECD or a portion thereof containing an IgSF domain or domains, in which is contained any of the amino acid modifications set forth in Table 6, such as the ECD set forth in any of SEQ ID NOS: 1178-1182 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1178-1182 and contains the one or more amino acid modifications.

[0252] In some embodiments, the at least one additional (e.g., second or third) vIgD is an IgSF domain (e.g. IgV) of a variant CD86 polypeptide that contains one or more amino acid modifications (e.g., substitutions, deletions or additions) in the IgSF domain (e.g., IgV) compared

to unmodified or wild-type CD86, which, in some aspects, result in increased binding to its cognate binding partner. Exemplary amino acid modifications, such as subtitutions, deletions or additions, in an IgSF domain (e.g. IgV or ECD containing IgV and IgC) of a variant CD86 polypeptide are set forth in Table 7. Among exemplary polypeptides include CD86 variants that contain the mutations Q35H/H90L/Q102H with reference to positions in the CD86 extracellular domain corresponding to positions set forth in SEQ ID NO: 29. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD86 polypeptide containing an IgV domain including any of the amino acid modifications set forth in Table 7, such as the IgV domain set forth in any of SEQ ID NOS: 1196-1199 or an IgV domain that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS: 1196-1199 and contains the one more amino acid modifications. In some embodiments, there is provided an immunomodulatory protein containing any of the provided variant PD-L1 polypeptides and a variant CD86 polypeptide containing an ECD or a portion thereof containing the IgV and/or IgC domains, in which is contained any of the amino acid modifications set forth in Table 7, such as the ECD set forth in any of SEQ ID NOS: 1191-1194 or an ECD that contains at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% to any of SEQ ID NOS:1191-1194 and contains the one or more amino acid modifications.

[0253] Tables 3-8 provide exemplary polypeptides containing one or more affinity-modified IgSF domains that can be used in stack constructs provided herein.

TABLE 3: Exemplary variant CD80 polypeptides

Mutation(s)	ECD SEQ ID NO	IgV SEQ ID NO
Wild-type	28	1005, 2030
L70P	932	1006, 1080
I30F/L70P	933	1007, 1081
Q27H/T41S/A71D	934	1008, 1082
I30T/L70R	935	1009, 1083
T13R/C16R/L70Q/A71D	936	1010, 1084
T57I	937	1011, 1085
M43I/C82R	938	1012, 1086
V22L/M38V/M47T/A71D/L85M	939	1013, 1087
I30V/T57I/L70P/A71D/A91T	940	1014, 1088
V22I/L70M/A71D	941	1015, 1089
N55D/L70P/E77G	942	1016, 1090
T57A/I69T	943	1017, 1091

TABLE 3: Exemplary variant CD80 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
N55D/K86M	944	1018, 1092
L72P/T79I	945	1019, 1093
L70P/F92S	946	1020, 1094
T79P	947	1021, 1095
E35D/M47I/L65P/D90N	948	1022, 1096
L25S/E35D/M47I/D90N	949	1023, 1097
A71D	951	1025, 1099
E81K/A91S	953	1027, 1101
A12V/M47V/L70M	954	1028, 1102
K34E/T41A/L72V	955	1029, 1103
T41S/A71D/V84A	956	1030, 1104
E35D/A71D	957	1031, 1105
E35D/M47I	958	1032, 1106
K36R/G78A	959	1033, 1107
Q33E/T41A	960	1034, 1108
M47V/N48H	961	1035, 1109
M47L/V68A	962	1036, 1110
S44P/A71D	963	1037, 1111
Q27H/M43I/A71D/R73S	964	1038, 1112
E35D/T57I/L70Q/A71D	966	1040, 1114
M47I/E88D	967	1041, 1115
M42I/I61V/A71D	968	1042, 1116
P51A/A71D	969	1043, 1117
H18Y/M47I/T57I/A71G	970	1044, 1118
V20I/M47V/T57I/V84I	971	1045, 1119
V20I/M47V/A71D	972	1046, 1120
A71D/L72V/E95K	973	1047, 1121
V22L/E35G/A71D/L72P	974	1048, 1122
E35D/A71D	975	1049, 1123
E35D/I67L/A71D	976	1050, 1124
Q27H/E35G/A71D/L72P/T79I	977	1051, 1125
T13R/M42V/M47I/A71D	978	1052, 1126
E35D	979	1053, 1127
E35D/M47I/L70M	980	1054, 1128
E35D/A71D/L72V	981	1055, 1129
E35D/M43L/L70M	982	1056, 1130
A26P/E35D/M43I/L85Q/E88D	983	1057, 1131
E35D/D46V/L85Q	984	1058, 1132
Q27L/E35D/M47I/T57I/L70Q/E88D	985	1059, 1133
M47V/I69F/A71D/V83I	986	1060, 1134
E35D/T57A/A71D/L85Q	987	1061, 1135
H18Y/A26T/E35D/A71D/L85Q	988	1062, 1136

TABLE 3: Exemplary variant CD80 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
E35D/M47L	989	1063, 1137
E23D/M42V/M43I/I58V/L70R	990	1064, 1138
V68M/L70M/A71D/E95K	991	1065, 1139
N55I/T57I/I69F	992	1066, 1140
E35D/M43I/A71D	993	1067, 1141
T41S/T57I/L70R	994	1068, 1142
H18Y/A71D/L72P/E88V	995	1069, 1143
V20I/A71D	996	1070, 1144
E23G/A26S/E35D/T62N/A71D/L72V/L85M	997	1071, 1145
A12T/E24D/E35D/D46V/I61V/L72P/E95V	998	1072, 1146
V22L/E35D/M43L/A71G/D76H	999	1073, 1147
E35G/K54E/A71D/L72P	1000	1074, 1148
L70Q/A71D	1001	1075, 1149
A26E/E35D/M47L/L85Q	1002	1076, 1150
D46E/A71D	1003	1077, 1151
Y31H/E35D/T41S/V68L/K93R/R94W	1004	1078, 1152

TABLE 4: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	48	666, 761
Y33H, A112V, G117D	667	714, 762
V19A, Y33H, S64G, S80G, G98S, N106Y, A112V	668	715, 763
L32P, A112V	669	716, 764
A95V, A112I	670	717, 765
P28S, A112V	671	718, 766
P27A, T38N, V101A, A112V	672	719, 767
S118F	673	720, 768
R12W, H48Y, F54S, S118F	674	721, 769
R12W, Q79R, S118F	675	722, 770
T113S, S118Y	676	723, 771
S118Y	677	724, 772
N106I, S118Y	678	725, 773
N106I, S118F	679	726, 774
A95T, L96P, S118Y	680	727, 775
Y33H, P67S, N106Y, A112V	681	728, 776
N106Y, A112V	682	729, 777
T18S, Y33H, A112V	683	730, 778
P9S, Y33H, N47S, A112V	684	731, 779
P42S, P67H, A112V	685	732, 780

TABLE 4: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
P27L, L32P, P42S, A112V	686	733, 781
G98D, A112V	687	734, 782
Y33H, S35P, N106Y, A112V	688	735, 783
L32P, P42S, T100A, A112V	689	736, 784
P27S, P45S, N106I, A112V	690	737, 785
Y33H, N47K, A112V	691	738, 786
Y33H, N106Y, A112V	692	739, 787
K78R, D84G, A112V, F114S	693	740, 788
Y33H, N47K, F54L, A112V	694	741, 789
Y33H, A112V	695	742, 790
A95V, A112V	696	743, 791
R12W, A112V	697	744, 792
R12W, P27S, A112V	698	745, 793
Y33H, V51M, A112V	699	746, 794
Y33H, A112V, S118T	700	747, 795
Y33H, V101A, A112V, P115S	701	748, 796
H24R, T38N, D43G, A112V	702	749, 797
A112V	703	750, 798
P27A, A112V	704	751, 799
A112V, S118T	705	752, 800
R12W, A112V, M122I	706	753, 801
Q83K, N106Y, A112V	707	754, 802
R12W, P27S, A112V, S118T	708	755, 803
P28S, Y33H, A112V	709	756, 804
P27S, Q90R, A112V	710	757, 805
L15V, P27A, A112V, S118T	711	758, 806
Y33H, N106Y, T108I, A112V	712	759, 807
Y33H, P56L, V75M, V101M, A112V	713	760, 808
N47K, Q79R, S118F	809	850, 891
Q40R, P60T, A112V, S118T	810	851, 892
F114Y, S118F	811	852, 893
Y33H, K78R, S118Y	812	853, 894
R12W, A46T, K66M, Q79R, N106I, T113A, S118F	813	854, 895
Y33H, A112V, S118F	814	855, 896
R12W, Y33H, N106I, S118F	815	856, 897
L15V, Q90R, S118F	816	857, 898
N47K, D84G, N106I, S118Y	817	858, 899
L32P, S118F	818	859, 900
Y33H, Q79R, A112V, S118Y	819	860, 901
T18A, N106I, S118T	820	861, 902
L15V, Y33H, N106Y, A112V, S118F	821	862, 903

TABLE 4: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
V37M, S118F	822	863, 904
N47K, A112V, S118Y	823	864, 905
A46T, A112V	824	865, 906
P28S, Y33H, N106I, S118Y	825	866, 907
P30S, Y33H, N47K, V75M, Q79R, N106I, S118Y	826	867, 908
V19A, N47K, N106Y, K116E, S118Y	827	868, 909
Q79R, T85A, A112V, S118Y	828	869, 910
V101M, N106I, S118Y	829	870, 911
Y33H, Q79R, N106I, A112V, S118T	830	871, 912
Q79R, A112V	831	872, 913
Y33H, A46T, Q79R, N106I, S118F	832	873, 914
A112V, G121S	833	874, 915
Y33H, Q79R, N106I, S118Y	834	875, 916
Y33H, N106I, A112V	835	876, 917
Y33H, A46T, V101M, A112V, S118T	836	877, 918
L32P, L99M, N106I, S118F	837	878, 919
L32P, T108A, S118F	838	879, 920
R12W, Q79R, A112V	839	880, 921
Y33H, N106Y, E110G, A112V	840	881, 922
Y33H, N106I, S118Y	841	882, 923
Q79R, S118F	842	883, 924
Y33H, Q79R, G98D, V101M, A112V	843	884, 925
N47K, T81S, V101M, A112V, S118F	844	885, 926
G82S, S118Y	845	886, 927
Y33H, A112V, S118Y	846	887, 928
Y33H, N47K, Q79R, N106Y, A112V	847	888, 929
Y33H, S118T	848	889, 930
R12W, Y33H, Q79R, V101M, A112V	849	890, 931
Y33H, Q83K, A112V, S118T	1433	1457, 1481
V29M, Y33H, N106I, S118F	1434	1458, 1482
Y33H, A46T, A112V	1435	1459, 1483
Y33H, Q79R, S118F	1436	1460, 1484
Y33H, N47K, F74L, S118F	1437	1461, 1485
R12W, V101M, N106I, S118Y	1438	1462, 1486
A46T, V101A, N106I, S118Y	1439	1463, 1487
N106Y, A112V, S118T	1440	1464, 1488
S76P, T81I, V101M, N106Y, A112V, S118F	1441	1465, 1489
P9R, L21V, P22L, I34M, S69F, F74L, A87V, A112V, L125A	1442	1466, 1490
Y33H, V101M, A112V	1443	1467, 1491
V29A, L32P, S118F	1444	1468, 1492
Y33H, V101M, N106I, A112V	1445	1469, 1493

TABLE 4: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
R12W, Y33H, N47K, Q79R, S118Y	1446	1470, 1494
Y33H, A46T, A112V, S118T	1447	1471, 1495
Y33H, A112V, F114L, S118T	1448	1472, 1496
Y33H, T38A, A46T, V101M, A112V	1449	1473, 1497
P28S, Y33H, S69P, N106I, A112V, S118Y	1450	1474, 1498
Y33H, P42L, N47K, V101M, A112V	1451	1475, 1499
Y33H, N47K, F74S, Q83K, N106I, F111L, A112V, S118T	1452	1476, 1500
Y33H, A112V, S118T, V119A	1453	1477, 1501
Y33H, N106I, A112V, S118F	1454	1478, 1502
Y33H, K66M, S118F, W124L	1455	1479, 1503
N106I, A112V	1456	1480, 1504

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	47	310, 353
P18S, P64S, F91S	311	332, 354
P18S, F91S, L104P	312	333, 355
L44P	313	334, 356
A56V	314	335, 357
P18L, L79V, F91S	315	336, 358
P18S, F91S	316	337, 359
P18T, F91S	317	338, 360
P18T, S42P, F91S	318	339, 361
G7E, P18T, Y30C, F91S	319	340, 362
P18T, F91S, G111D	320	341, 363
P18S, F91P	321	342, 364
P18T, F91S, F108L	322	343, 365
P18T, T45A, F91S	323	344, 366
P18T, F91S, R94H	324	345, 367
P18S, Y30C, F91S	325	346, 368
A81V, L83P	326	347, 369
L88P	327	348, 370
R94H	328	349, 371
A13E, P18S, A56V, F91S	329	350, 372
P18T, F91S, V115A	330	351, 373
P18T, Q60K	331	352, 374
S52M	375	472, 569
T45Q, S52L, L104E, G111R	376	473, 570

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
S42G	377	474, 571
Q62F	378	475, 572
S52Q	379	476, 573
S42A, L104Q, G111R	380	477, 574
S42A, S52Q, L104Q, G111R	381	478, 575
S52W, L104E	382	479, 576
S42C	383	480, 577
S52W	384	481, 578
S52M, L104Q	385	482, 579
S42L, S52L, Q62F, L104Q	386	483, 580
S42W	387	484, 581
S42Q	388	485, 582
S52L	389	486, 583
S52R	390	487, 584
L104E	391	488, 585
G111R	392	489, 586
S52E	393	490, 587
Q62Y	394	491, 588
T45Q, S52M, L104E	395	492, 589
S42N, L104Q, G111R	396	493, 590
S52M, V57L	397	494, 591
S42N, S52Q, Q62F	398	495, 592
S42A, S52L, L104E, G111R	399	496, 593
S42W, S52Q, V57L, Q62Y	400	497, 594
L104Q	401	498, 595
S42L, S52Q, L104E	402	499, 596
S42C, S52L	403	500, 597
S42W, S52R, Q62Y, L104Q	404	501, 598
T45Q, S52R, L104E	405	502, 599
S52R, Q62F, L104Q, G111R	406	503, 600
T45Q, S52L, V57L, L104E	407	504, 601
S52M, Q62Y	408	505, 602
Q62F, L104E, G111R	409	506, 603
T45Q, S52Q	410	507, 604
S52L, L104E	411	508, 605
S42V, S52E	412	509, 606
T45Q, S52R, G111R	413	510, 607
S42G, S52Q, L104E, G111R	414	511, 608
S42N, S52E, V57L, L104E	415	512, 609
S42C, S52M, Q62F	416	513, 610
S42L	417	514, 611

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
S42A	418	515, 612
S42G, S52L, Q62F, L104Q	419	516, 613
S42N	420	517, 614
P18T, S65A, S67V, F91S	421	518, 615
P18F, T39A, T45Q, T61R, S65N, S67L, E73G, R78G	422	519, 616
P18T, T45Q, T61R, S65N, S67L	423	520, 617
P18F, S65A, S67V, F91S	424	521, 618
P18F, T45Q, T61R, S65N, S67L, F91S, L104P	425	522, 619
P18S, L79P, L104M	426	523, 620
P18S, L104M	427	524, 621
L79P, L104M	428	525, 622
P18T, T45Q, L79P	429	526, 623
P18T, T45Q, T61R, S65H, S67H	430	527, 624
P18T, A81E	431	528, 625
P18S, D23Y, E37P, S52G, Q62M, G80S, A81P, G99Y, S112N	432	529, 626
A13R, D23Y, E37P, S42P, Q62Y, A81E	433	530, 627
A13R, D23Y, E37P, G99Y, S112N	434	531, 628
A13R, D23Y, E37P, Q62M, A77V, G80S, A81P, G99Y	435	532, 629
P18L, E37S, Q62M, G80S, A81P, G99Y, S112N	436	533, 630
P18S, L104T	437	534, 631
P18S, Q62H, L79Q, F91S	438	535, 632
T45Q, S52K, Q62F, L104Q, G111R	439	536, 633
T45Q, S52Q, Q62Y, L104Q, G111R	440	537, 634
T45Q, S52Q, Q62Y, L104E, G111R	441	538, 635
V57A, T61M, S65W, S67A, E96D, L104T	442	539, 636
P18L, V57T, T61S, S65Y, S67A, L104T	443	540, 637
P18T, T45Q	444	541, 638
P18L, V57A, T61M, S65W, S67A, L104T	445	542, 639
T61M, S65W, S67A, L104T	446	543, 640
P18S, V41A, S42G, T45G, L104N	447	544, 641
P18H, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104N	448	545, 642
P18S, S42G, T45V, F58L, S67W, L104N	449	546, 643
P18S, T45I, L104N	450	547, 644
P18S, S42G, T45G, L104N, V106A	451	548, 645
P18H, H40R, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104Y, V106L, F108H	452	549, 646
E37V, S42G, T45G, L104N	453	550, 647
P18S, T45Q, L79P, L104T	454	551, 648
P18L, Q62R	455	552, 649
A13R, D23Y, E37P, S42L, S52G, Q62Y, A81E	456	553, 650

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
P18L, H49R, L104T, D116N	457	554, 651
A13R, D23Y, E37P, Q62M, G80S, A81P, L104T	458	555, 652
S65T, L104T	459	556, 653
A13R, D23Y, E37P, S52G, V57A, Q62M, K70E, L104T	460	557, 654
P18L, A47V, Q62Y, E73D, L104T	461	558, 655
H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, D97G, E98S, L104T, D116N	462	559, 656
P18L, S42P, T45Q, T61G, S65H, S67E, L104T, D116N	463	560, 657
P18S, H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, L104M, V106A	464	561, 658
H40T, V41M, A47V, S52Q, Q62L, S65T, E68G, E73R, D97G, E98S, L104T	465	562, 659
T45Q, S52E, L104E	466	563, 660
T45Q, S52E, Q62F, L104E	467	564, 661
P18F, T26M, L44V, Q62K, L79P, F91S, L104M, G111D	468	565, 662
P18S, T45S, T61K, S65W, S67A, F91S, G111R	469	566, 663
P18S, L79P, L104M, T107M	470	567, 664
P18S, S65W, S67A, M90V, V95A, L104Q, G111R	471	568, 665
P18S, A47G, L79P, F91S, L104M, T107A, R113W	1551	1505, 1528
P18T, D23G, S24A, N35D, H49L, L79P, F91S, L104M, G111R	1552	1506, 1529
V9L, P18S, Q60R, V75L, L79P, R89K, F91S, L104E, G111R	1553	1507, 1530
P18S, H49R, E73D, L79P, N85D, F91S, V95A, L104M, G111R	1554	1508, 1531
V11A, P18S, L79P, F91S, L104M, G111R	1555	1509, 1532
V11A, P18S, S54R, Q60P, Q62K, L79P, N85D, F91S, T107M	1556	1510, 1533
P18T, S52P, S65A, S67V, L79P, F91S, L104M, G111R	1557	1511, 1534
P18T, M36T, L79P, F91S, G111R	1558	1512, 1535
D8G, P18S, M36I, V38A, H49Q, A76E, F91S, L104M, T107A, R113W	1559	1513, 1536
P18S, S52P, S65A, S67V, L79P, F91S, L104M, T107S, R113W	1560	1514, 1537
T15I, P18T, L79P, F91S, L104M, G111R	1561	1515, 1538
P18F, T26M, L44V, Q62K, L79P, E82D, F91S, L104M, G111D	1562	1516, 1539
P18T, E37G, G53R, Q62K, L79P, F91S, E98D, L104M, T107M	1563	1517, 1540
P18L, K70E, L79P, F91S, V95A, G111R	1564	1518, 1541
V9I, Q12K, P18F, S65A, S67V, L79P, L104T, G111R, S112I	1565	1519, 1542
P18F, S65A, S67V, F91S, L104M, G111R	1566	1520, 1543
V9I, V10I, P18S, F20S, T45A, L79P, F91S, L104M, F108Y, G111R, S112V	1567	1521, 1544
V9L, P18L, L79P, M90I, F91S, T102S, L104M, G111R	1568	1522, 1545
P18C, T26M, L44V, M55I, Q62K, L79P, F91S, L104M, T107M	1569	1523, 1546
V9I, P18T, D23G, L79P, F91S, G111R	1570	1524, 1547
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1571	1525, 1548
P18T, M36T, S65A, S67E, L79Q, A81T, F91S, G111R	1572	1526, 1549
V9L, P18T, Q62R, L79P, F91S, L104M, G111R	1573	1527, 1550
P18S, S65W, S67A, L104Q, G111R	1574	1575, 1576
P18T, G19D, M36T, S54N, L79P, L83Q, F91S, T107M, F108Y	1577	1623, 1669

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
V9L, P18L, M55V, S69L, L79P, A81E, F91S, T107M	1578	1624, 1670
P18F, H40Q, T61K, Q62K, L79P, F91S, L104M, T107V	1579	1625, 1671
P18S, Q32R, Q62K, R78G, L79P, F91S, T107A, R113W	1580	1626, 1672
Q12H, P18T, L21S, G22S, V57A, Q62R, L79P, F91S, T107M	1581	1627, 1673
V9I, P18S, S24P, H49Q, F58Y, Q60R, Q62K, L79P, F91S, T107M	1582	1628, 1674
P18T, W46C, H49R, S65A, S67V, A76T, L79P, S87T, L104M	1583	1629, 1675
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1584	1630, 1676
V10F, T15S, P18L, R48Q, L79P, F91S, T107M, V115M	1585	1631, 1677
P18S, L21M, Y30F, N35D, R84W, F91S, T107M, D116G	1586	1632, 1678
P18F, E51V, S54G, Q60R, L79Q, E82G, S87T, M90I, F91S, G92R, T107M	1587	1633, 1679
Q16H, P18F, F91S, T107M	1588	1634, 1680
P18T, D23G, Q60R, S67L, L79P, F91S, T107M, V115A	1589	1635, 1681
D8G, V9I, V11A, P18T, T26M, S52P, L79P, F91S, G92A, T107L, V115A	1590	1636, 1682
V9I, P18F, A47E, G50S, E68G, L79P, F91S, T107M	1591	1637, 1683
P18S, M55I, Q62K, S69P, L79P, F91S, T107M	1592	1638, 1684
P18T, T39S, S52P, S54R, L79P, F91S, T107M	1593	1639, 1685
P18S, D23N, L79P, F91S, T107M, S114N	1594	1640, 1686
P18S, P34S, E51V, L79P, F91S, G111R	1595	1641, 1687
P18S, H59N, V75A, L79P, A81T, F91S, L104M, T107M	1596	1642, 1688
P18S, W46R, E68D, L79P, F91S, T107M, R113G	1597	1643, 1689
V9L, P18F, T45A, S65A, S67V, R78K, L79V, F91S, T107M, S114T	1598	1644, 1690
P18T, M55L, T61R, L79P, F91S, V106I, T107M	1599	1645, 1691
T15I, P18S, V33M, N35F, T39S, M55L, R78S, L79P, F91S, T107M	1600	1646, 1692
P18S, Q62K, K70E, L79P, F91S, G92E, R113W	1601	1647, 1693
P18F, F20I, T26M, A47V, E51K, L79P, F91S	1602	1648, 1694
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1603	1649, 1695
P18S, D23G, C29R, N35D, E37G, M55I, Q62K, S65A, S67G, R78G, L79P, F91S, L104M, T107M, Q110R	1604	1650, 1696
A13E, P18S, M36R, Q62K, S67T, L79P, N85D, F91S, T107M	1605	1651, 1697
V9I, P18T, H49R, L79P, N85D, F91S, L104T, T107M	1606	1652, 1698
V9A, P18F, T61S, Q62L, L79P, F91S, G111R	1607	1653, 1699
D8E, P18T, T61A, L79P, F91S, T107M	1608	1654, 1700
P18S, V41A, H49R, S54C, L79S, N85Y, L88P, F91S, L104M, T107M	1609	1655, 1701
V11E, P18H, F20Y, V25E, N35S, H49R, L79P, F91S, T107M, G111R	1610	1656, 1702
V11A, P18F, D23A, L79P, G80D, V95A, T107M	1611	1657, 1703
P18S, K70R, L79P, F91S, G111R	1612	1658, 1704
V9L, V11M, P18S, N35S, S54G, Q62K, L79P, L104M, T107M, V115M	1613	1659, 1705
V9L, P18Y, V25A, V38G, M55V, A77T, L79P, M90I, F91S, L104M	1614	1660, 1706
V10G, P18T, L72Q, L79P, F91S, T107M	1615	1661, 1707
P18S, H59R, A76G, R78S, L79P	1616	1662, 1708
V9A, P18S, M36T, S65G, L79P, F91S, L104T, G111R, S112I	1617	1663, 1709

TABLE 5: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
P18T, S52A, V57A, Q60R, Q62K, S65C, L79P, F91T, N100Y, T107M	1618	1664, 1710
V11A, P18F, N35D, A47E, Q62K, L79P, F91S, G99D, T107M, S114N	1619	1665, 1711
V11A, P18T, N35S, L79P, S87T, F91S	1620	1666, 1712
V9D, V11M, Q12L, P18S, E37V, M55I, Q60R, K70Q, L79P, F91S, L104M, T107M	1621	1667, 1713
T15S, P18S, Y30H, Q32L, Q62R, L79P, F91S, T107M	1622	1668, 1714

TABLE 6: Exemplary variant NKp30 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgC-like domain SEQ ID NO**
Wild-type	54	1183
L30V/A60V/S64P/S86G	1178	1184
L30V	1179	1185
A60V	1180	1186
S64P	1181	1187
S86G	1182	1188

TABLE 7: Exemplary variant CD86 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	29	1195
Q35H/H90L/Q102H	1191	1196
Q35H	1192	1197
H90L	1193	1198
Q102H	1194	1199

TABLE 8: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	31	1203, 1263
H15Q	1204	1281, 1357
N24D	1205	1282, 1358
E44D	1206	1283, 1359
V89D	1207	1284, 1360
Q82R/V89D	1208	1285, 1361

TABLE 8: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
E59G/Q82R	1209	1286, 1362
S39I/V89D	1210	1287, 1363
S67L/V89D	1211	1288, 1364
S67L/I85F	1212	1289, 1365
S67L/I86T	1213	1290, 1366
H15Q/K65R	1214	1291, 1367
H15Q/Q72H/V89D	1215	1292, 1368
H15Q/S67L/R76G	1216	1293, 1369
H15Q/R76G/I85F	1217	1294, 1370
H15Q/T47A/Q82R	1218	1295, 1371
H15Q/Q82R/V89D	1219	1296, 1372
H15Q/C23S/I86T	1220	1297, 1373
H15Q/S39I/I86T	1221	1298, 1374
H15Q/R76G/I85F	1222	1299, 1375
E44D/V89D/W91R	1223	1300, 1376
I13V/S67L/V89D	1224	1301, 1377
H15Q/S67L/I86T	1225	1302, 1378
I13V/H15Q/S67L/I86T	1226	1303, 1379
I13V/H15Q/E44D/V89D	1227	1304, 1380
I13V/S39I/E44D/Q82R/V89D	1228	1305, 1381
I13V/E44D/Q82R/V89D	1229	1306, 1382
I13V/Q72H/R76G/I86T	1230	1307, 1383
I13V/H15Q/R76G/I85F	1231	1308, 1384
H15Q/S39I/R76G/V89D	1232	1309, 1385
H15Q/S67L/R76G/I85F	1233	1310, 1386
H15Q/T47A/Q72H/R76G/I86T	1234	1311, 1387
H15Q/T47A/Q72H/R76G	1235	1312, 1388
I13V/H15Q/T47A/Q72H/R76G	1236	1313, 1389
H15Q/E44D/R76G/I85F	1237	1314, 1390
H15Q/S39I/S67L/V89D	1238	1315, 1391
H15Q/N32D/S67L/V89D	1239	1316, 1392
N32D/S67L/V89D	1240	1317, 1393
H15Q/S67L/Q72H/R76G/V89D	1241	1318, 1394
H15Q/Q72H/Q74R/R76G/I86T	1242	1319, 1395
G28V/Q72H/R76G/I86T	1243	1320, 1396
I13V/H15Q/S39I/E44D/S67L	1244	1321, 1397
E44D/S67L/Q72H/Q82R/V89D	1245	1322, 1398
H15Q/V89D	1246	1323, 1399
H15Q/T47A	1247	1324, 1400
I13V/H15Q/Q82R	1248	1325, 1401
I13V/H15Q/V89D	1249	1326, 1402
I13V/S67L/Q82R/V89D	1250	1327, 1403

TABLE 8: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
I13V/H15Q/Q82R/V89D	1251	1328, 1404
H15Q/V31M/S67L/Q82R/V89D	1252	1329, 1405
I13V/H15Q/T47A/Q82R	1253	1330, 1406
I13V/H15Q/V31A/N45S/Q82R/V89D	1254	1331, 1407
H15Q/T47A/H69L/Q82R/V89D	1256	1333, 1409
I13V/H15Q/T47A/H69L/R76G/V89D	1257	1334, 1410
I12V/I13V/H15Q/T47A/Q82R/V89D	1258	1335, 1411
I13V/H15Q/R76G/D77N/Q82R/V89D	1259	1336, 1412
I13V/H15Q/T47A/R76G/V89D	1260	1337, 1413
I13V/H15Q/T47A/Q82R/V89D	1261	1338, 1414
I13V/H15Q/N24D/Q82R/V89D	1262	1339, 1415
I13V/H15Q/I36V/T47A/S67L/V89D	1264	1340, 1416
H15Q/T47A/K65R/S67L/Q82R/V89D	1265	1341, 1417
H15Q/L33P/T47A/S67L/P71S/V89D	1266	1342, 1418
I13V/H15Q/Q72H/R76G/I86T	1267	1343, 1419
H15Q/T47A/S67L/Q82R/V89D	1268	1344, 1420
F2L/H15Q/D46E/T47A/Q72H/R76G/Q82R/V89D	1269	1345, 1421
I13V/H15Q/L33F/T47A/Q82R/V89D	1270	1346, 1422
I13V/H15Q/T47A/E58G/S67L/Q82R/V89D	1271	1347, 1423
H15Q/N24S/T47A/Q72H/R76G/V89D	1272	1348, 1424
I13V/H15Q/E44V/T47A/Q82R/V89D	1273	1349, 1425
H15Q/N18D/T47A/Q72H/V73A/R76G/I86T/V89D	1274	1350, 1426
I13V/H15Q/T37A/E44D/S48C/S67L/Q82R/V89D	1275	1351, 1427
H15Q/L33H/S67L/R76G/Q82R/V89D	1276	1352, 1428
I13V/H15Q/T47A/Q72H/R76G/I86T	1277	1353, 1429
H15Q/S39I/E44D/Q72H/V75G/R76G/Q82R/V89D	1278	1354, 1430
H15Q/T47A/S67L/R76G/Q82R/V89D	1279	1355, 1431
I13V/H15Q/T47A/S67L/Q72H/R76G/Q82R/V89D	1280	1356, 1432

[0254] The number of such non-affinity modified or affinity modified IgSF domains present in a "stacked" immunomodulatory protein construct (whether non-wild type combinations or non-wild type arrangements) is at least 2, 3, 4, or 5 and in some embodiments exactly 2, 3, 4, or 5 IgSF domains (whereby determination of the number of affinity modified IgSF domains disregards any non-specific binding fractional sequences thereof and/or substantially immunologically inactive fractional sequences thereof).

[0255] In some embodiments of a stacked immunomodulatory protein provided herein, the number of IgSF domains is at least 2 wherein the number of affinity modified and the number of non-affinity modified IgSF domains is each independently at least: 0, 1, 2, 3, 4, 5, or 6. Thus, the

number of affinity modified IgSF domains and the number of non-affinity modified IgSF domains, respectively, (affinity modified IgSF domain: non-affinity modified IgSF domain), can be exactly or at least: 2:0 (affinity modified: wild-type), 0:2, 2:1, 1:2, 2:2, 2:3, 3:2, 2:4, 4:2, 1:1, 1:3, 3:1, 1:4, 4:1, 1:5, or 5:1.

[0256] In some embodiments of a stacked immunomodulatory protein, at least two of the non-affinity modified and/or affinity modified IgSF domains are identical IgSF domains.

[0257] In some embodiments, a stacked immunomodulatory protein provided herein comprises at least two affinity modified and/or non-affinity modified IgSF domains from a single IgSF member but in a non-wild-type arrangement (alternatively, "permutation"). One illustrative example of a non-wild type arrangement or permutation is an immunomodulatory protein comprising a non-wild-type order of affinity modified and/or non-affinity modified IgSF domain sequences relative to those found in the wild-type PD-L1 whose IgSF domain sequences served as the source of the variant IgSF domains as provided herein. Thus, in one example, the immunomodulatory protein can comprise an IgV proximal and an IgC distal to the transmembrane domain albeit in a non-affinity modified and/or affinity modified form. The presence, in an immunomodulatory protein provided herein, of both non-wild-type combinations and non-wild-type arrangements of non-affinity modified and/or affinity modified IgSF domain is also within the scope of the provided subject matter.

[0258] In some embodiments of a stacked immunomodulatory protein, the non-affinity modified and/or affinity modified IgSF domains are non-identical (i.e., different) IgSF domains. Non-identical affinity modified IgSF domains specifically bind, under specific binding conditions, different cognate binding partners and are "non-identical" irrespective of whether or not the wild-type or unmodified IgSF domains from which they are engineered was the same. Thus, for example, a non-wild-type combination of at least two non-identical IgSF domains in an immunomodulatory protein can comprise at least one IgSF domain sequence whose origin is from and unique to one PD-L1, and at least one of a second IgSF domain sequence whose origin is from and unique to another IgSF family member that is not PD-L1, wherein the IgSF domains of the immunomodulatory protein are in non-affinity modified and/or affinity modified form. However, in alternative embodiments, the two non-identical IgSF domains originate from the same IgSF domain sequence but at least one is affinity modified such that they specifically bind to different cognate binding partners.

[0259] A plurality of non-affinity modified and/or affinity modified IgSF domains in a stacked immunomodulatory protein polypeptide chain need not be covalently linked directly to one another. In some embodiments, an intervening span of one or more amino acid residues indirectly covalently bonds the non-affinity modified and/or affinity modified IgSF domains to each other. The linkage can be via the N-terminal to C-terminal residues.

[0260] In some embodiments, the two or more IgSF domain, including a vIgD of PD-L1 and one or more additional IgSF domain (e.g. second or third variant IgSF domain) from another IgSF family member, are covalently or non-covalently linked. In some embodiments, the two or more IgSF domains are linked directly or indirectly, such as via a linker. In some embodiments, an intervening span of one or more amino acid residues indirectly covalently bonds IgSF domains to each other. The linkage can be via the N-terminal to C-terminal residues. In some embodiments, the linkage can be made via side chains of amino acid residues that are not located at the N-terminus or C-terminus of the IgSF domain(s). Thus, linkages can be made via terminal or internal amino acid residues or combinations thereof.

[0261] In some embodiments, the immunomodulatory protein contains at least two IgSF domains, each linked directly or indirectly via a linker. In some embodiments, the immunomodulatory protein contains at least three immunomodulatory proteins, each linked directly or indirectly via a linker. Various configurations are shown in FIG. 5A and 5B.

[0262] In some embodiments, one or more "peptide linkers" link the vIgD of PD-L1 and an one or more additional IgSF domain (e.g. second or third variant IgSF domain). In some embodiments, a peptide linker can be a single amino acid residue or greater in length. In some embodiments, the peptide linker has at least one amino acid residue but is no more than 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid residues in length. In some embodiments, the linker is a flexible linker. In some embodiments, the linker is (in one-letter amino acid code): GGGGS ("4GS"; SEQ ID NO: 1942) or multimers of the 4GS linker, such as repeats of 2, 3, 4, or 5 4GS linkers. In some embodiments, the peptide linker is $(GGGGS)_2$ (SEQ ID NO: 240) or $(GGGGS)_3$ (SEQ ID NO: 239). In some embodiments, the linker (in one-letter amino acid code) is GSGGGGS (SEQ ID NO:1941). In some embodiments, the linker also can include a series of alanine residues alone or in addition to another peptide linker (such as a 4GS linker or multimer thereof). In some embodiments, the number of alanine residues in each series is: 2, 3, 4, 5, or 6 alanines. In some embodiments, the linker also can include a series of alanine residues alone or in addition to another peptide linker (such as a 4GS linker or multimer thereof).

In some embodiments, the number of alanine residues in each series is: 2, 3, 4, 5, or 6 alanines. In some embodiments, the linker is a rigid linker. For example, the linker is an α-helical linker. In some embodiments, the linker is (in one-letter amino acid code): EAAAK or multimers of the EAAAK linker, such as repeats of 2, 3, 4, or 5 EAAAK linkers, such as set forth in SEQ ID NO: 2022 (1xEAAAK), SEQ ID NO: 2023 (3xEAAAK) or SEQ ID NO: 2024 (5xEAAAK). In some embodiments, the linker can further include amino acids introduced by cloning and/or from a restriction site, for example the linker can include the amino acids GS (in one-letter amino acid code) as introduced by use of the restriction site BAMHI. For example, in some embodiments, the linker (in one-letter amino acid code) is GSGGGGS (SEQ ID NO:1941), $GS(G_4S)_3$ (SEQ ID NO: 2031), or $GS(G_4S)_5$ (SEQ ID NO: 2032). In some examples, the linker is a 2xGGGGS followed by three alanines (GGGGSGGGGSAAA; SEQ ID NO: 241). In some cases, various combinations of peptide is used linkers.

[0263] In some embodiments, the non-affinity modified and/or affinity modified IgSF domains are linked by "wild-type peptide linkers" inserted at the N-terminus and/or C-terminus of a non-affinity modified and/or affinity modified IgSF domains. These linkers are also called leading sequences (N-terminal to non-affinity modified or affinity modified IgSF domain) or trailing sequences (C-terminal to non-affinity modified or affinity modified IgSF domain), and sequences that exist in the wild-type protein that span immediately outside the structural prediction of the Ig fold of the IgSF. In some embodiments, the "wild-type linker" is an amino acid sequence that exists after the signal sequence, but before in the IgSF domain, such as the defined IgV domain, in the amino acid sequence of the wild-type protein. In some embodiments, the "wild-type" linker is an amino acid sequence that exists immediately after the IgSF domain, such as immediately after the defined IgV domain but before the IgC domain, in the amino acid sequence of the wild-type protein. These linker sequences can contribute to the proper folding and function of the neighboring IgSF domain(s). In some embodiments, there is present a leading peptide linker inserted at the N-terminus of the first IgSF domain and/or a trailing sequence inserted at the C-terminus of the first non-affinity modified and/or affinity modified IgSF domain. In some embodiments, there is present a second leading peptide linker inserted at the N-terminus of the second IgSF domain and/or a second trailing sequence inserted at the C-terminus of the second non-affinity modified and/or affinity modified IgSF domain. When the first and second non-affinity modified and/or affinity modified IgSF domains are derived from the same parental protein and are connected in the same orientation, wild-type peptide linkers between the

first and second non-affinity modified and/or affinity modified IgSF domains are not duplicated. For example, when the first trailing wild-type peptide linker and the second leading wild-type peptide linker are the same, the Type II immunomodulatory protein does not comprise either the first trailing wild-type peptide linker or the second leading wild-type peptide linker.

[0264] In some embodiments, the Type II immunomodulatory protein comprises a first leading wild-type peptide linker inserted at the N-terminus of the first non-affinity modified and/or affinity modified IgSF domain, wherein the first leading wild-type peptide linker comprises at least 5 (such as at least about any of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more) consecutive amino acids from the intervening sequence in the wild-type protein from which the first non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately preceding domain (such as a signal peptide or an IgSF domain). In some embodiments, the first leading wild-type peptide linker comprises the entire intervening sequence in the wild-type protein from which the first non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately preceding domain (such as a signal peptide or an IgSF domain).

[0265] In some embodiments, the Type II immunomodulatory protein further comprises a first trailing wild-type peptide linker inserted at the C-terminus of the first non-affinity modified and/or affinity modified IgSF domain, wherein the first trailing wild-type peptide linker comprises at least 5 (such as at least about any of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more) consecutive amino acids from the intervening sequence in the wild-type protein from which the first non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately following domain (such as an IgSF domain or a transmembrane domain). In some embodiments, the first trailing wild-type peptide linker comprises the entire intervening sequence in the wild-type protein from which the first non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately following domain (such as an IgSF domain or a transmembrane domain).

[0266] In some embodiments, the Type II immunomodulatory protein further comprises a second leading wild-type peptide linker inserted at the N-terminus of the second non-affinity modified and/or affinity modified IgSF domain, wherein the second leading wild-type peptide linker comprises at least 5 (such as at least about any of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more) consecutive amino acids from the intervening sequence in the wild-type protein from which the

second non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately preceding domain (such as a signal peptide or an IgSF domain). In some embodiments, the second leading wild-type peptide linker comprises the entire intervening sequence in the wild-type protein from which the second non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately preceding domain (such as a signal peptide or an IgSF domain).

[0267] In some embodiments, the Type II immunomodulatory protein further comprises a second trailing wild-type peptide linker inserted at the C-terminus of the second non-affinity modified and/or affinity modified IgSF domain, wherein the second trailing wild-type peptide linker comprises at least 5 (such as at least about any of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more) consecutive amino acids from the intervening sequence in the wild-type protein from which the second non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately following domain (such as an IgSF domain or a transmembrane domain). In some embodiments, the second trailing wild-type peptide linker comprises the entire intervening sequence in the wild-type protein from which the second non-affinity modified and/or affinity modified IgSF domain is derived between the parental IgSF domain and the immediately following domain (such as an IgSF domain or a transmembrane domain).

[0268] In some embodiments, the two or more IgSF domain, including a vIgD of PD-L1 and one or more additional IgSF domain (e.g. second and/or third variant IgSF domain) from another IgSF family member, are linked or attached to a multimerization domain, such as to an Fc to form an Fc fusion, which, upon expression in a cell can, in some aspects, produce a dimeric multi-domain stack immunomodulatory protein. Thus, also provided are dimeric multi-domain immunomodulatory proteins.

[0269] In some embodiments, the variant PD-L1 polypeptide and one or more additional IgSF domain are independently linked, directly or indirectly, to the N- or C-terminus of a multimerization domain, such as an Fc region. In some embodiments, the variant PD-L1 polypeptide and at least one of the one or more additional IgSF domain are linked, directly or indirectly, and one of the variant PD-L1 and one of the one or more additional IgSF domain is also linked, directly or indirectly, to the N- or C-terminus of a multimerization domain, such as an Fc region. In some embodiments, the N- or C-terminus of a multimerization domain, such as an Fc region is linked to the variant PD-L1 polypeptide or the one or more additional IgSF

domain and the other of the N- or C-terminus of the Fc region is linked to the other of the PD-L1 variant or another of the one or more additional IgSF domain. In some embodiments, linkage to the multimerization domain, such as to an Fc is via a peptide linker, e.g. a peptide linker, such as described above. In some embodiments, linkage between the variant PD-L1 and the one or more additional IgSF domain is via a peptide linker, e.g. a peptide linker, such as described above. In some embodiments, the vIgD of PD-L1, the one or more additional IgSF domains, and the multimerization domain, such as an Fc domain can be linked together in any of numerous configurations as depicted in FIG. 5A and 5B. Exemplary configurations are described in the Examples.

[0270] In some embodiments, the stacked immunomodulatory protein is a dimer formed by two immunomodulatory Fc fusion polypeptides. Also provided are nucleic acid molecules encoding any of the stacked immunomodulatory proteins. In some embodiments, the dimeric multi-domain stack immunomodulatory protein can be produced in cells by expression, or in some cases co-expression, of stack immunomodulatory Fc fusion polypeptides, such as described above in accord with generating dimeric Fc fusion proteins.

[0271] In some embodiments, the dimeric multi-domain stack immunomodulatory protein is divalent for each Fc region, monovalent for each subunit, or divalent for one subunit and tetravalent for the other.

[0272] In some embodiments, the dimeric multi-domain stack immunomodulatory protein is a homodimeric multi-domain stack Fc protein. In some embodiments, the dimeric multi-domain stack immunomodulatory protein comprises a first stack immunomodulatory Fc fusion polypeptide and a second stack immunomodulatory Fc fusion polypeptide in which the first and second polypeptide are the same. In some embodiments, the multi-domain stack molecule contains a first Fc fusion polypeptide containing a variant PD-L1 and a second IgSF domain and a second Fc fusion polypeptide containing the variant PD-L1 and the second IgSF domain. In some embodiments, the multi-domain stack molecule contains a first Fc fusion polypeptide containing a variant PD-L1, a second IgSF domain, and a third IgSF domain and a second Fc fusion polypeptide containing the variant PD-L1, the second IgSF domain, and the third IgSF domain. In some embodiments, the Fc portion of the first and/or second fusion polypeptide can be any Fc as described above. In some embodiments, the Fc portion or region of the first and second fusion polypeptide is the same.

[0273] In some embodiments, the multi-domain stack molecule is heterodimeric, comprising two different Fc fusion polypeptides, e.g. a first and a second Fc fusion polypeptide, wherein at least one is an Fc fusion polypeptide containing at least one is an Fc fusion polypeptide containing a variant PD-L1 polypeptide and/or at least one second IgSF domain (e.g. second variant IgSF domain). In some embodiments, the first or second Fc fusion polypeptide further contains a third IgSF domain (e.g. third variant IgSF domain).

[0274] In some embodiments, the multi-domain stack molecule contains a first Fc fusion polypeptide containing a variant PD-L1and a second Fc fusion polypeptide containing at a second IgSF domain, in which, in some cases, the first or second Fc fusion polypeptide additionally contains a third IgSF domain. In some embodiments, the multi-domain stack molecule contains a first Fc fusion polypeptide containing a variant PD-L1, a second IgSF domain, and in some cases, a third IgSF domain and a second Fc fusion polypeptide that is not linked to either a variant PD-L1 polypeptide or an additional IgSF domain. In some embodiments, the Fc portion or region of the first and second fusion polypeptide is the same. In some embodiments, the Fc portion or region of the first and second fusion polypeptide is different.

[0275] In some embodiments, the multi-domain stack molecule contains a first Fc fusion polypeptide containing 1, 2, 3, 4 or more variant PD-L1 polypeptides and 1, 2, 3, 4 or more additional IgSF domains, wherein the total number of IgSF domains in the first stack Fc fusion polypeptide is greater than 2, 3, 4, 5, 6 or more. In one example of such an embodiment, the second stack Fc fusion polypeptide contains 1, 2, 3, 4 or more variant PD-L1 polypeptides and 1, 2, 3, 4 or more additional IgSF domains, wherein the total number of IgSF domains in the second stack Fc fusion polypeptide is greater than 2, 3, 4, 5, 6 or more. In another example of such an embodiment, the second Fc fusion polypeptide is not linked to either a variant PD-L1 polypeptide or additional IgSF domain.

[0276] In some embodiments, the heterodimeric stack molecule contains a first stack immunomodulatory Fc fusion polypeptide and a second stack immunomodulatory Fc fusion polypeptide in which the first and second polypeptide are different. In some embodiments, a heterodimeric stack molecule contains a first Fc polypeptide fusion containing an Fc region and a a first variant PD-L1 polypeptide and/or second IgSF domain (e.g. second variant IgSF domain) and a second polypeptide fusion containing an Fc region and the other of the first variant PD-L1 polypeptide or the second IgSF domain. In some embodiments, a heterodimeric stack molecule

contains a first Fc polypeptide fusion containing an Fc region and a first variant PD-L1 polypeptide and/or second IgSF domain (e.g. second variant IgSF domain) and a second Fc polypeptide fusion containing an Fc region and the first variant PD-L1 polypeptide and second IgSF domain (e.g. second variant IgSF domain) but in a different orientation or configuration from the first Fc region. In some embodiments, the first and/or second Fc fusion polypeptide also contains a third IgSF domain (e.g. third variant IgSF domain).

[0277] In some embodiments, the Fc domain of one or both of the first and second stacked immunomodulatory Fc fusion polypeptide comprises a modification (e.g. substitution) such that the interface of the Fc molecule is modified to facilitate and/or promote heterodimerization. In some embodiments, modifications include introduction of a protuberance (knob) into a first Fc polypeptide and a cavity (hole) into a second Fc polypeptide such that the protuberance is positionable in the cavity to promote complexing of the first and second Fc-containing polypeptides. Amino acids targeted for replacement and/or modification to create protuberances or cavities in a polypeptide are typically interface amino acids that interact or contact with one or more amino acids in the interface of a second polypeptide.

[0278] In some embodiments, a sequence of amino acids is added preceding the Fc sequence for constructs in which the Fc sequence was the N-terminal portion of the sequence. In some cases, the sequence of amino acids HMSSVSAQ (SEQ ID NO:1156) is added immediately preceding the Fc sequence for constructs in which the Fc sequence was the N-terminal portion of the sequence. In some embodiments, a heterodimeric stack molecule contains a first Fc polypeptide fusion containing an Fc region (knob) and a first variant polypeptide and/or second IgSF domain (e.g. second variant IgSF domain) and a second Fc polypeptide fusion containing an Fc region (hole) contains a stuffer sequence HMSSVSAQ (SEQ ID NO:1156) immediately preceding both Fc regions of the first and second Fc polypeptide fusion.

[0279] In some embodiments, a first polypeptide that is modified to contain protuberance (hole) amino acids include replacement of a native or original amino acid with an amino acid that has at least one side chain which projects from the interface of the first polypeptide and is therefore positionable in a compensatory cavity (hole) in an adjacent interface of a second polypeptide. Most often, the replacement amino acid is one which has a larger side chain volume than the original amino acid residue. One of skill in the art knows how to determine and/or assess the properties of amino acid residues to identify those that are ideal replacement amino acids to create a protuberance. In some embodiments, the replacement residues for the formation of a

protuberance are naturally occurring amino acid residues and include, for example, arginine (R), phenylalanine (F), tyrosine (Y), or tryptophan (W). In some examples, the original residue identified for replacement is an amino acid residue that has a small side chain such as, for example, alanine, asparagine, aspartic acid, glycine, serine, threonine, or valine.

[0280] In some embodiments, a second polypeptide that is modified to contain a cavity (hole) is one that includes replacement of a native or original amino acid with an amino acid that has at least one side chain that is recessed from the interface of the second polypeptide and thus is able to accommodate a corresponding protuberance from the interface of a first polypeptide. Most often, the replacement amino acid is one which has a smaller side chain volume than the original amino acid residue. One of skill in the art knows how to determine and/or assess the properties of amino acid residues to identify those that are ideal replacement residues for the formation of a cavity. Generally, the replacement residues for the formation of a cavity are naturally occurring amino acids and include, for example, alanine (A), serine (S), threonine (T) and valine (V). In some examples, the original amino acid identified for replacement is an amino acid that has a large side chain such as, for example, tyrosine, arginine, phenylalanine, or tryptophan.

[0281] The CH3 interface of human IgG1, for example, involves sixteen residues on each domain located on four anti-parallel β-strands which buries 1090 Å2 from each surface (see e.g., Deisenhofer et al. (1981) Biochemistry, 20:2361-2370; Miller et al., (1990) J Mol. Biol., 216, 965-973; Ridgway et al., (1996) Prot. Engin., 9: 617-621; U.S. Pat. No. 5,731,168). Modifications of a CH3 domain to create protuberances or cavities are described, for example, in U.S. Pat. No. 5,731,168; International Patent Applications WO98/50431 and WO 2005/063816; and Ridgway et al., (1996) Prot. Engin., 9: 617-621. In some examples, modifications of a CH3 domain to create protuberances or cavities are typically targeted to residues located on the two central anti-parallel β-strands. The aim is to minimize the risk that the protuberances which are created can be accommodated by protruding into the surrounding solvent rather than being accommodated by a compensatory cavity in the partner CH3 domain.

[0282] In some embodiments, the heterodimeric molecule contains a T366W mutation in the CH3 domain of the "knobs chain" and T366S, L368A, Y407V mutations in the CH3 domain of the "hole chain". In some cases, an additional interchain disulfide bridge between the CH3 domains can also be used (Merchant, A. M., et al., Nature Biotech. 16 (1998) 677-681) e.g. by introducing a Y349C mutation into the CH3 domain of the "knobs" or "hole" chain and a E356C

mutation or a S354C mutation into the CH3 domain of the other chain. In some embodiments, the heterodimeric molecule contains S354C, T366W mutations in one of the two CH3 domains and Y349C, T366S, L368A, Y407V mutations in the other of the two CH3 domains. In some embodiments, the heterodimeric molecule comprises E356C, T366W mutations in one of the two CH3 domains and Y349C, T366S, L368A, Y407V mutations in the other of the two CH3 domains. In some embodiments, the heterodimeric molecule comprises Y349C, T366W mutations in one of the two CH3 domains and E356C, T366S, L368A, Y407V mutations in the other of the two CH3 domains. In some embodiments, the heterodimeric molecule comprises Y349C, T366W mutations in one of the two CH3 domains and S354C, T366S, L368A, Y407V mutations in the other of the two CH3 domains. Examples of other knobs-in-holes technologies are known in the art, e.g. as described by EP 1 870 459 A1.

[0283] In some embodiments, the Fc region of the heterodimeric molecule additionally can contain one or more other Fc mutation, such as any described above. In some embodiments, the heterodimer molecule contains an Fc region with a mutation that reduces effector function.

[0284] In some embodiments, an Fc variant containing CH3 protuberance(knob) or cavity(hole) modifications can be joined to a stacked immunomodulatory polypeptide anywhere, but typically via its N- or C-terminus, to the N- or C-terminus of a first and/or second stacked immunomodulatory polypeptide, such as to form a fusion polypeptide. The linkage can be direct or indirect via a linker. Typically, a knob and hole molecule is generated by co-expression of a first stacked immunomodulatory polypeptide linked to an Fc variant containing CH3 protuberance modification(s) with a second stacked immunomodulatory polypeptide linked to an Fc variant containing CH3 cavity modification(s).

[0285] There is provided herein a homodimeric multi-domain stack molecule produced from a stack immunomodulatory Fc fusion polypeptide containing an IgSF domain, e.g. IgV domain, of a variant PD-L1 polypeptide and a second IgSF domain, e.g. IgV, of a variant CD155 polypeptide. In some embodiments, the first and second immunomodulatory Fc fusion polypeptide of the multi-domain stack molecule has the sequence set forth in any of SEQ ID NOS: 1716, 1717, 1718, 1719, 1720 or 1721 or a sequence of amino acids that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to any of SEQ ID NOS: 1716, 1717, 1718, 1719, 1720 or 1721 and contains the one more amino acid modifications in the variant PD-L1 and/or CD155 IgSF domain. In some embodiments, the resulting multi-domain stack molecules bind to both TIGIT and PD-1. In some

aspects, the binding to TIGIT is to the same or similar degree or, in some cases, is increased, compared to the binding to TIGIT of the corresponding IgSF domain of unmodified or wild-type PD-L1 or CD155. In some aspects, the binding to PD-1 is to the same or similar degree, or, in some cases, is increased, compared to the binding to PD-1 of the corresponding IgSF domain of unmodified or wild-type PD-L1. In some embodiments, the binding to TIGIT or PD-1 is at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or more of the binding to TIGIT or PD-1 of the non-stacked form of the variant PD-L1 IgSF-Fc. In some embodiments, the binding to TIGIT is at least 30%, 40%, 50%, 60%, 70%, 80%, 90% or more of the binding to TIGIT of the non-stacked form of the variant CD155 IgSF-Fc. In some embodiments, the resulting multi-domain stack molecule increases T cell immune responses compared to the non-stack variant PD-L1 IgSF-Fc and/or variant CD155-IgSF-Fc, such as determined in a reporter assay. In some embodiments, the increase is greater than 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 2.0-fold, 3.0-fold, 4.0-fold, 5.0-fold or more.

[0286] There is provided herein a homodimeric multi-domain stack molecule produced from a stack immunomodulatory Fc fusion polypeptide containing an IgSF domain, e.g. IgV domain, of a variant PD-L1 polypeptide, a second IgSF domain, e.g. IgV, of a variant CD155 polypeptide and a third IgSF domain, e.g. IgV, of a variant CD112 polypeptide. In some embodiments, the first and second immunomodulatory Fc fusion polypeptide of the multi-domain stack molecule has the sequence set forth in any of SEQ ID NOS: 1722, 1723 and 1724 or a sequence of amino acids that has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to any of SEQ ID NOS: 1722, 1723 and 1724 and contains the one more amino acid modifications in the variant CD112, CD155 and/or PD-L1 IgSF domain. In some embodiments, the resulting multi-domain stack molecules bind to both TIGIT, CD112R and PD-1. In some aspects, the binding to TIGIT is to the same or similar degree or, in some cases, is increased, compared to the binding to TIGIT of the corresponding IgSF domain of unmodified or wild-type CD112 or CD155. In some aspects, the binding to CD112R is to the same or similar degree, or, in some cases, is increased, compared to the binding to CD112R of the corresponding IgSF domain of unmodified or wild-type CD112. In some aspects, the binding to PD-1 is to the same or similar degree, or, in some cases, is increased, compared to the binding to PD-1 of the corresponding IgSF domain of unmodified or wild-type PD-L1. In some embodiments, the binding to TIGIT or CD112R is at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or more of the binding to TIGIT or CD112R of the non-stacked form of the variant CD112

IgSF-Fc. In some embodiments, the binding to TIGIT is at least 30%, 40%, 50%, 60%, 70%, 80%, 90% or more of the binding to TIGIT of the non-stacked form of the variant CD155 IgSF-Fc. In some embodiments, the binding to PD-1 is at least 30%, 40%, 50%, 60%, 70%, 80%, 90% or more of the binding to PD-1 of the non-stacked form of the variant PD-1 IgSF-Fc. In some embodiments, the resulting multi-domain stack molecule increases T cell immune responses compared to the non-stack variant CD112 IgSF-Fc, variant CD155-IgSF-Fc and/or variant PD-L1-IgSF-Fc, such as determined in a reporter assay. In some embodiments, the increase is greater than 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 2.0-fold, 3.0-fold, 4.0-fold, 5.0-fold or more.

C. Conjugates and Fusions of Variant Polypeptides and Immunomodulatory Proteins

[0287] In some embodiments, the variant polypeptides provided herein, which are immunomodulatory proteins comprising variants of an Ig domain of the IgSF family (vIgD), can be conjugated with or fused with a moiety, such as an effector moiety, such as another protein, directly or indirectly, to form a conjugate ("IgSF conjugate"). In some embodiments, the attachment can be covalent or non-covalent, e.g., via a biotin-streptavidin non-covalent interaction. In some embodiments, the moiety can be a targeting moiety, a small molecule drug (non-polypeptide drug of less than 500 daltons molar mass), a toxin, a cytostatic agent, a cytotoxic agent, an immunosuppressive agent, a radioactive agent suitable for diagnostic purposes, a radioactive metal ion for therapeutic purposes, a prodrug-activating enzyme, an agent that increases biological half-life, or a diagnostic or detectable agent.

[0288] In some embodiments the effector moiety is a therapeutic agent, such as a cancer therapeutic agent, which is either cytotoxic, cytostatic or otherwise provides some therapeutic benefit. In some embodiments, the effector moiety is a targeting moiety or agent, such as an agent that targets a cell surface antigen, e.g., an antigen on the surface of a tumor cell. In some embodiments, the effector moiety is a label, which can generate a detectable signal, either directly or indirectly. In some embodiments, the effector moiety is a toxin. In some embodiments, the effector moiety is a protein, peptide, nucleic acid, small molecule or nanoparticle.

[0289] In some embodiments, 1, 2, 3, 4, 5 or more effector moieties, which can be the same or different, are conjugated, linked or fused to the variant polypeptide or protein to form an IgSF conjugate. In some embodiments, such effector moieties can be attached to the variant polypeptide or immunomodulatory protein using various molecular biological or chemical

conjugation and linkage methods known in the art and described below. In some embodiments, linkers such as peptide linkers, cleavable linkers, non-cleavable linkers or linkers that aid in the conjugation reaction, can be used to link or conjugate the effector moieties to the variant polypeptide or immunomodulatory protein.

[0290] In some embodiments, the IgSF conjugate comprises the following components: (protein or polypeptide), $(L)_q$ and (effector moiety)$_m$, wherein the protein or polypeptide is any of the described variant polypeptides or immunomodulatory proteins capable of binding one or more cognate counter structure ligands as described; L is a linker for linking the protein or polypeptide to the moiety; m is at least 1; q is 0 or more; and the resulting IgSF conjugate binds to the one or more counter structure ligands. In particular embodiments, m is 1 to 4 and q is 0 to 8.

[0291] In some embodiments, there is provided an IgSF conjugate comprising a variant polypeptide or immunomodulatory protein provided herein conjugated with a targeting agent that binds to a cell surface molecule, for example, for targeted delivery of the variant polypeptide or immunomodulatory protein to a specific cell. In some embodiments, the targeting agent is a molecule(s) that has the ability to localize and bind to a molecule present on a normal cell/tissue and/or tumor cell/tumor in a subject. In other words, IgSF conjugates comprising a targeting agent can bind to a ligand (directly or indirectly), which is present on a cell, such as a tumor cell. The targeting agents of the invention contemplated for use include antibodies, polypeptides, peptides, aptamers, other ligands, or any combination thereof, that can bind a component of a target cell or molecule.

[0292] In some embodiments, the targeting agent binds a tumor cell(s) or can bind in the vicinity of a tumor cell(s) (e.g., tumor vasculature or tumor microenvironment) following administration to the subject. The targeting agent may bind to a receptor or ligand on the surface of the cancer cell. In another aspect of the invention, a targeting agent is selected which is specific for a noncancerous cells or tissue. For example, a targeting agent can be specific for a molecule present normally on a particular cell or tissue. Furthermore, in some embodiments, the same molecule can be present on normal and cancer cells. Various cellular components and molecules are known. For example, if a targeting agent is specific for EGFR, the resulting IgSF conjugate can target cancer cells expressing EGFR as well as normal skin epidermal cells expressing EGFR. Therefore, in some embodiments, an IgSF conjugate of the invention can operate by two separate mechanisms (targeting cancer and non-cancer cells).

[0293] In various aspects of the invention disclosed herein an IgSF conjugate of the invention comprises a targeting agent which can bind/target a cellular component, such as a tumor antigen, a bacterial antigen, a viral antigen, a mycoplasm antigen, a fungal antigen, a prion antigen, an antigen from a parasite. In some aspects, a cellular component, antigen or molecule can each be used to mean, a desired target for a targeting agent. For example, in various embodiments, a targeting agent is specific for or binds to a component, which includes but is not limited to, epidermal growth factor receptor (EGFR, ErbB-1, HERl), ErbB-2 (HER2/neu), ErbB-3/HER3, ErbB-4/HER4, EGFR ligand family; insulin-like growth factor receptor (IGFR) family, IGF-binding proteins (IGFBPs), IGFR ligand family; platelet derived growth factor receptor (PDGFR) family, PDGFR ligand family; fibroblast growth factor receptor (FGFR) family, FGFR ligand family, vascular endothelial growth factor receptor (VEGFR) family, VEGF family; HGF receptor family; TRK receptor family; ephrin (EPH) receptor family; AXL receptor family; leukocyte tyrosine kinase (LTK) receptor family; TIE receptor family, angiopoietin 1,2; receptor tyrosine kinase-like orphan receptor (ROR) receptor family, e.g. ROR1; CD171 (L1CAM); B7-H6 (NCR3LG1); PD-L1, tumor glycosylation antigen, e.g. sTn or Tn, such as sTn Ag of MUC1; LHR (LHCGR); phosphatidylserine, discoidin domain receptor (DDR) family; RET receptor family; KLG receptor family; RYK receptor family; MuSK receptor family; Transforming growth factor-α (TGF-α) receptors, TGF-β; Cytokine receptors, Class I (hematopoietin family) and Class II (interferon/IL-10 family) receptors, tumor necrosis factor (TNF) receptor superfamily (TNFRSF), death receptor family; cancer-testis (CT) antigens, lineage-specific antigens, differentiation antigens, alpha-actinin-4, ARTCl, breakpoint cluster region-Abelson (Bcr-abl) fusion products, B-RAF, caspase-5 (CASP-5), caspase-8 (CASP-8), β-catenin (CTNNBl), cell division cycle 27 (CDC27), cyclin-dependent kinase 4 (CDK4), CDKN2A, COA-I, dek-can fusion protein, EFTUD-2, Elongation factor 2 (ELF2), Ets variant gene 6/acute myeloid leukemia 1 gene ETS (ETC6-AML1) fusion protein, fibronectin (FN), e.g. the extradomain A (EDA) of fibronectin, GPNMB, low density lipid receptor/GDP-L fucose: β-D-galactose 2-α-L-fucosyltransferase (LDLR/FUT) fusion protein, HLA-A2. arginine to isoleucine exchange at residue 170 of the α-helix of the α2-domain in the HLA-A2gene (HLA-A*201-R170I), HLA-Al 1, heat shock protein 70-2 mutated (HSP70-2M), K1AA0205, MART2, melanoma ubiquitous mutated 1, 2, 3 (MUM-I, 2, 3), prostatic acid phosphatase (PAP), neo-PAP, Myosin class I, NFYC, OGT, OS-9, pml-RARα fusion protein, PRDX5, PTPRK, K-ras (KRAS2), N-ras (NRAS), HRAS, RBAF600, SIRT2, SNRPDl, SYT-SSXl or -SSX2 fusion

protein, Triosephosphate Isomerase, BAGE, BAGK- 1, BAGE-2,3,4,5, GAGE-1,2,3,4,5,6,7,8, GnT-V (aberrant N-acetyl glucosaminyl transferase V, MGAT5), HERV-K-MEL, KK-LC, KM-HN-I, LAGE, LAGE-I, CTL-recognized antigen on melanoma (CAMEL), MAGE-Al (MAGE-I), MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A8, MAGE-A9, MAGE-AlO, MAGE-AI l, MAGE-A12, MAGE-3, MAGE-Bl, MAGE-B2, MAGE-B5, MAGE-B6, MAGE- Cl, MAGE-C2, mucin 1 (MUCl), MART-1/Melan-A (MLANA), gplOO, gplOO/ Pmell7 (SILV), tyrosinase (TYR), TRP-I, HAGE, NA-88, NY-ESO-I, NY-ESO-l/LAGE-2, SAGE, Spl7, SSX-1,2,3,4, TRP2-INT2, carcino-embryonic antigen (CEA), Kallikrein 4, mammaglobin-A, OAl, prostate specific antigen (PSA), TRP- 1/ gp75, TRP-2, adipophilin, interferon inducible protein absent in melanoma 2 (AIM-2), BING-4, CPSF, cyclin Dl, epithelial cell adhesion molecule (Ep-CAM), EphA3, fibroblast growth factor-5 (FGF-5), glycoprotein 250 (gp250), EGFR (ERBBl), HER-2/neu (ERBB2), interleukin 13 receptor α2 chain (IL13Rα2), IL-6 receptor, intestinal carboxyl esterase (iCE), alpha-feto protein (AFP), M-CSF, mdm-2, MUCl, p53 (TP53), PBF, PRAME, PSMA, RAGE-I, RNF43, RU2AS, SOXlO, STEAPl, survivin (BIRC5), human telomerase reverse transcriptase (hTERT), telomerase, Wilms' tumor gene (WTl), SYCPl, BRDT, SPANX, XAGE, ADAM2, PAGE-5, LIPl, CTAGE-I, CSAGE, MMAl, CAGE, BORIS, HOM-TES-85, AF15ql4, HCA661, LDHC, MORC, SGY-I, SPOl 1, TPXl, NY-SAR-35, FTHL17, NXF2, TDRDl, TEX15, FATE, TPTE, immunoglobulin idiotypes, Bence-Jones protein, estrogen receptors (ER), androgen receptors (AR), CD40, CD30, CD20, CD 19, CD33, cancer antigen 72-4 (CA 72-4), cancer antigen 15-3 (CA 15-3), cancer antigen 27- 29 (CA 27-29), cancer antigen 125 (CA 125), cancer antigen 19-9 (CA 19-9), β-human chorionic gonadotropin, β-2 microglobulin, squamous cell carcinoma antigen, neuron-specific enolase, heat shock protein gp96, GM2, sargramostim, CTLA-4, 707 alanine proline (707-AP), adenocarcinoma antigen recognized by T cells 4 (ART- 4), carcinoembryogenic antigen peptide-1 (CAP-I), calcium-activated chloride channel-2 (CLCA2), cyclophilin B (Cyp-B), human signet ring tumor-2 (HST-2), Human papilloma virus (HPV) proteins (HPV-E6, HPV-E7, major or minor capsid antigens, others), Epstein-Barr virus (EBV) proteins (EBV latent membrane proteins - LMPl, LMP2; others), Hepatitis B or C virus proteins, and HIV proteins.

[0294] In some embodiments, an IgSF conjugate, through its targeting agent, will bind a cellular component of a tumor cell, tumor vasculature or tumor microenvironment, thereby promoting killing of targeted cells via modulation of the immune response, (e.g., by activation of co-stimulatory molecules or inhibition of negative regulatory molecules of immune cell

activation), inhibition of survival signals (e.g., growth factor or cytokine or hormone receptor antagonists), activation of death signals, and/or immune-mediated cytotoxicity, such as through antibody dependent cellular cytotoxicity. Such IgSF conjugates can function through several mechanisms to prevent, reduce or eliminate tumor cells, such as to facilitate delivery of conjugated effector moieties to the tumor target, such as through receptor-mediated endocytosis of the IgSF conjugate; or such conjugates can recruit, bind, and/or activate immune cells (e.g. NK cells, monocytes/macrophages, dendritic cells, T cells, B cells). Moreover, in some instances one or more of the foregoing pathways may operate upon administration of one or more IgSF conjugates of the invention.

[0295] In some embodiments, an IgSF conjugate, through its targeting agent, will be localized to, such as bind to, a cellular component of a tumor cell, tumor vasculature or tumor microenvironment, thereby modulating cells of the immune response in the vicinity of the tumor. In some embodiments, the targeting agent facilitates delivery of the conjugated IgSF (e.g. vIgD) to the tumor target, such as to interact with its cognate binding partner to alter signaling of immune cells (e.g. NK cells, monocytes/macrophages, dendritic cells, T cells, B cells) bearing the cognate binding partner. In some embodiments, localized delivery mediates an antagonizing or blocking activity of the PD-1 inhibitory receptor. In some embodiments, localized delivery agonizes the PD-1 inhibitory receptor, which, in some cases, can occur where there is proximal clustering of an activating receptor.

[0296] In some embodiments, the targeting agent is an immunoglobulin. As used herein, the term "immunoglobulin" includes natural or artificial mono- or polyvalent antibodies including, but not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, signle chain Fv (scFv); anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, e.g., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA, and IgY), class (e.g., IgGl, IgG2, IgG3, IgG4, IgAl , and IgA2) or subclass of immunoglobulin molecule.

[0297] In some embodiments, an IgSF conjugate, through its antibody targeting moiety, will bind a cellular component of a tumor cell, tumor vasculature or tumor microenvironment, thereby

promoting apoptosis of targeted cells via modulation of the immune response, (e.g., by activation of co-stimulatory molecules or inhibition of negative regulatory molecules of immune cell activation), inhibition of survival signals (e.g., growth factor or cytokine or hormone receptor antagonists), activation of death signals, and/or immune-mediated cytotoxicity, such as through antibody dependent cellular cytotoxicity. Such IgSF conjugates can function through several mechanisms to prevent, reduce or eliminate tumor cells, such as to facilitate delivery of conjugated effector moieties to the tumor target, such as through receptor-mediated endocytosis of the IgSF conjugate; or such conjugates can recruit, bind, and/or activate immune cells (e.g. NK cells, monocytes/macrophages, dendritic cells, T cells, B cells).

[0298] In some embodiments, an IgSF conjugate, through its antibody targeting moiety, will bind a cellular component of a tumor cell, tumor vasculature or tumor microenvironment, thereby modulating the immune response (e.g., by activation of co-stimulatory molecules or inhibition of negative regulatory molecules of immune cell activation). In some embodiments, such conjugates can recognize, bind, and/or modulate (e.g. inhibit or activate) immune cells (e.g. NK cells, monocytes/macrophages, dendritic cells, T cells, B cells).

[0299] Antibody targeting moieties of the invention include antibody fragments that include, but are not limited to, Fab, Fab' and F(ab')2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. Also included in the invention are Fc fragments, antigen-Fc fusion proteins, and Fc-targeting moiety conjugates or fusion products (Fc-peptide, Fc-aptamer). The antibody targeting moieties of the invention may be from any animal origin including birds and mammals. In one aspect, the antibody targeting moieties are human, murine (e.g., mouse and rat), donkey, sheep, rabbit, goat, guinea pig, camel, horse, or chicken. Further, such antibodies may be humanized versions of animal antibodies. The antibody targeting moieties of the invention may be monospecific, bispecific, trispecific, or of greater multispecificity.

[0300] In various embodiments, an antibody/targeting moiety recruits, binds, and/or activates immune cells (e.g. NK cells, monocytes/macrophages, dendritic cells) via interactions between Fc (in antibodies) and Fc receptors (on immune cells) and via the conjugated variant

polypeptides or immunomodulatory proteins provided herein. In some embodiments, an antibody/targeting moiety recognizes or binds a tumor agent via and localizes to the tumor cell the conjugated variant polypeptides or immunomodulatory proteins provided herein to facilitate modulation of immune cells in the vicinity of the tumor.

[0301] Examples of antibodies which can be incorporated into IgSF conjugates include but are not limited to antibodies such as Cetuximab (IMC-C225; Erbitux®), Trastuzumab (Herceptin®), Rituximab (Rituxan®; MabThera®), Bevacizumab (Avastin®), Alemtuzumab (Campath®; Campath-1H®; Mabcampath®), Panitumumab (ABX-EGF; Vectibix®), Ranibizumab (Lucentis®), Ibritumomab, Ibritumomab tiuxetan, (Zevalin ®), Tositumomab, Iodine I 131 Tositumomab (BEXXAR®), Catumaxomab (Removab®), Gemtuzumab, Gemtuzumab ozogamicine (Mylotarg®), Abatacept (CTLA4-Ig; Orencia®), Belatacept (L104EA29YIg; LEA29Y; LEA), Ipilimumab (MDX-010; MDX-101), Tremelimumab (ticilimumab; CP-675,206), PRS-010, PRS-050, Aflibercept (VEGF Trap, AVE005), Volociximab (M200), F200, MORAb-009, SS1P (CAT-5001), Cixutumumab (IMC-A12), Matuzumab (EMD72000), Nimotuzumab (h-R3), Zalutumumab (HuMax-EGFR), Necitumumab IMC-11F8, mAb806 / ch806, Sym004, mAb-425, Panorex @ (17-1A) (murine monoclonal antibody); Panorex @ (17-1A) (chimeric murine monoclonal antibody); IDEC- Y2B8 (murine, anti- CD2O MAb) ; BEC2 (anti-idiotypic MAb, mimics the GD epitope) (with BCG); Oncolym (Lym-1 monoclonal antibody); SMART MI95 Ab, humanized 13' I LYM-I (Oncolym), Ovarex (B43.13, anti-idiotypic mouse MAb); MDX-210 (humanized anti-HER-2 bispecific antibody); 3622W94 MAb that binds to EGP40 (17-1A) pancarcinoma antigen on adenocarcinomas; Anti-VEGF, Zenapax (SMART Anti-Tac (IL-2 receptor); SMART MI95 Ab, humanized Ab, humanized); MDX-210 (humanized anti- HER-2 bispecific antibody); MDX-447 (humanized anti-EGF receptor bispecific antibody); NovoMAb-G2 (pancarcinoma specific Ab); TNT (chimeric MAb to histone antigens); TNT (chimeric MAb to histone antigens); Gliomab-H (Monoclon s - Humanized Abs); GNI-250 Mab; EMD-72000 (chimeric-EGF antagonist); LymphoCide (humanized LL2 antibody); and MDX-260 bispecific, targets GD-2, ANA Ab, SMART IDlO Ab, SMART ABL 364 Ab or ImmuRAIT-CEA. As illustrated by the forgoing list, it is conventional to make antibodies to a particular target epitope.

[0302] In some embodiments, the antibody targeting moiety is a full length antibody, or antigen-binding fragment thereof, containing an Fc domain. In some embodiments, the variant

polypeptide or immunomodulatory protein is conjugated to the Fc portion of the antibody targeting moiety, such as by conjugation to the N-terminus of the Fc portion of the antibody.

[0303] In some embodiments, the vIgD is linked, directly or indirectly, to the N- or C-terminus of the light and/or heavy chain of the antibody. In some embodiments, linkage can be via a peptide linker, such as any described above. Various configurations can be constructed. Fig. 7A-7C depict exemplary configurations. In some embodiments, the antibody conjugate can be produced by co-expression of the heavy and light chain of the antibody in a cell.

[0304] In one aspect of the invention, the targeting agent is an aptamer molecule. For example, in some embodiments, the aptamer is comprised of nucleic acids that function as a targeting agent. In various embodiments, an IgSF conjugate of the invention comprises an aptamer that is specific for a molecule on a tumor cell, tumor vasculature, and/or a tumor microenvironment. In some embodiments, the aptamer itself can comprise a biologically active sequence, in addition to the targeting module (sequence), wherein the biologically active sequence can induce an immune response to the target cell. In other words, such an aptamer molecule is a dual use agent. In some embodiments, an IgSF conjugate of the invention comprises conjugation of an aptamer to an antibody, wherein the aptamer and the antibody are specific for binding to separate molecules on a tumor cell, tumor vasculature, tumor microenvironment, and/or immune cells.

[0305] The term "aptamer" includes DNA, RNA or peptides that are selected based on specific binding properties to a particular molecule. For example, an aptamer(s) can be selected for binding a particular gene or gene product in a tumor cell, tumor vasculature, tumor microenvironment, and/or an immune cell, as disclosed herein, where selection is made by methods known in the art and familiar to one of skill in the art.

[0306] In some aspects of the invention the targeting agent is a peptide. For example, the variant polypeptides or immunomodulatory proteins provided herein can be conjugated to a peptide which can bind with a component of a cancer or tumor cells. Therefore, such IgSF conjugates of the invention comprise peptide targeting agents which binds to a cellular component of a tumor cell, tumor vasculature, and/or a component of a tumor microenvironment. In some embodiments, targeting agent peptides can be an antagonist or agonist of an integrin. Integrins, which comprise an alpha and a beta subunit, include numerous types well known to a skilled artisan.

[0307] In one embodiment, the targeting agent is Vvβ3. Integrin Vvβ3 is expressed on a variety of cells and has been shown to mediate several biologically relevant processes, including adhesion of osteoclasts to bone matrix, migration of vascular smooth muscle cells, and angiogenesis. Suitable targeting molecules for integrins include RGD peptides or peptidomimetics as well as non-RGD peptides or peptidomimetics (see, e.g., U.S. Pat. Nos. 5,767,071 and 5,780,426) for other integrins such as V4.βi (VLA-4), V4-P7 (see, e.g., U.S. Pat. No. 6,365,619; Chang et al, Bioorganic & Medicinal Chem Lett, 12:159-163 (2002); Lin et al., Bioorganic & Medicinal Chem Lett, 12:133-136 (2002)), and the like.

[0308] In some embodiments, there is provided an IgSF conjugate comprising a variant polypeptide or immunomodulatory protein provided herein conjugated with a therapeutic agent. In some embodiments, the therapeutic agent includes, for example, daunomycin, doxorubicin, methotrexate, and vindesine (Rowland et al., Cancer Immunol. Immunother. 21:183-187, 1986). In some embodiments, the therapeutic agent has an intracellular activity. In some embodiments, the IgSF conjugate is internalized and the therapeutic agent is a cytotoxin that blocks the protein synthesis of the cell, therein leading to cell death. In some embodiments, the therapeutic agent is a cytotoxin comprising a polypeptide having ribosome-inactivating activity including, for example, gelonin, bouganin, saporin, ricin, ricin A chain, bryodin, diphtheria toxin, restrictocin, Pseudomonas exotoxin A and variants thereof. In some embodiments, where the therapeutic agent is a cytotoxin comprising a polypeptide having a ribosome-inactivating activity, the IgSF conjugate must be internalized upon binding to the target cell in order for the protein to be cytotoxic to the cells.

[0309] In some embodiments, there is provided an IgSF conjugate comprising a variant polypeptide or immunomodulatory protein provided herein conjugated with a toxin. In some embodiments, the toxin includes, for example, bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin (Mandler et al., J.Nat. Cancer Inst. 92(19):1573-1581 (2000); Mandler et al., Bioorganic & Med. Chem. Letters 10:1025- 1028 (2000); Mandler et al., Bioconjugate Chem. 13:786-791 (2002)), maytansinoids (EP 1391213; Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996)), and calicheamicin (Lode et al., Cancer Res. 58:2928 (1998); Hinman et al., Cancer Res. 53:3336-3342 (1993)). The toxins may exert their cytotoxic and cytostatic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition.

[0310] In some embodiments, there is provided an IgSF conjugate comprising a variant polypeptide or immunomodulatory protein provided herein conjugated with a label, which can generate a detectable signal, indirectly or directly. These IgSF conjugates can be used for research or diagnostic applications, such as for the in vivo detection of cancer. The label is preferably capable of producing, either directly or indirectly, a detectable signal. For example, the label may be radio-opaque or a radioisotope, such as 3H, 14C, 32P, 35S, 123I, 125I, 131I; a fluorescent (fluorophore) or chemiluminescent (chromophore) compound, such as fluorescein isothiocyanate, rhodamine or luciferin; an enzyme, such as alkaline phosphatase, β-galactosidase or horseradish peroxidase; an imaging agent; or a metal ion. In some embodiments, the label is a radioactive atom for scintigraphic studies, for example 99Tc or 123I, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, MRI), such as zirconium-89, iodine-123, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron. Zirconium-89 may be complexed to various metal chelating agents and conjugated to antibodies, e.g., for PET imaging (WO 2011/056983). In some embodiments, the IgSF conjugate is detectable indirectly. For example, a secondary antibody that is specific for the IgSF conjugate and contains a detectable label can be used to detect the IgSF conjugate.

[0311] The IgSF conjugates may be prepared using any methods known in the art. See, e.g., WO 2009/067800, WO 2011/133886, and U.S. Patent Application Publication No. 2014322129, incorporated by reference herein in their entirety.

[0312] The variant polypeptides or immunomodulatory proteins of an IgSF conjugate may be "attached to" the effector moiety by any means by which the variant polypeptides or immunomodulatory proteins can be associated with, or linked to, the effector moiety. For example, the variant polypeptides or immunomodulatory proteins of an IgSF conjugate may be attached to the effector moiety by chemical or recombinant means. Chemical means for preparing fusions or conjugates are known in the art and can be used to prepare the IgSF conjugate. The method used to conjugate the variant polypeptides or immunomodulatory proteins and effector moiety must be capable of joining the variant polypeptides or immunomodulatory proteins with the effector moiety without interfering with the ability of the variant polypeptides or immunomodulatory proteins to bind to their one or more counter structure ligands.

[0313] The variant polypeptides or immunomodulatory proteins of an IgSF conjugate may be linked indirectly to the effector moiety. For example, the variant polypeptides or

immunomodulatory proteins of an IgSF conjugate may be directly linked to a liposome containing the effector moiety of one of several types. The effector moiety(s) and/or the variant polypeptides or immunomodulatory proteins may also be bound to a solid surface.

[0314] In some embodiments, the variant polypeptides or immunomodulatory proteins of an IgSF conjugate and the effector moiety are both proteins and can be conjugated using techniques well known in the art. There are several hundred crosslinkers available that can conjugate two proteins. (See for example "Chemistry of Protein Conjugation and Crosslinking," 1991, Shans Wong, CRC Press, Ann Arbor). The crosslinker is generally chosen based on the reactive functional groups available or inserted on the variant polypeptides or immunomodulatory proteins and/or effector moiety. In addition, if there are no reactive groups, a photoactivatible crosslinker can be used. In certain instances, it may be desirable to include a spacer between the variant polypeptides or immunomodulatory proteins and the effector moiety. Crosslinking agents known to the art include the homobifunctional agents: glutaraldehyde, dimethyladipimidate and Bis(diazobenzidine) and the heterobifunctional agents: m Maleimidobenzoyl-N-Hydroxysuccinimide and Sulfo-m Maleimidobenzoyl-N-Hydroxysuccinimide.

[0315] In some embodiments, the variant polypeptides or immunomodulatory proteins of an IgSF conjugate may be engineered with specific residues for chemical attachment of the effector moiety. Specific residues used for chemical attachment of molecule known to the art include lysine and cysteine. The crosslinker is chosen based on the reactive functional groups inserted on the variant polypeptides or immunomodulatory proteins, and available on the effector moiety.

[0316] An IgSF conjugate may also be prepared using recombinant DNA techniques. In such a case a DNA sequence encoding the variant polypeptides or immunomodulatory proteins is fused to a DNA sequence encoding the effector moiety, resulting in a chimeric DNA molecule. The chimeric DNA sequence is transfected into a host cell that expresses the fusion protein. The fusion protein can be recovered from the cell culture and purified using techniques known in the art.

[0317] Examples of attaching an effector moiety, which is a label, to the variant polypeptides or immunomodulatory proteins include the methods described in Hunter, et al., Nature 144:945 (1962); David, et al., Biochemistry 13:1014 (1974); Pain, et al., J. Immunol. Meth. 40:219 (1981); Nygren, J. Histochem. and Cytochem. 30:407 (1982); Wensel and Meares, Radioimmunoimaging And Radioimmunotherapy, Elsevier, N.Y. (1983); and Colcher et al.,

"Use Of Monoclonal Antibodies As Radiopharmaceuticals For The Localization Of Human Carcinoma Xenografts In Athymic Mice", Meth. Enzymol., 121:802-16 (1986).

[0318] The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as 99Tc or 123I, 186Re, 188Re and 111In can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al., Biochem. Biophys. Res. Commun. 80:49-57 (1978)) can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

[0319] Conjugates of the variant polypeptides or immunomodulatory proteins and a cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1 -carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCI), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)- ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1 ,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-p-isothiocyanatobenzyl-3-methyldiethylenetriaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See, e.g., WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Research 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

[0320] The IgSF conjugates of the invention expressly contemplate, but are not limited to, drug conjugates prepared with cross-linker reagents: BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, IL, U.S.A). See pages 467-498, 2003-2004 Applications Handbook and Catalog.

D. Transmembrane and Secretable Immunomodulatory Proteins and Engineered Cells

[0321] Provided herein are engineered cells which express the immunomodulatory variant PD-L1 polypeptides (alternatively, "engineered cells"). In some embodiments, the expressed immunomodulatory variant PD-L1 polypeptide is a transmembrane protein and is surface expressed. In some embodiments, the expressed immunomodulatory variant PD-L1 polypeptide is expressed and secreted from the cell.

1. Transmembrane Immunomodulatory Proteins

[0322] In some embodiments, an immunomodulatory polypeptide comprising a variant PD-L1 can be a membrane bound protein. As described in more detail below, the immunomodulatory polypeptide can be a transmembrane immunomodulatory polypeptide comprising a variant PD-L1 in which is contained: an ectodomain containing at least one affinity modified IgSF domain (IgV or IgC), a transmembrane domain and, optionally, a cytoplasmic domain. In some embodiments, the transmembrane immunomodulatory protein can be expressed on the surface of an immune cell, such as a mammalian cell, including on the surface of a lymphocyte (e.g. T cell or NK cell) or antigen presenting cell. In some embodiments, the transmembrane immunomodulatory protein is expressed on the surface of a mammalian T-cell, including such T-cells as: a T helper cell, a cytotoxic T-cell (alternatively, cytotoxic T lymphocyte or CTL), a natural killer T-cell, a regulatory T-cell, a memory T-cell, or a gamma delta T-cell. In some embodiments, the mammalian cell is an antigen presenting cell (APC). Typically, but not exclusively, the ectodomain (alternatively, "extracellular domain") of comprises the one or more amino acid variations (e.g. amino acid substitutions) of the variant PD-L1 of the invention. Thus, for example, in some embodiments a transmembrane protein will comprise an ectodomain that comprises one or more amino acid substitutions of a variant PD-L1 of the invention.

[0323] In some embodiments, the engineered cells express a variant PD-L1 polypeptides are transmembrane immunomodulatory polypeptides (TIPs) that can be a membrane protein such as a transmembrane protein. In typical embodiments, the ectodomain of a membrane protein comprises an extracellular domain or IgSF domain thereof of a variant PD-L1 provided herein in which is contained one or more amino acid substitutions in at least one IgSF domain as described. The transmembrane immunomodulatory proteins provided herein further contain a

transmembrane domain linked to the ectodomain. In some embodiments, the transmembrane domain results in an encoded protein for cell surface expression on a cell. In some embodiments, the transmembrane domain is linked directly to the ectodomain. In some embodiments, the transmembrane domain is linked indirectly to the ectodomain via one or more linkers or spacers. In some embodiments, the transmembrane domain contains predominantly hydrophobic amino acid residues, such as leucine and valine.

[0324] In some embodiments, a full length transmembrane anchor domain can be used to ensure that the TIPs will be expressed on the surface of the engineered cell, such as engineered T cell. Conveniently, this could be from a particular native protein that is being affinity modified (e.g. PD-L1 or other native IgSF protein), and simply fused to the sequence of the first membrane proximal domain in a similar fashion as the native IgSF protein (e.g. PD-L1). In some embodiments, the transmembrane immunomodulatory protein comprises a transmembrane domain of the corresponding wild-type or unmodified IgSF member, such as a transmembrane domain contained in the sequence of amino acids set forth in SEQ ID NO:3 (Table 2). In some embodiments, the membrane bound form comprises a transmembrane domain of the corresponding wild-type or unmodified polypeptide, such as corresponding to residues 239-259 of SEQ ID NO:3.

[0325] In some embodiments, the transmembrane domain is a non-native transmembrane domain that is not the transmembrane domain of native PD-L1. In some embodiments, the transmembrane domain is derived from a transmembrane domain from another non- PD-L1 family member polypeptide that is a membrane-bound or is a transmembrane protein. In some embodiments, a transmembrane anchor domain from another protein on T cells can be used. In some embodiments, the transmembrane domain is derived from CD8. In some embodiments, the transmembrane domain can further contain an extracellular portion of CD8 that serves as a spacer domain. An exemplary CD8 derived transmembrane domain is set forth in SEQ ID NO: 242 or 1164 or a portion thereof containing the CD8 transmembrane domain. In some embodiments, the transmembrane domain is a synthetic transmembrane domain.

[0326] In some embodiments, the transmembrane immunomodulatory protein further contains an endodomain, such as a cytoplasmic signaling domain, linked to the transmembrane domain. In some embodiments, the cytoplasmic signaling domain induces cell signaling. In some embodiments, the endodomain of the transmembrane immunomodulatory protein comprises the cytoplasmic domain of the corresponding wild-type or unmodified polypeptide,

such as a cytoplasmic domain contained in the sequence of amino acids set forth in SEQ ID NO:3 (see Table 2).

[0327] In some embodiments, a provided transmembrane immunomodulatory protein that is or comprises a variant PD-L1 comprises a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO: 191 and contains an ectodomain comprising at least one affinity-modified PD-L1 IgSF domain as described and a transmembrane domain. In some embodiments, the transmembrane immunomodulatory protein contains any one or more amino acid substitutions in an IgSF domain (e.g. IgV domain) as described, including any set forth in Table 1. In some embodiments, the transmembrane immunomodulatory protein can further comprise a cytoplasmic domain as described. In some embodiments, the transmembrane immunomodulatory protein can further contain a signal peptide. In some embodiments, the signal peptide is the native signal peptide of wild-type IgSF member, such as contained in the sequence of amino acids set forth in SEQ ID NO:3 (see e.g. Table 2).

[0328] Also provided is a nucleic acid molecule encoding such transmembrane immunomodulatory proteins. In some embodiments, a nucleic acid molecule encoding a transmembrane immunomodulatory protein comprises a nucleotide sequence that encodes a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NOS: 191 and contains an ectodomain comprising at least one affinity-modified IgSF domain as described, a transmembrane domain and, optionally, a cytoplasmic domain. In some embodiments, the nucleic acid molecule can further comprise a sequence of nucleotides encoding a signal peptide. In some embodiments, the signal peptide is the native signal peptide of the corresponding wild-type IgSF member (see e.g. Table 2).

[0329] In some embodiments, provided are CAR-related transmembrane immunomodulatory proteins in which the endodomain of a transmembrane immunomodulatory protein comprises a cytoplasmic signaling domain that comprises at least one ITAM (immunoreceptor tyrosine-based activation motif)-containing signaling domain. ITAM is a conserved motif found in a number of protein signaling domains involved in signal transduction of immune cells, including in the CD3-zeta chain ("CD3-z") involved in T-cell receptor signal transduction. In some embodiments, the endodomain comprises at CD3-zeta signaling domain. In some embodiments, the CD3-zeta signaling domain comprises the sequence of amino acids set forth in SEQ ID NO: 243 or a

sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% to SEQ ID NO:243 and retains the activity of T cell signaling. In some embodiments, the endodomain of a CAR-related transmembrane immunomodulatory protein can further comprise a costimulatory signaling domain to further modulate immunomodulatory responses of the T-cell. In some embodiments, the costimulatory signaling domain is CD28, ICOS, 41BB or OX40. In some embodiments, the costimulatory signaling domain is a derived from CD28 or 4-1BB and comprises the sequence of amino acids set forth in any of SEQ ID NOS: 1165-1168 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% to SEQ ID NO:1165-1168 and retains the activity of T cell costimulatory signaling. In some embodiments, the provided CAR-related transmembrane immunomodulatory proteins have features of CARs to stimulate T cell signaling upon binding of an affinity modified IgSF domain to a cognate binding partner or counter structure. In some embodiments, upon specific binding by the affinity-modified IgSF domain to its counter structure can lead to changes in the immunological activity of the T-cell activity as reflected by changes in cytotoxicity, proliferation or cytokine production.

[0330] In some embodiments, the transmembrane immunomodulatory protein does not contain an endodomain capable of mediating cytoplasmic signaling. In some embodiments, the transmembrane immunomodulatory protein lacks the signal transduction mechanism of the wild-type or unmodified polypeptide and therefore does not itself induce cell signaling. In some embodiments, the transmembrane immunomodulatory protein lacks an intracellular (cytoplasmic) domain or a portion of the intracellular domain of the corresponding wild-type or unmodified polypeptide, such as a cytoplasmic signaling domain contained in the sequence of amino acids set forth in SEQ ID NO:3 (see Table 2). In some embodiments, the transmembrane immunomodulatory protein does not contain an ITIM (immunoreceptor tyrosine-based inhibition motif), such as contained in certain inhibitory receptors, including inhibitory receptors of the IgSF family (e.g. PD-1 or TIGIT). Thus, in some embodiments, the transmembrane immunomodulatory protein only contains the ectodomain and the transmembrane domain, such as any as described.

2. Secreted Immunomodulatory Proteins and Engineered Cells

[0331] In some embodiments, the PD-L1 variant immunomodulatory polypeptide containing any one or more of the amino acid mutations as described herein, is secretable, such as when expressed from a cell. Such a variant PD-L1 immunomodulatory protein does not comprise a transmembrane domain. In some embodiments, the variant PD-L1 immunomodulatory protein is not conjugated to a half-life extending moiety (such as an Fc domain or a multimerization domain). In some embodiments, the variant PD-L1 immunomodulatory protein comprises a signal peptide, e.g. an antibody signal peptide or other efficient signal sequence to get domains outside of cell. When the immunomodulatory protein comprises a signal peptide and is expressed by an engineered cell, the signal peptide causes the immunomodulatory protein to be secreted by the engineered cell. Generally, the signal peptide, or a portion of the signal peptide, is cleaved from the immunomodulatory protein with secretion. The immunomodulatory protein can be encoded by a nucleic acid (which can be part of an expression vector). In some embodiments, the immunomodulatory protein is expressed and secreted by a cell (such as an immune cell, for example a primary immune cell).

[0332] Thus, in some embodiments, there are provided variant PD-L1 immunomodulatory proteins that further comprises a signal peptide. In some embodiments, provided herein is a nucleic acid molecule encoding the variant PD-L1 immunomodulatory protein operably connected to a secretion sequence encoding the signal peptide.

[0333] A signal peptide is a sequence on the N-terminus of an immunomodulatory protein that signals secretion of the immunomodulatory protein from a cell. In some embodiments, the signal peptide is about 5 to about 40 amino acids in length (such as about 5 to about 7, about 7 to about 10, about 10 to about 15, about 15 to about 20, about 20 to about 25, or about 25 to about 30, about 30 to about 35, or about 35 to about 40 amino acids in length).

[0334] In some embodiments, the signal peptide is a native signal peptide from the corresponding wild-type PD-L1 (see Table 2). In some embodiments, the signal peptide is a non-native signal peptide. For example, in some embodiments, the non-native signal peptide is a mutant native signal peptide from the corresponding wild-type PD-L1, and can include one or more (such as 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more) substitutions insertions or deletions. In some embodiments, the non-native signal peptide is a signal peptide or mutant thereof of a family member from the same IgSF family as the wild-type IgSF family member. In some embodiments, the non-native signal peptide is a signal peptide or mutant thereof from an IgSF family member from a different IgSF family that the wild-type IgSF family member. In some

embodiments, the signal peptide is a signal peptide or mutant thereof from a non-IgSF protein family, such as a signal peptide from an immunoglobulin (such as IgG heavy chain or IgG-kappa light chain), a cytokine (such as interleukin-2 (IL-2), or CD33), a serum albumin protein (e.g. HSA or albumin), a human azurocidin preprotein signal sequence, a luciferase, a trypsinogen (e.g. chymotrypsinogen or trypsinogen) or other signal peptide able to efficiently secrete a protein from a cell. Exemplary signal peptides include any described in the Table 9.

TABLE 9. Exemplary Signal Peptides

SEQ ID NO	Signal Peptide	Peptide Sequence
SEQ ID NO: 221	HSA signal peptide	MKWVTFISLLFLFSSAYS
SEQ ID NO: 222	Ig kappa light chain	MDMRAPAGIFGFLLVLFPGYRS
SEQ ID NO: 223	human azurocidin preprotein signal sequence	MTRLTVLALLAGLLASSRA
SEQ ID NO: 224	IgG heavy chain signal peptide	MELGLSWIFLLAILKGVQC
SEQ ID NO: 225	IgG heavy chain signal peptide	MELGLRWVFLVAILEGVQC
SEQ ID NO: 226	IgG heavy chain signal peptide	MKHLWFFLLLVAAPRWVLS
SEQ ID NO: 227	IgG heavy chain signal peptide	MDWTWRILFLVAAATGAHS
SEQ ID NO: 228	IgG heavy chain signal peptide	MDWTWRFLFVVAAATGVQS
SEQ ID NO: 229	IgG heavy chain signal peptide	MEFGLSWLFLVAILKGVQC
SEQ ID NO: 230	IgG heavy chain signal peptide	MEFGLSWVFLVALFRGVQC
SEQ ID NO: 231	IgG heavy chain signal peptide	MDLLHKNMKHLWFFLLLVAAPRWVLS
SEQ ID NO: 232	IgG Kappa light chain signal sequences:	MDMRVPAQLLGLLLLWLSGARC
SEQ ID NO: 233	IgG Kappa light chain signal sequences:	MKYLLPTAAAGLLLLAAQPAMA
SEQ ID NO: 234	Gaussia luciferase	MGVKVLFALICIAVAEA
SEQ ID NO: 235	Human albumin	MKWVTFISLLFLFSSAYS
SEQ ID NO: 236	Human chymotrypsinogen	MAFLWLLSCWALLGTTFG
SEQ ID NO: 237	Human interleukin-2	MQLLSCIALILALV
SEQ ID NO: 238	Human trypsinogen-2	MNLLLILTFVAAAVA

[0335] In some embodiments of a secretable variant PD-L1 immunomodulatory protein, the immunomodulatory protein comprises a signal peptide when expressed, and the signal peptide (or a portion thereof) is cleaved from the immunomodulatory protein upon secretion.

[0336] In some embodiments, the engineered cells express a variant PD-L1 polypeptides that are secreted from the cell. In some embodiments, such a variant PD-L1 polypeptide is encoded by a nucleic acid molecule encoding an immunomodulatory protein under the operable control of a signal sequence for secretion. In some embodiments, the encoded immunomodulatory protein is secreted when expressed from a cell. In some embodiments, the immunomodulatory protein encoded by the nucleic acid molecule does not comprise a transmembrane domain. In some embodiments, the immunomodulatory protein encoded by the nucleic acid molecule does not comprise a half-life extending moiety (such as an Fc domain or a multimerization domain). In some embodiments, the immunomodulatory protein encoded by the nucleic acid molecule comprises a signal peptide. In some embodiments, a nucleic acid of the invention further comprises nucleotide sequence that encodes a secretory or signal peptide operably linked to the nucleic acid encoding the immunomodulatory protein, thereby allowing for secretion of the immunomodulatory protein

3. Cells and Engineering Cells

[0337] Provided herein are engineered cells expressing any of the provided immunomodulatory polypeptide. In some embodiments, the engineered cells express on their surface any of the provided transmembrane immunomodulatory polypeptides. In some embodiments, the engineered cells express and are capable of or are able to secrete the immunomodulatory protein from the cells under conditions suitable for secretion of the protein. In some embodiments, the immunomodulatory protein is expressed on a lymphocyte such as a tumor infiltrating lymphocyte (TIL), T-cell or NK cell, or on a myeloid cell. In some embodiments, the engineered cells are antigen presenting cells (APCs). In some embodiments, the engineered cells are engineered mammalian T-cells or engineered mammalian antigen presenting cells (APCs). In some embodiments, the engineered T-cells or APCs are human or murine cells.

[0338] In some embodiments, engineered T-cells include, but are not limited to, T helper cell, cytotoxic T-cell (alternatively, cytotoxic T lymphocyte or CTL), natural killer T-cell, regulatory T-cell, memory T-cell, or gamma delta T-cell. In some embodiments, the engineered T cells are CD4+ or CD8+.

[0339] In some embodiments, the engineered APCs include, for example, MHC II expressing APCs such as macrophages, B cells, and dendritic cells, as well as artificial APCs

(aAPCs) including both cellular and acellular (e.g., biodegradable polymeric microparticles) aAPCs. Artificial APCs (aAPCs) are synthetic versions of APCs that can act in a similar manner to APCs in that they present antigens to T-cells as well as activate them. Antigen presentation is performed by the MHC (Class I or Class II). In some embodiments, in engineered APCs such as aAPCs, the antigen that is loaded onto the MHC is, in some embodiments, a tumor specific antigen or a tumor associated antigen. The antigen loaded onto the MHC is recognized by a T-cell receptor (TCR) of a T cell, which, in some cases, can express PD-1 or CD80 or other molecule recognized by the variant PD-L1 polypeptides provided herein. Materials which can be used to engineer an aAPC include: poly (glycolic acid), poly(lactic-co-glycolic acid), iron-oxide, liposomes, lipid bilayers, sepharose, and polystyrene.

[0340] In some embodiments a cellular aAPC can be engineered to contain a TIP and TCR agonist which is used in adoptive cellular therapy. In some embodiments, a cellular aAPC can be engineered to contain a TIP and TCR agonist which is used in ex vivo expansion of human T cells, such as prior to administration, e.g., for reintroduction into the patient. In some aspects, the aAPC may include expression of at least one anti-CD3 antibody clone, e.g. such as, for example, OKT3 and/or UCHT1. In some aspects, the aAPCs may be inactivated (e.g. irradiated). In some embodiment, the TIP can include any variant IgSF domain that exhibits binding affinity for a cognate binding partner on a T cell.

[0341] In some embodiments, an immunomodulatory protein provided herein, such as a transmembrane immunomodulatory protein or a secretable immunomodulatory protein, is co-expressed or engineered into a cell that expresses an antigen-binding receptor, such as a recombinant receptor, such as a chimeric antigen receptor (CAR) or T cell receptor (TCR). In some embodiments, the engineered cell, such as an engineered T cell, recognizes a desired antigen associated with cancer, inflammatory and autoimmune disorders, or a viral infection. In specific embodiments, the antigen-binding receptor contains an antigen-binding moiety that specifically binds a tumor specific antigen or a tumor associated antigen. In some embodiments, the engineered T-cell is a CAR (chimeric antigen receptor) T-cell that contains an antigen-binding domain (e.g. scFv) that specifically binds to an antigen, such as a tumor specific antigen or tumor associated antigen. Iin some embodiments, the TIP protein is expressed in an engineered T-cell receptor cell or and engineered chimeric antigen receptor cell. In such embodiments, the engineered cell co-expresses the TIP and the CAR or TCR. In some embodiments, the SIP protein is expressed in an engineered T-cell receptor cell or an engineered

chimeric antigen receptor cell. In such embodiments, the engineered cell co-expresses the SIP and the CAR or TCR.

[0342] Chimeric antigen receptors (CARs) are recombinant receptors that include an antigen-binding domain (ectodomain), a transmembrane domain and an intracellular signaling region (endodomain) that is capable of inducing or mediating an activation signal to the T cell after the antigen is bound. In some example, CAR-expressing cells are engineered to express an extracellular single chain variable fragment (scFv) with specificity for a particular tumor antigen linked to an intracellular signaling part comprising an activating domain and, in some cases, a costimulatory domain. The costimulatory domain can be derived from, e.g., CD28, OX-40, 4-1BB/CD137, inducible T cell costimulator (ICOS). The activating domain can be derived from, e.g., CD3, such as CD3 zeta, epsilon, delta, gamma, or the like. In certain embodiments, the CAR is designed to have two, three, four, or more costimulatory domains. The CAR scFv can be designed to target an antigen expressed on a cell associated with a disease or condition, e.g. a tumor antigen, such as, for example, CD19, which is a transmembrane protein expressed by cells in the B cell lineage, including all normal B cells and B cell malignances, including but not limited to NHL, CLL, and non-T cell ALL. Example CAR+ T cell therapies and constructs are described in U.S. Patent Publication Nos. 2013/0287748, 2014/0227237, 2014/0099309, and 2014/0050708, and these references are incorporated by reference in their entirety.

[0343] In some aspects, the antigen-binding domain is an antibody or antigen-binding fragment thereof, such as a single chain fragment (scFv). In some embodiments, the antigen is expressed on a tumor or cancer cell. Exemplary of an antigen is CD19. Exemplary of a CAR is an anti-CD19 CAR, such as a CAR containing an anti-CD19 scFv set forth in SEQ ID NO:1163 or SEQ ID NO:1174. In some embodiments, the CAR further contains a spacer, a transmembrane domain, and an intracellular signaling domain or region comprising an ITAM signaling domain, such as a CD3zeta signaling domain. In some embodiments, the CAR further includes a costimulatory signaling domain.

[0344] In some embodiments, the spacer and transmembrane domain are the hinge and transmembrane domain derived from CD8, such as having an exemplary sequence set forth in SEQ ID NO: 242, 1164, 2014 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 242, 1164, or 2014. In some embodiments, the endodomain comprises at CD3-zeta signaling domain. In some embodiments, the CD3-zeta signaling domain comprises the

sequence of amino acids set forth in SEQ ID NO: 243 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to SEQ ID NO:243 and retains the activity of T cell signaling. In some embodiments, the endodomain of a CAR can further comprise a costimulatory signaling region to further modulate immunomodulatory responses of the T-cell. In some embodiments, the costimulatory signaling domain is or comprises a costimulatory region, or is derived from a costimulatory region, of CD28, ICOS, 41BB or OX40. In some embodiments, the costimulatory signaling domain is a derived from CD28 or 4-1BB and comprises the sequence of amino acids set forth in any of SEQ ID NOS: 1165-1168 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to SEQ ID NO:1165-1168 and retains the activity of T cell costimulatory signaling.

[0345] In some embodiments, the construct encoding the CAR further encodes a second protein, such as a marker, e.g. detectable protein, separated from the CAR by a self-cleaving peptide sequence. In some embodiments, the self-cleaving peptide sequence is an F2A, T2A, E2A or P2A self-cleaving peptide. Exemplary sequences of a T2A self-cleaving peptide are set for the in any one of SEQ ID NOS: 1167, 1177 or 2021 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to any of SEQ ID NOS: 1167, 1177 or 2021. In some embodiments, the T2A is encoded by the sequence of nucleotides set forth in SEQ ID NO:1176 or a sequence that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to any of SEQ ID NO: 1176. An exemplary sequence of a P2A self-cleaving peptide is set in SEQ ID NO: 2026 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to SEQ ID NOS: 2026. In some cases, a nucleic acid construct that encodes more than one P2A self-cleaving peptide (such as a P2A1 and P2A2), in which the nucleotide sequence P2A1 and P2A2 each encode the P2A set forth in SEQ ID NO:2026, the nucleotide sequence may be different to avoid recombination between sequences.

[0346] In some embodiments, the marker is a detectable protein, such as a fluorescent protein, e.g. a green fluorescent protein (GFP) or blue fluorescent protein (BFP). Exemplary sequences of a fluorescent protein marker are set forth in SEQ ID NO: 1170, 2020, 2027-2029 or

a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to SEQ ID NO: 1170 or 2020.

[0347] In some embodiments, the CAR has the sequence of amino acids set forth in any of SEQ ID NOS: 1160, 1171, 1172, 1173, 2015, 2016, 2018 or 2019 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to any one of SEQ ID NOS: 1160, 1171, 1172, 1173, 2015, 2016, 2018 or 2019. In some embodiments, the CAR is encoded by a sequence of nucleotides set forth in SEQ ID NO: 1175 or 2017 or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to any one of SEQ ID NO: 1175 or 2017.

[0348] In another embodiment, the engineered T-cell possesses a TCR, including a recombinant or engineered TCR. In some embodiments, the TCR can be a native TCR. Those of skill in the art will recognize that generally native mammalian T-cell receptors comprise an alpha and a beta chain (or a gamma and a delta chain) involved in antigen specific recognition and binding. In some embodiments, the TCR is an engineered TCR that is modified. In some embodiments, the TCR of an engineered T-cell specifically binds to a tumor associated or tumor specific antigen presented by an APC.

[0349] In some embodiments, the immunomodulatory polypeptides, such as transmembrane immunomodulatory polypeptides or secretable immunomodulatory polypeptides, can be incorporated into engineered cells, such as engineered T cells or engineered APCs, by a variety of strategies such as those employed for recombinant host cells. A variety of methods to introduce a DNA construct into primary T cells are known in the art. In some embodiments, viral transduction or plasmid electroporation are employed. In typical embodiments, the nucleic acid molecule encoding the immunomodulatory protein, or the expression vector, comprises a signal peptide that localizes the expressed transmembrane immunomodulatory proteins to the cellular membrane or for secretion. In some embodiments, a nucleic acid encoding a transmembrane immunomodulatory proteins of the invention is sub-cloned into a viral vector, such as a retroviral vector, which allows expression in the host mammalian cell. The expression vector can be introduced into a mammalian host cell and, under host cell culture conditions, the immunomodulatory protein is expressed on the surface or is secreted.

[0350] In an exemplary example, primary T-cells can be purified ex vivo (CD4 cells or CD8 cells or both) and stimulated with an activation protocol consisting of various TCR/CD28 agonists, such as anti-CD3/anti-CD28 coated beads. After a 2 or 3 day activation process, a recombinant expression vector containing an immunomodulatory polypeptide can be stably introduced into the primary T cells through art standard lentiviral or retroviral transduction protocols or plasmid electroporation strategies. Cells can be monitored for immunomodulatory polypeptide expression by, for example, flow cytometry using anti-epitope tag or antibodies that cross-react with native parental molecule and polypeptides comprising variant PD-L1. T-cells that express the immunomodulatory polypeptide can be enriched through sorting with anti-epitope tag antibodies or enriched for high or low expression depending on the application.

[0351] Upon immunomodulatory polypeptide expression the engineered T-cell can be assayed for appropriate function by a variety of means. The engineered CAR or TCR co-expression can be validated to show that this part of the engineered T cell was not significantly impacted by the expression of the immunomodulatory protein. Once validated, standard in vitro cytotoxicity, proliferation, or cytokine assays (e.g., IFN-gamma expression) can be used to assess the function of engineered T-cells. Exemplary standard endpoints are percent lysis of the tumor line, proliferation of the engineered T-cell, or IFN-gamma protein expression in culture supernatants. An engineered construct which results in statistically significant increased lysis of tumor line, increased proliferation of the engineered T-cell, or increased IFN-gamma expression over the control construct can be selected for. Additionally, non-engineered, such as native primary or endogenous T-cells could also be incorporated into the same in vitro assay to measure the ability of the immunomodulatory polypeptide construct expressed on the engineered cells, such as engineered T-cells, to modulate activity, including, in some cases, to activate and generate effector function in bystander, native T-cells. Increased expression of activation markers such as CD69, CD44, or CD62L could be monitored on endogenous T cells, and increased proliferation and/or cytokine production could indicate desired activity of the immunomodulatory protein expressed on the engineered T cells.

[0352] In some embodiments, the similar assays can be used to compare the function of engineered T cells containing the CAR or TCR alone to those containing the CAR or TCR and a TIP construct. Typically, these in vitro assays are performed by plating various ratios of the engineered T cell and a "tumor" cell line containing the cognate CAR or TCR antigen together in culture. Standard endpoints are percent lysis of the tumor line, proliferation of the engineered T

cell, or IFN-gamma production in culture supernatants. An engineered immunomodulatory protein which resulted in statistically significant increased lysis of tumor line, increased proliferation of the engineered T cell, or increased IFN-gamma production over the same TCR or CAR construct alone can be selected for. Engineered human T cells can be analyzed in immunocompromised mice, like the NSG strain, which lacks mouse T, NK and B cells. Engineered human T cells in which the CAR or TCR binds a target counter-structure on the xenograft and is co-expressed with the TIP affinity modified IgSF domain can be adoptively transferred in vivo at different cell numbers and ratios compared to the xenograft. For example, engraftment of CD19+ leukemia tumor lines containing a luciferase/GFP vector can be monitored through bioluminescence or ex vivo by flow cytometry. In a common embodiment, the xenograft is introduced into the murine model, followed by the engineered T cells several days later. Engineered T cells containing the immunomodulatory protein can be assayed for increased survival, tumor clearance, or expanded engineered T cells numbers relative to engineered T cells containing the CAR or TCR alone. As in the in vitro assay, endogenous, native (i.e., non-engineered) human T cells could be co-adoptively transferred to look for successful epitope spreading in that population, resulting in better survival or tumor clearance.

E. Infectious Agents Expressing Variant Polypeptides and Immunomodulatory Proteins

[0353] Also provided are infectious agents that contain nucleic acids encoding any of the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable or transmembrane immunomodulatory proteins described herein. In some embodiments, such infectious agents can deliver the nucleic acids encoding the variant immunomodulatory polypeptides described herein, such as PD-L1 vIgD polypeptides, to a target cell in a subject, e.g., immune cell and/or antigen-presenting cell (APC) or tumor cell in a subject. Also provided are nucleic acids contained in such infectious agents, and/or nucleic acids for generation or modification of such infectious agents, such as vectors and/or plasmids, and compositions containing such infectious agents.

[0354] In some embodiments, the infectious agent is a microorganism or a microbe. In some embodiments, the infectious agent is a virus or a bacterium. In some embodiments, the infectious agent is a virus. In some embodiments, the infectious agent is a bacterium. In some embodiments, such infectious agents can deliver nucleic acid sequences encoding any of the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable or transmembrane immunomodulatory proteins, described herein. Thus, in some embodiments, the cell in a subject

that is infected or contacted by the infectious agents can be rendered to express on the cell surface or secrete, the variant immunomodulatory polypeptides. In some embodiments, the infectious agent can also deliver one or more other therapeutics or nucleic acids encoding other therapeutics to the cell and/or to an environment within the subject. In some embodiments, other therapeutics that can be delivered by the infectious agents include cytokines or other immunomodulatory molecules.

[0355] In some embodiments, the infectious agent, e.g., virus or bacteria, contains nucleic acid sequences that encode any of the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable or transmembrane immunomodulatory proteins, described herein, and by virtue of contact and/or infection of a cell in the subject, the cell expresses the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable or transmembrane immunomodulatory proteins, encoded by the nucleic acid sequences contained in the infectious agent. In some embodiments, the infectious agent can be administered to the subject. In some embodiments, the infectious agent can be contacted with cells from the subject *ex vivo*.

[0356] In some embodiments, the variant polypeptides, such as PD-L1 vIgD polypeptides, including transmembrane immunomodulatory proteins, expressed by the cell infected by the infectious agent is a transmembrane protein and is surface expressed. In some embodiments, the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable immunomodulatory proteins, expressed by the cell infected by the infectious agent is expressed and secreted from the cell. The transmembrane immunomodulatory protein or secreted immunomodulatory protein can be any described herein.

[0357] In some embodiments, the cells in the subject that are targeted by the infectious agent include a tumor cell, an immune cell, and/or an antigen-presenting cell (APC). In some embodiments, the infectious agent targets a cell in the tumor microenvironment (TME). In some embodiments, the infectious agent delivers the nucleic acids encoding the variant polypeptides, such as PD-L1 vIgD polypeptides, including secretable or transmembrane immunomodulatory proteins, to an appropriate cell (for example, an APC, such as a cell that displays a peptide/MHC complex on its cell surface, such as a dendritic cell) or tissue (e.g., lymphoid tissue) that will induce and/or augment the desired effect, e.g., immunomodulation and/or a specific cell-medicated immune response, e.g., CD4 and/or CD8 T cell response, which CD8 T cell response may include a cytotoxic T cell (CTL) response. In some embodiments, the infectious agent targets an APC, such as a dendritic cell (DC). In some embodiments, the nucleic acid molecule

delivered by the infectious agents described herein include appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequences encoding the variant immunomodulatory polypeptides, in a particular target cell, e.g., regulatory elements such as promoters.

[0358] In some embodiments, the infectious agent that contains nucleic acid sequences encoding the immunomodulatory polypeptides can also contain nucleic acid sequences that encode one or more additional gene products, e.g., cytokines, prodrug converting enzymes, cytotoxins and/or detectable gene products. For example, in some embodiments, the infectious agent is an oncolytic virus and the virus can include nucleic acid sequences encoding additional therapeutic gene products (see, e.g., Kirn et al., (2009) Nat Rev Cancer 9:64-71; Garcia-Aragoncillo et al., (2010) Curr Opin Mol Ther 12:403-411; see U.S. Pat. Nos. 7,588,767, 7,588,771, 7,662,398 and 7,754,221 and U.S. Pat. Publ. Nos. 2007/0202572, 2007/0212727, 2010/0062016, 2009/0098529, 2009/0053244, 2009/0155287, 2009/0117034, 2010/0233078, 2009/0162288, 2010/0196325, 2009/0136917 and 2011/0064650. In some embodiments, the additional gene product can be a therapeutic gene product that can result in death of the target cell (e.g., tumor cell) or gene products that can augment or boost or regulate an immune response (e.g., cytokine). Exemplary gene products also include among an anticancer agent, an anti-metastatic agent, an antiangiogenic agent, an immunomodulatory molecule, an immune checkpoint inhibitor, an antibody, a cytokine, a growth factor, an antigen, a cytotoxic gene product, a pro-apoptotic gene product, an anti-apoptotic gene product, a cell matrix degradative gene, genes for tissue regeneration or reprogramming human somatic cells to pluripotency, and other genes described herein or known to one of skill in the art. In some embodiments, the additional gene product is Granulocyte-macrophage colony-stimulating factor (GM-CSF).

1. Viruses

[0359] In some embodiments, the infectious agent is a virus. In some embodiments, the infectious agent is an oncolytic virus, or a virus that targets particular cells, e.g., immune cells. In some embodiments, the infectious agent targets a tumor cell and/or cancer cell in the subject. In some embodiments, the infectious agent targets an immune cell or an antigen-presenting cell (APC).

[0360] In some embodiments, the infectious agent is an oncolytic virus. Oncolytic viruses are viruses that accumulate in tumor cells and replicate in tumor cells. By virtue of replication in the

cells, and optional delivery of nucleic acids encoding variant PD-L1 polypeptide or immunomodulatory polypeptides described herein, tumor cells are lysed, and the tumor shrinks and can be eliminated. Oncolytic viruses can also have a broad host and cell type range. For example, oncolytic viruses can accumulate in immunoprivileged cells or immunoprivileged tissues, including tumors and/or metastases, and also including wounded tissues and cells, thus allowing the delivery and expression of nucleic acids encoding the variant immunomodulatory polypeptides described herein in a broad range of cell types. Oncolytic viruses can also replicate in a tumor cell specific manner, resulting in tumor cell lysis and efficient tumor regression.

[0361] Exemplary oncolytic viruses include adenoviruses, adeno-associated viruses, herpes viruses, Herpes Simplex Virus, Vesticular Stomatic virus, Reovirus, Newcastle Disease virus, parvovirus, measles virus, vesticular stomatitis virus (VSV), Coxsackie virus and Vaccinia virus. In some embodiments, oncolytic viruses can specifically colonize solid tumors, while not infecting other organs, and can be used as an infectious agent to deliver the nucleic acids encoding the variant immunomodulatory polypeptides described herein to such solid tumors.

[0362] Oncolytic viruses for use in delivering the nucleic acids encoding variant PD-L1 polypeptides or immunomodulatory polypeptides described herein, can be any of those known to one of skill in the art and include, for example, vesicular stomatitis virus, see, e.g., U.S. Pat. Nos. 7,731,974, 7,153,510, 6,653,103 and U.S. Pat. Pub. Nos. 2010/0178684, 2010/0172877, 2010/0113567, 2007/0098743, 20050260601, 20050220818 and EP Pat. Nos. 1385466, 1606411 and 1520175; herpes simplex virus, see, e.g., U.S. Pat. Nos. 7,897,146, 7,731,952, 7,550,296, 7,537,924, 6,723,316, 6,428,968 and U.S. Pat. Pub. Nos., 2014/0154216, 2011/0177032, 2011/0158948, 2010/0092515, 2009/0274728, 2009/0285860, 2009/0215147, 2009/0010889, 2007/0110720, 2006/0039894, 2004/0009604, 2004/0063094, International Patent Pub. Nos., WO 2007/052029, WO 1999/038955; retroviruses, see, e.g., U.S. Pat. Nos. 6,689,871, 6,635,472, 5,851,529, 5,716,826, 5,716,613 and U.S. Pat. Pub. No. 20110212530; vaccinia viruses, see, e.g., 2016/0339066, and adeno-associated viruses, see, e.g., U.S. Pat. Nos. 8,007,780, 7,968,340, 7,943,374, 7,906,111, 7,927,585, 7,811,814, 7,662,627, 7,241,447, 7,238,526, 7,172,893, 7,033,826, 7,001,765, 6,897,045, and 6,632,670.

[0363] Oncolytic viruses also include viruses that have been genetically altered to attenuate their virulence, to improve their safety profile, enhance their tumor specificity, and they have also been equipped with additional genes, for example cytotoxins, cytokines, prodrug converting enzymes to improve the overall efficacy of the viruses (see, e.g., Kirn et al., (2009) Nat Rev

Cancer 9:64-71; Garcia-Aragoncillo et al., (2010) Curr Opin Mol Ther 12:403-411; see U.S. Pat. Nos. 7,588,767, 7,588,771, 7,662,398 and 7,754,221 and U.S. Pat. Publ. Nos. 2007/0202572, 2007/0212727, 2010/0062016, 2009/0098529, 2009/0053244, 2009/0155287, 2009/0117034, 2010/0233078, 2009/0162288, 2010/0196325, 2009/0136917 and 2011/0064650). In some embodiments, the oncolytic viruses can be those that have been modified so that they selectively replicate in cancerous cells, and, thus, are oncolytic. For example, the oncolytic virus is an adenovirus that has been engineered to have modified tropism for tumor therapy and also as gene therapy vectors. Exemplary of such is ONYX-015, H101 and Ad5ΔCR (Hallden and Portella (2012) Expert Opin Ther Targets, 16:945-58) and TNFerade (McLoughlin et al. (2005) Ann. Surg. Oncol., 12:825-30), or a conditionally replicative adenovirus Oncorine®.

[0364] In some embodiments, the infectious agent is a modified herpes simplex virus. In some embodiments, the infectious agent is a modified version of Talimogene laherparepvec (also known as T-Vec, Imlygic or OncoVex GM-CSF), that is modified to contain nucleic acids encoding any of the variant immunomodulatory polypeptides described herein, such as variant PD-L1 polypeptide described herein. In some embodiments, the infectious agent is a modified herpes simplex virus that is described, e.g., in WO 2007/052029, WO 1999/038955, US 2004/0063094, US 2014/0154216, or, variants thereof.

[0365] In some embodiments, the infectious agent is a virus that targets a particular type of cells in a subject that is administered the virus, e.g., a virus that targets immune cells or antigen-presenting cells (APCs). Dendritic cells (DCs) are essential APCs for the initiation and control of immune responses. DCs can capture and process antigens, migrate from the periphery to a lymphoid organ, and present the antigens to resting T cells in a major histocompatibility complex (MHC)-restricted fashion. In some embodiments, the infectious agent is a virus that specifically can target DCs to deliver nucleic acids encoding the variant PD-L1 polypeptides or immunomodulatory polypeptides for expression in DCs. In some embodiments, the virus is a lentivirus or a variant or derivative thereof, such as an integration-deficient lentiviral vector. In some embodiments, the virus is a lentivirus that is pseudotyped to efficiently bind to and productively infect cells expressing the cell surface marker dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin (DC-SIGN), such as DCs. In some embodiments, the virus is a lentivirus pseudotyped with a Sindbis virus E2 glycoprotein or modified form thereof, such as those described in WO 2013/149167. In some embodiments, the virus allows for delivery and expression of a sequence of interest (e.g., a nucleic acid encoding any of the variant

PD-L1 polypeptides or immunomodulatory polypeptides described herein) to a DC. In some embodiments, the virus includes those described in WO 2008/011636 or US 2011/0064763, Tareen et al. (2014) Mol. Ther., 22:575-587, or variants thereof. Exemplary of a dendritic cell-tropic vector platform is ZVex™.

2. Bacteria

[0366] In some embodiments, the infectious agent is a bacterium. For example, in some embodiments, the bacteria can deliver nucleic acids encoding any of the variant immunomodulatory polypeptides described herein to a target cell in the subject, such as a tumor cell, an immune cell, an antigen-presenting cell and/or a phagocytic cell. In some embodiments, the bacterium can be preferentially targeted to a specific environment within a subject, such as a tumor microenvironment (TME), for expression and/or secretion of the variant immunomodulatory polypeptides and/or to target specific cells in the environment for expression of the variant immunomodulatory polypeptides.

[0367] In some embodiments, the bacterium delivers the nucleic acids to the cells via bacterial-mediated transfer of plasmid DNA to mammalian cells (also referred to as "bactofection"). For example, in some embodiments, delivery of genetic material is achieved through entry of the entire bacterium into target cells. In some embodiments, spontaneous or induced bacterial lysis can lead to the release of plasmid for subsequent eukaryotic cell expression. In some embodiments, the bacterium can deliver nucleic acids to non-phagocytic mammalian cells (e.g., tumor cells) and/or to phagocytic cells, e.g., certain immune cells and/or APCs. In some embodiments, the nucleic acids delivered by the bacterium can be transferred to the nucleus of the cell in the subject for expression. In some embodiments, the nucleic acids also include appropriate nucleic acid sequences necessary for the expression of the operably linked sequences encoding the variant immunomodulatory polypeptides in a particular host cell, e.g., regulatory elements such as promoters or enhancers. In some embodiments, the infectious agent that is a bacterium can deliver nucleic acids encoding the immunomodulatory proteins in the form of an RNA, such as a pre-made translation-competent RNA delivered to the cytoplasm of the target cell for translation by the target cell's machinery.

[0368] In some embodiments, the bacterium can replicate and lyse the target cells, e.g., tumor cells. In some embodiments, the bacterium can contain and/or release nucleic acid sequences and/or gene products in the cytoplasm of the target cells, thereby killing the target cell, e.g.,

tumor cell. In some embodiments, the infectious agent is bacterium that can replicate specifically in a particular environment in the subject, e.g., tumor microenvironment (TME). For example, in some embodiments, the bacterium can replicate specifically in anaerobic or hypoxic microenvironments. In some embodiments, conditions or factors present in particular environments, e.g., aspartate, serine, citrate, ribose or galactose produced by cells in the TME, can act as chemoattractants to attract the bacterium to the environment. In some embodiments, the bacterium can express and/or secrete the immunomodulatory proteins described herein in the environment, e.g., TME.

[0369] In some embodiments, the infectious agent is a bacterium that is a Listeria sp., a Bifidobacterium sp., an Escherichia sp., a Clostridium sp., a Salmonella sp., a Shigella sp., a Vibrio sp. or a Yersinia sp. In some embodiments, the bacterium is selected from among one or more of *Listeria monocytogenes, Salmonella typhimurium, Salmonella choleraesuis, Escherichia coli, Vibrio cholera, Clostridium perfringens, Clostridium butyricum, Clostridium novyi, Clostridium acetobutylicum, Bifidobacterium infantis, Bifidobacterium longum* and *Bifidobacterium adolescentis.* In some embodiments, the bacterium is an engineered bacterium. In some embodiments, the bacterium is an engineered bacterium such as those described in, e.g., Seow and Wood (2009) Molecular Therapy 17(5):767–777; Baban et al. (2010) Bioengineered Bugs 1:6, 385-394; Patyar et al. (2010) J Biomed Sci 17:21; Tangney et al. (2010) Bioengineered Bugs 1:4, 284-287; van Pijkeren et al. (2010) Hum Gene Ther. 21(4):405-416; WO 2012/149364; WO 2014/198002; US 9103831; US 9453227; US 2014/0186401; US 2004/0146488; US 2011/0293705; US 2015/0359909 and EP 3020816. The bacterium can be modified to deliver nucleic acid sequences encoding any of the variant immunomodulatory polypeptides, conjugates and/or fusions provided herein, and/or to express such variant immunomodulatory polypeptides in the subject.

F. Nucleic Acids, Vectors and Methods for Producing the Polypeptides or Cells

[0370] Provided herein are isolated or recombinant nucleic acids collectively referred to as "nucleic acids" which encode any of the various provided embodiments of the variant PD-L1 polypeptides or immunomodulatory polypeptides provided herein. In some embodiments, nucleic acids provided herein, including all described below, are useful in recombinant production (e.g., expression) of variant PD-L1 polypeptides or immunomodulatory polypeptides provided herein. In some embodiments, nucleic acids provided herein, including all described below, are useful in expression of variant PD-L1 polypeptides or immunomodulatory polypeptides provided herein in

cells, such as in engineered cells, e.g. immune cells, or infectious agent cells. The nucleic acids provided herein can be in the form of RNA or in the form of DNA, and include mRNA, cRNA, recombinant or synthetic RNA and DNA, and cDNA. The nucleic acids provided herein are typically DNA molecules, and usually double-stranded DNA molecules. However, single-stranded DNA, single-stranded RNA, double-stranded RNA, and hybrid DNA/RNA nucleic acids or combinations thereof comprising any of the nucleotide sequences of the invention also are provided.

[0371] Also provided herein are recombinant expression vectors and recombinant host cells useful in producing the variant PD-L1 polypeptides or immunomodulatory polypeptides provided herein.

[0372] Also provided herein are engineered cells, such as engineered immune cells, containing any of the provided nucleic acids or encoded variant PD-L1 polypeptides or immunomodulatory polypeptides, such as any of the transmembrane immunomodulatory polypeptides or secretable immunomodulatory polypeptides.

[0373] Also provided herein are infectious agents, such as bacterial or viral cells, containing any of the provided nucleic acids or encoded variant PD-L1 polypeptides or immunomodulatory polypeptides, such as any of the transmembrane immunomodulatory polypeptides or secretable immunomodulatory polypeptides.

[0374] In any of the above provided embodiments, the nucleic acids encoding the immunomodulatory polypeptides provided herein can be introduced into cells using recombinant DNA and cloning techniques. To do so, a recombinant DNA molecule encoding an immunomodulatory polypeptide is prepared. Methods of preparing such DNA molecules are well known in the art. For instance, sequences coding for the peptides could be excised from DNA using suitable restriction enzymes. Alternatively, the DNA molecule could be synthesized using chemical synthesis techniques, such as the phosphoramidite method. Also, a combination of these techniques could be used. In some instances, a recombinant or synthetic nucleic acid may be generated through polymerase chain reaction (PCR). In some embodiments, a DNA insert can be generated encoding one or more variant PD-L1 polypeptides containing at least one affinity-modified IgSF domain and, in some embodiments, a signal peptide, a transmembrane domain and/or an endodomain in accord with the provided description. This DNA insert can be cloned into an appropriate transduction/transfection vector as is known to those of skill in the art. Also provided are expression vectors containing the nucleic acid molecules.

[0375] In some embodiments, the expression vectors are capable of expressing the immunomodulatory proteins in an appropriate cell under conditions suited to expression of the protein. In some aspects, nucleic acid molecule or an expression vector comprises the DNA molecule that encodes the immunomodulatory protein operatively linked to appropriate expression control sequences. Methods of effecting this operative linking, either before or after the DNA molecule is inserted into the vector, are well known. Expression control sequences include promoters, activators, enhancers, operators, ribosomal binding sites, start signals, stop signals, cap signals, polyadenylation signals, and other signals involved with the control of transcription or translation.

[0376] In some embodiments, expression of the immunomodulatory protein is controlled by a promoter or enhancer to control or regulate expression. The promoter is operably linked to the portion of the nucleic acid molecule encoding the variant polypeptide or immunomodulatory protein. In some embodiments, the promotor is a constitutively active promotor (such as a tissue-specific constitutively active promotor or other constitutive promotor). In some embodiments, the promotor is an inducible promotor, which may be responsive to an inducing agent (such as a T cell activation signal).

[0377] In some embodiments, a constitutive promoter is operatively linked to the nucleic acid molecule encoding the variant polypeptide or immunomodulatory protein. Exemplary constitutive promoters include the Simian vacuolating virus 40 (SV40) promoter, the cytomegalovirus (CMV) promoter, the ubiquitin C (UbC) promoter, and the EF-1 alpha (EF1a) promoter. In some embodiments, the constitutive promoter is tissue specific. For example, in some embodiments, the promoter allows for constitutive expression of the immunomodulatory protein in specific tissues, such as immune cells, lymphocytes, or T cells. Exemplary tissue-specific promoters are described in U.S. Patent No. 5,998,205, including, for example, a fetoprotein, DF3, tyrosinase, CEA, surfactant protein, and ErbB2 promoters.

[0378] In some embodiments, an inducible promoter is operatively linked to the nucleic acid molecule encoding the variant polypeptide or immunomodulatory protein such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. For example, the promoter can be a regulated promoter and transcription factor expression system, such as the published tetracycline-regulated systems or other regulatable systems (see, e.g. published International PCT Appl. No. WO 01/30843), to allow regulated expression of the encoded polypeptide. An exemplary regulatable promoter system is the Tet-On

(and Tet-Off) system available, for example, from Clontech (Palo Alto, CA). This promoter system allows the regulated expression of the transgene controlled by tetracycline or tetracycline derivatives, such as doxycycline. Other regulatable promoter systems are known (see e.g., published U.S. Application No. 2002-0168714, entitled "Regulation of Gene Expression Using Single-Chain, Monomeric, Ligand Dependent Polypeptide Switches," which describes gene switches that contain ligand binding domains and transcriptional regulating domains, such as those from hormone receptors).

[0379] In some embodiments, the promotor is responsive to an element responsive to T-cell activation signaling. Solely by way of example, in some embodiments, an engineered T cell comprises an expression vector encoding the immunomodulatory protein and a promotor operatively linked to control expression of the immunomodulatory protein. The engineered T cell can be activated, for example by signaling through an engineered T cell receptor (TCR) or a chimeric antigen rector (CAR), and thereby triggering expression and secretion of the immunomodulatory protein through the responsive promotor.

[0380] In some embodiments, an inducible promoter is operatively linked to the nucleic acid molecule encoding the immunomodulatory protein such that the immunomodulatory protein is expressed in response to a nuclear factor of activated T-cells (NFAT) or nuclear factor kappa-light-chain enhancer of activated B cells (NF-κB). For example, in some embodiments, the inducible promoter comprises a binding site for NFAT or NF-κB. For example, in some embodiments, the promoter is an NFAT or NF-κB promoter or a functional variant thereof. Thus, in some embodiments, the nucleic acids make it possible to control the expression of immunomodulatory protein while also reducing or eliminating the toxicity of the immunomodulatory protein. In particular, engineered immune cells comprising the nucleic acids of the invention express and secrete the immunomodulatory protein only when the cell (e.g., a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) expressed by the cell) is specifically stimulated by an antigen and/or the cell (e.g., the calcium signaling pathway of the cell) is non-specifically stimulated by, e.g., phorbol myristate acetate (PMA)/Ionomycin. Accordingly, the expression and, in some cases, secretion, of immunomodulatory protein can be controlled to occur only when and where it is needed (e.g., in the presence of an infectious disease-causing agent, cancer, or at a tumor site), which can decrease or avoid undesired immunomodulatory protein interactions.

[0381] In some embodiments, the nucleic acid encoding an immunomodulatory protein described herein comprises a suitable nucleotide sequence that encodes a NFAT promoter, NF-κB promoter, or a functional variant thereof. "NFAT promoter" as used herein means one or more NFAT responsive elements linked to a minimal promoter. "NF-κB promoter" refers to one or more NF-κB responsive elements linked to a minimal promoter. In some embodiments, the minimal promoter of a gene is a minimal human IL-2 promoter or a CMV promoter. The NFAT responsive elements may comprise, e.g., NFAT1, NFAT2, NFAT3, and/or NFAT4 responsive elements. The NFAT promoter, NF-κB promoter, or a functional variant thereof may comprise any number of binding motifs, e.g., at least two, at least three, at least four, at least five, or at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or up to twelve binding motifs.

[0382] The resulting recombinant expression vector having the DNA molecule thereon is used to transform an appropriate host. This transformation can be performed using methods well known in the art. In some embodiments, a nucleic acid provided herein further comprises nucleotide sequence that encodes a secretory or signal peptide operably linked to the nucleic acid encoding an immunomodulatory polypeptide such that a resultant soluble immunomodulatory polypeptide is recovered from the culture medium, host cell, or host cell periplasm. In other embodiments, the appropriate expression control signals are chosen to allow for membrane expression of an immunomodulatory polypeptide. Furthermore, commercially available kits as well as contract manufacturing companies can also be utilized to make engineered cells or recombinant host cells provided herein.

[0383] In some embodiments, the resulting expression vector having the DNA molecule thereon is used to transform, such as transduce, an appropriate cell. The introduction can be performed using methods well known in the art. Exemplary methods include those for transfer of nucleic acids encoding the receptors, including via viral, e.g., retroviral or lentiviral, transduction, transposons, and electroporation. In some embodiments, the expression vector is a viral vector. In some embodiments, the nucleic acid is transferred into cells by lentiviral or retroviral transduction methods.

[0384] Any of a large number of publicly available and well-known mammalian host cells, including mammalian T-cells or APCs, can be used in the preparing the polypeptides or engineered cells. The selection of a cell is dependent upon a number of factors recognized by the art. These include, for example, compatibility with the chosen expression vector, toxicity of the

peptides encoded by the DNA molecule, rate of transformation, ease of recovery of the peptides, expression characteristics, bio-safety and costs. A balance of these factors must be struck with the understanding that not all cells can be equally effective for the expression of a particular DNA sequence.

[0385] In some embodiments, the host cells can be a variety of eukaryotic cells, such as in yeast cells, or with mammalian cells such as Chinese hamster ovary (CHO) or HEK293 cells. In some embodiments, the host cell is a suspension cell and the polypeptide is engineered or produced in cultured suspension, such as in cultured suspension CHO cells, e.g. CHO-S cells. In some examples, the cell line is a CHO cell line that is deficient in DHFR (DHFR-), such as DG44 and DUXB11. In some embodiments, the cell is deficient in glutamine synthase (GS), e.g. CHO-S cells, CHOK1 SV cells, and CHOZN((R)) GS-/- cells. In some embodiments, the CHO cells, such as suspension CHO cells, may be CHO-S-2H2 cells, CHO-S-clone 14 cells, or ExpiCHO-S cells.

[0386] In some embodiments, host cells can also be prokaryotic cells, such as with *E. coli*. The transformed recombinant host is cultured under polypeptide expressing conditions, and then purified to obtain a soluble protein. Recombinant host cells can be cultured under conventional fermentation conditions so that the desired polypeptides are expressed. Such fermentation conditions are well known in the art. Finally, the polypeptides provided herein can be recovered and purified from recombinant cell cultures by any of a number of methods well known in the art, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, and affinity chromatography. Protein refolding steps can be used, as desired, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed in the final purification steps.

[0387] In some embodiments, the cell is an immune cell, such as any described above in connection with preparing engineered cells. In some embodiments, such engineered cells are primary cells. In some embodiments, the engineered cells are autologous to the subject. In some embodiment, the engineered cells are allogeneic to the subject. In some embodiments, the engineered cells are obtained from a subject, such as by leukapheresis, and transformed ex vivo for expression of the immunomodulatory polypeptide, e.g. transmembrane immunomodulatory polypeptide or secretable immunomodulatory polypeptide.

[0388] Also provided are nucleic acids encoding any of the variant immunomodulatory polypeptides contained in infectious agents described herein. In some embodiments, the infectious agents deliver the nucleic acids to a cell in the subject, and/or permit expression of the encoded variant polypeptides in the cell. Also provided are nucleic acids that are used to generate, produce or modify such infectious agents. For example, in some embodiments, provided are vectors and/or plasmids that contain nucleic acids encoding the variant immunomodulatory polypeptides, for generation of the infectious agents, delivery to the cells in a subject and/or expression of the variant immunomodulatory polypeptides in the cells in the subject.

[0389] In some embodiments, the provided nucleic acids are recombinant viral or bacterial vectors containing nucleic acid sequences encoding the variant immunomodulatory polypeptides. In some embodiments, the recombinant vectors can be used to produce an infectious agent that contains nucleic acid sequences encoding the variant immunomodulatory polypeptides and/or to be delivered to a target cell in the subject for expression by the target cell. In some embodiments, the recombinant vector is an expression vector. In some embodiments, the recombinant vector includes appropriate sequences necessary for generation and/or production of the infectious agent and expression in the target cell.

[0390] In some embodiments, the recombinant vector is a plasmid or cosmid. Plasmid or cosmid containing nucleic acid sequences encoding the variant immunomodulatory polypeptides, as described herein, is readily constructed using standard techniques well known in the art. For generation of the infectious agent, the vector or genome can be constructed in a plasmid form that can then be transfected into a packaging or producer cell line or a host bacterium. The recombinant vectors can be generated using any of the recombinant techniques known in the art. In some embodiments, the vectors can include a prokaryotic origin of replication and/or a gene whose expression confers a detectable or selectable marker such as a drug resistance for propagation and/or selection in prokaryotic systems.

[0391] In some embodiments, the recombinant vector is a viral vector. Exemplary recombinant viral vectors include a lentiviral vector genome, poxvirus vector genome, vaccinia virus vector genome, adenovirus vector genome, adenovirus-associated virus vector genome, herpes virus vector genome, and alpha virus vector genome. Viral vectors can be live, attenuated, replication conditional or replication deficient, non-pathogenic (defective), replication competent viral vector, and/or is modified to express a heterologous gene product, e.g., the variant

immunomodulatory polypeptides provided herein. Vectors for generation of viruses also can be modified to alter attenuation of the virus, which includes any method of increasing or decreasing the transcriptional or translational load.

[0392] Exemplary viral vectors that can be used include modified vaccinia virus vectors (see, e.g., Guerra et al., J. Virol. 80:985-98 (2006); Tartaglia et al., AIDS Research and Human Retroviruses 8: 1445-47 (1992); Gheradi et al., J. Gen. Virol. 86:2925-36 (2005); Mayr et al., Infection 3:6-14 (1975); Hu et al., J. Virol. 75: 10300-308 (2001); U.S. Patent Nos. 5,698,530, 6,998,252, 5,443,964, 7,247,615 and 7,368,116); adenovirus vector or adenovirus-associated virus vectors (see., e.g., Molin et al., J. Virol. 72:8358-61 (1998); Narumi et al., Am J. Respir. Cell Mol. Biol. 19:936-41 (1998); Mercier et al., Proc. Natl. Acad. Sci. USA 101:6188-93 (2004); U.S. Patent Nos. 6,143,290; 6,596,535; 6,855,317; 6,936,257; 7,125,717; 7,378,087; 7,550,296); retroviral vectors including those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), ecotropic retroviruses, simian immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations (see, e.g., Buchscher et al., J. Virol. 66:2731-39 (1992); Johann et al., J. Virol. 66: 1635-40 (1992); Sommerfelt et al., Virology 176:58-59 (1990); Wilson et al., J. Virol. 63:2374-78 (1989); Miller et al., J. Virol. 65:2220-24 (1991); Miller et al., Mol. Cell Biol. 10:4239 (1990); Kolberg, NIH Res. 4:43 1992; Cornetta et al., Hum. Gene Ther. 2:215 (1991)); lentiviral vectors including those based upon Human Immunodeficiency Virus (HIV-1), HIV-2, feline immunodeficiency virus (FIV), equine infectious anemia virus, Simian Immunodeficiency Virus (SIV), and maedi/visna virus (see, e.g., Pfeifer et al., Annu. Rev. Genomics Hum. Genet. 2: 177-211 (2001); Zufferey et al., J. Virol. 72: 9873, 1998; Miyoshi et al., J. Virol. 72:8150, 1998; Philpott and Thrasher, Human Gene Therapy 18:483, 2007; Engelman et al., J. Virol. 69: 2729, 1995; Nightingale et al., Mol. Therapy, 13: 1121, 2006; Brown et al., J. Virol. 73:9011 (1999); WO 2009/076524; WO 2012/141984; WO 2016/011083; McWilliams et al., J. Virol. 77: 11150, 2003; Powell et al., J. Virol. 70:5288, 1996) or any, variants thereof, and/or vectors that can be used to generate any of the viruses described above. In some embodiments, the recombinant vector can include regulatory sequences, such as promoter or enhancer sequences, that can regulate the expression of the viral genome, such as in the case for RNA viruses, in the packaging cell line (see, e.g., U.S. Patent Nos.5,385,839 and 5,168,062).

[0393] In some embodiments, the recombinant vector is an expression vector, e.g., an expression vector that permits expression of the encoded gene product when delivered into the

target cell, e.g., a cell in the subject, e.g., a tumor cell, an immune cell and/or an APC. In some embodiments, the recombinant expression vectors contained in the infectious agent are capable of expressing the immunomodulatory proteins in the target cell in the subject, under conditions suited to expression of the protein.

[0394] In some aspects, nucleic acids or an expression vector comprises a nucleic acid sequence that encodes the immunomodulatory protein operatively linked to appropriate expression control sequences. Methods of affecting this operative linking, either before or after the nucleic acid sequence encoding the immunomodulatory protein is inserted into the vector, are well known. Expression control sequences include promoters, activators, enhancers, operators, ribosomal binding sites, start signals, stop signals, cap signals, polyadenylation signals, and other signals involved with the control of transcription or translation. The promoter can be operably linked to the portion of the nucleic acid sequence encoding the immunomodulatory protein. In some embodiments, the promotor is a constitutively active promotor in the target cell (such as a tissue-specific constitutively active promotor or other constitutive promotor). For example, the recombinant expression vector may also include, lymphoid tissue-specific transcriptional regulatory elements (TRE) such as a B lymphocyte, T lymphocyte, or dendritic cell specific TRE. Lymphoid tissue specific TRE are known in the art (see, e.g., Thompson et al., Mol. Cell. Biol. 12:1043-53 (1992); Todd et al., J. Exp. Med. 177:1663-74 (1993); Penix et al., J. Exp. Med. 178:1483-96 (1993)). In some embodiments, the promotor is an inducible promotor, which may be responsive to an inducing agent (such as a T cell activation signal). In some embodiments, nucleic acids delivered to the target cell in the subject, e.g., tumor cell, immune cell and/or APC, can be operably linked to any of the regulatory elements described above.

[0395] In some embodiments, the vector is a bacterial vector, e.g., a bacterial plasmid or cosmid. In some embodiments, the bacterial vector is delivered to the target cell, e.g., tumor cells, immune cells and/or APCs, via bacterial-mediated transfer of plasmid DNA to mammalian cells (also referred to as "bactofection"). In some embodiments, the delivered bacterial vector also contains appropriate expression control sequences for expression in the target cells, such as a promoter sequence and/or enhancer sequences, or any regulatory or control sequences described above. In some embodiments, the bacterial vector contains appropriate expression control sequences for expression and/or secretion of the encoded variant polypeptides in the infectious agent, e.g., the bacterium.

[0396] In some embodiments, polypeptides provided herein can also be made by synthetic methods. Solid phase synthesis is the preferred technique of making individual peptides since it is the most cost-effective method of making small peptides. For example, well known solid phase synthesis techniques include the use of protecting groups, linkers, and solid phase supports, as well as specific protection and deprotection reaction conditions, linker cleavage conditions, use of scavengers, and other aspects of solid phase peptide synthesis. Peptides can then be assembled into the polypeptides as provided herein.

IV. METHODS OF ASSESSING ACTIVITY IMMUNE MODULATION OF VARIANT PD-L1 POLYPEPTIDES AND IMMUNOMODULATORY PROTEINS

[0397] In some embodiments, the variant PD-L1 polypeptides provided herein (e.g. full-length and/or specific binding fragments or conjugates, stack constructs or fusion thereof, engineered cells or infectious agents) exhibit immunomodulatory activity to modulate T cell activation. In some embodiments, PD-L1 polypeptides modulate IFN-gamma expression in a T cell assay relative to a wild-type or unmodified PD-L1 control. In some cases, modulation of IFN-gamma expression can increase or decrease IFN-gamma expression relative to the control. Assays to determine specific binding and IFN-gamma expression are well-known in the art and include the MLR (mixed lymphocyte reaction) assays measuring interferon-gamma cytokine levels in culture supernatants (Wang et al., Cancer Immunol Res. 2014 Sep: 2(9):846-56), SEB (staphylococcal enterotoxin B) T cell stimulation assay (Wang et al., Cancer Immunol Res. 2014 Sep: 2(9):846-56), and anti-CD3 T cell stimulation assays (Li and Kurlander, J Transl Med. 2010: 8: 104).

[0398] In some embodiments, a variant PD-L1 polypeptide can in some embodiments increase or, in alternative embodiments, decrease IFN-gamma (interferon-gamma) expression in a primary T-cell assay relative to a wild-type PD-L1 control. In some embodiments, such activity may depend on whether the variant PD-L1 polypeptide is provided in a form for antagonist activity or in a form for agonist activity. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein is an antagonist of the inhibitory receptor, such as blocks an inhibitory signal in the cell that may occur to decrease response to an activating stimuli, e.g. CD3 and/or CD28 costimulatory signal or a mitogenic signal. Those of skill will

recognize that different formats of the primary T-cell assay used to determine an increase or decrease in IFN-gamma expression exist.

[0399] In assaying for the ability of a variant PD-L1 to increase or decrease IFN-gamma expression in a primary T-cell assay, a Mixed Lymphocyte Reaction (MLR) assay can be used. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein provided in antagonist form, such as soluble form, e.g. variant PD-L1-Fc or secretable immunomodulatory protein, block activity of the PD-1 inhibitory receptor and thereby increase MLR activity in the assay, such as observed by increased production of IFN-gamma in the assay. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein provided in agonist form, such as a localizing vIgD stack or conjugate containing a tumor-localizing moiety or an engineered cell expressing a transmembrane immunomodulatory protein as provided, may stimulate activity of the PD-1 inhibitory receptor and thereby decrease MLR activity, such as evidenced by decreased IFN-gamma production. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein provided in agonist form, such as a localizing vIgD stack or conjugate containing a tumor-localizing moiety or an engineered cell expressing a transmembrane immunomodulatory protein as provided, may block activity of the PD-1 inhibitory receptor and thereby increase MLR activity, such as increase IFN-gamma production.

[0400] Alternatively, in assaying for the ability of a variant PD-L1 to modulate an increase or decrease IFN-gamma expression in a primary T-cell assay, a co-immobilization assay can be used. In a co-immobilization assay, a TCR signal, provided in some embodiments by anti-CD3 antibody, is used in conjunction with a co-immobilized variant PD-L1 to determine the ability to increase or decrease IFN-gamma expression relative to a PD-L1 unmodified or wild-type control. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein, e.g. a co-immobilized variant PD-L1 (e.g., PD-L1-Fc), decreases IFN-gamma production in a co-immobilization assay.

[0401] In some embodiments, in assaying for the ability of a variant PD-L1 to modulate an increase or decrease IFN-gamma expression a T cell reporter assay can be used. In some embodiments, the T cell is a Jurkat T cell line or is derived from Jurkat T cell lines. In reporter assays, the reporter cell line (e.g. Jurkat reporter cell) also is generated to overexpress an inhibitory receptor that is the cognate binding partner of the variant IgSF domain polypeptide. For example, in the case of a variant PD-L1, the reporter cell line (e.g. Jurkat reporter cell) is generated to overexpress PD-1. In some embodiments, the reporter T cells also contain a

reporter construct containing an inducible promoter responsive to T cell activation operably linked to a reporter. In some embodiments, the reporter is a fluorescent or luminescent reporter. In some embodiments, the reporter is luciferase. In some embodiments, the promoter is responsive to CD3 signaling. In some embodiments, the promoter is an NFAT promoter. In some embodiments, the promoter is responsive to costimulatory signaling, e.g. CD28 costimulatory signaling. In some embodiments, the promoter is an IL-2 promoter.

[0402] In aspects of a reporter assay, a reporter cell line is stimulated, such as by co-incubation with antigen presenting cells (APCs) expressing the wild-type ligand of the inhibitory receptor, e.g. PD-L1. In some embodiments, the APCs are artificial APCs. Artificial APCs are well known to a skilled artisan. In some embodiments, artificial APCs are derived from one or more mammalian cell line, such as K562, CHO or 293 cells.

[0403] In some embodiments, the Jurkat reporter cells are co-incubated with artificial APCs overexpressing the inhibitory ligand in the presence of the variant IgSF domain molecule or immunomodulatory protein, e.g., variant PD-L1 polypeptide or immunomodulatory protein. In some embodiments, reporter expression is monitored, such as by determining the luminescence or fluorescence of the cells. In some embodiments, normal interactions between its inhibitory receptor and ligand result in a repression of or decrease in the reporter signal, such as compared to control, e.g. reporter expression by co-incubation of control T cells and APCs in which the inhibitory receptor and ligand interaction is not present, e.g. APCs that do not overexpress PD-L1. In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein provided herein antagonizes the interaction, e.g. when provided in soluble form as a variant PD-L1-Fc or when expressed from the APC as a secretable immunomodulatory protein, thereby resulting in an increase in the reporter signal compared to the absence of the variant PD-L1 polypeptide or immunomodulatory protein. In some cases, certain formats of a variant PD-L1 polypeptide or immunomodulatory protein as provided herein may provide an agonist activity, thereby decreasing reporter expression compared to the absence of the variant PD-L1 polypeptide or immunomodulatory protein.,

[0404] Use of proper controls is known to those of skill in the art, however, in the aforementioned embodiments, a control typically involves use of the unmodified PD-L1, such as a wild-type of native PD-L1 isoform from the same mammalian species from which the variant PD-L1 was derived or developed. In some embodiments, the wild-type or native PD-L1 is of the same form or corresponding form as the variant. For example, if the variant PD-L1 is a soluble

form containing a variant ECD fused to an Fc protein, then the control is a soluble form containing the wild-type or native ECD of PD-L1 fused to the Fc protein. Irrespective of whether the binding affinity and/or selectivity to either one or more of PD-1 and CD80 is increased or decreased, a variant PD-L1 in some embodiments will increase IFN-gamma expression and, in alternative embodiments, decrease IFN-gamma expression in a T-cell assay relative to a wild-type PD-L1 control.

[0405] In some embodiments, a variant PD-L1 polypeptide or immunomodulatory protein, increases IFN-gamma expression (i.e., protein expression) relative to a wild-type or unmodified PD-L1 control by at least: 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or higher. In other embodiments, a variant PD-L1 or immunomodulatory protein decreases IFN-gamma expression (i.e. protein expression) relative to a wild-type or unmodified PD-L1 control by at least: 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or higher. In some embodiments, the wild-type PD-L1 control is murine PD-L1, such as would typically be used for a variant PD-L1 altered in sequence from that of a wild-type murine PD-L1 sequence. In some embodiments, the wild-type PD-L1 control is human PD-L1, such as would typically be used for a variant PD-L1 altered in sequence from that of a wild-type human PD-L1 sequence such as an PD-L1 sequence comprising the sequence of amino acids of SEQ ID NO: 30 or 1728, or SEQ ID NO: 55 or 309.

V. PHARMACEUTICAL FORMULATIONS

[0406] Provided herein are compositions containing any of the variant PD-L1 polypeptides, immunomodulatory proteins, conjugates, engineered cells or infectious agents described herein. The pharmaceutical composition can further comprise a pharmaceutically acceptable excipient. For example, the pharmaceutical composition can contain one or more excipients for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption, or penetration of the composition. In some aspects, a skilled artisan understands that a pharmaceutical composition containing cells may differ from a pharmaceutical composition containing a protein.

[0407] In some embodiments, the pharmaceutical composition is a solid, such as a powder, capsule, or tablet. For example, the components of the pharmaceutical composition can be lyophilized. In some embodiments, the solid pharmaceutical composition is reconstituted or dissolved in a liquid prior to administration.

[0408] In some embodiments, the pharmaceutical composition is a liquid, for example variant PD-L1 polypeptides dissolved in an aqueous solution (such as physiological saline or Ringer's solution). In some embodiments, the pH of the pharmaceutical composition is between about 4.0 and about 8.5 (such as between about 4.0 and about 5.0, between about 4.5 and about 5.5, between about 5.0 and about 6.0, between about 5.5 and about 6.5, between about 6.0 and about 7.0, between about 6.5 and about 7.5, between about 7.0 and about 8.0, or between about 7.5 and about 8.5).

[0409] In some embodiments, the pharmaceutical composition comprises a pharmaceutically-acceptable excipient, for example a filler, binder, coating, preservative, lubricant, flavoring agent, sweetening agent, coloring agent, a solvent, a buffering agent, a chelating agent, or stabilizer. Examples of pharmaceutically-acceptable fillers include cellulose, dibasic calcium phosphate, calcium carbonate, microcrystalline cellulose, sucrose, lactose, glucose, mannitol, sorbitol, maltol, pregelatinized starch, corn starch, or potato starch. Examples of pharmaceutically-acceptable binders include polyvinylpyrrolidone, starch, lactose, xylitol, sorbitol, maltitol, gelatin, sucrose, polyethylene glycol, methyl cellulose, or cellulose. Examples of pharmaceutically-acceptable coatings include hydroxypropyl methylcellulose (HPMC), shellac, corn protein zein, or gelatin. Examples of pharmaceutically-acceptable disintegrants include polyvinylpyrrolidone, carboxymethyl cellulose, or sodium starch glycolate. Examples of pharmaceutically-acceptable lubricants include polyethylene glycol, magnesium stearate, or stearic acid. Examples of pharmaceutically-acceptable preservatives include methyl parabens, ethyl parabens, propyl paraben, benzoic acid, or sorbic acid. Examples of pharmaceutically-acceptable sweetening agents include sucrose, saccharine, aspartame, or sorbitol. Examples of pharmaceutically-acceptable buffering agents include carbonates, citrates, gluconates, acetates, phosphates, or tartrates.

[0410] In some embodiments, the pharmaceutical composition further comprises an agent for the controlled or sustained release of the product, such as injectable microspheres, bio-erodible particles, polymeric compounds (polylactic acid, polyglycolic acid), beads, or liposomes.

[0411] In some embodiments, the pharmaceutical composition is sterile. Sterilization may be accomplished by filtration through sterile filtration membranes or radiation. Where the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. The composition for parenteral administration may be stored in lyophilized form or in solution. In addition, parenteral compositions generally are

placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0412] In some embodiments, provided are pharmaceutical compositions containing the transmembrane immunomodulatory proteins, including engineered cells expressing such transmembrane immunomodulatory proteins. In some embodiments, the pharmaceutical compositions and formulations include one or more optional pharmaceutically acceptable carrier or excipient. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present invention are preferably formulated for intravenous administration.

[0413] Such a formulation may, for example, be in a form suitable for intravenous infusion. A pharmaceutically acceptable carrier may be a pharmaceutically acceptable material, composition, or vehicle that is involved in carrying or transporting cells of interest from one tissue, organ, or portion of the body to another tissue, organ, or portion of the body. For example, the carrier may be a liquid or solid filler, diluent, excipient, solvent, or encapsulating material, or some combination thereof. Each component of the carrier must be "pharmaceutically acceptable" in that it must be compatible with the other ingredients of the formulation. It also must be suitable for contact with any tissue, organ, or portion of the body that it may encounter, meaning that it must not carry a risk of toxicity, irritation, allergic response, immunogenicity, or any other complication that excessively outweighs its therapeutic benefits.

VI. ARTICLES OF MANUFACTURE AND KITS

[0414] Also provided herein are articles of manufacture comprising the pharmaceutical compositions described herein in suitable packaging. Suitable packaging for compositions (such as ophthalmic compositions) described herein are known in the art, and include, for example, vials (such as sealed vials), vessels, ampules, bottles, jars, flexible packaging (e.g., sealed Mylar or plastic bags), and the like. These articles of manufacture may further be sterilized and/or sealed.

[0415] Further provided are kits comprising the pharmaceutical compositions (or articles of manufacture) described herein, which may further comprise instruction(s) on methods of using the composition, such as uses described herein. The kits described herein may also include other

materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for performing any methods described herein.

VII. THERAPEUTIC APPLICATIONS

[0416] Provided herein are methods using the provided pharmaceutical compositions containing a variant PD-L1 polypeptide, immunomodulatory protein, conjugate engineered cell or infectious agent described herein, for modulating an immune response, including in connection with treating a disease or condition in a subject, such as in a human patient. The pharmaceutical compositions described herein (including pharmaceutical composition comprising the variant PD-L1 polypeptides, the immunomodulatory proteins, the conjugates, the engineered cells and the infectious agents described herein) can be used in a variety of therapeutic applications, such as the treatment of a disease. For example, in some embodiments the pharmaceutical composition is used to treat inflammatory or autoimmune disorders, cancer, organ transplantation, viral infections, and/or bacterial infections in a mammal. The pharmaceutical composition can modulate (e.g. increase or decrease) an immune response to treat the disease.

[0417] In some embodiments, the provided methods are applicable to therapeutic administration of variant PD-L1 polypeptides, the immunomodulatory proteins, the conjugates, the engineered cells and infectious agents described herein. It is within the level of a skilled artisan, in view of the provided disclosure, to choose a format for the indication depending on the type of modulation of the immune response, e.g. increase or decrease that is desired.

[0418] In some embodiments, a pharmaceutical composition provided herein that stimulates the immune response is administered, which can be useful, for example, in the treatment of cancer, viral infections, or bacterial infections. In some embodiments, the pharmaceutical composition contains a variant PD-L1 polypeptide in a format that exhibits antagonist activity of its cognate binding partner PD-1 and/or that inhibits costimulatory signaling via PD-1. Exemplary formats of PD-L1 polypeptide for use in connection with such therapeutic applications include, for example, a variant PD-L1 polypeptide that is soluble (e.g. variant PD-L1-Fc fusion protein), an immunomodulatory protein or "stack" of a variant PD-L1 polypeptide and another IgSF domain, including soluble forms thereof that are Fc fusions, an engineered cell expressing a secretable immunomodulatory protein, or an infectious agent comprising a nucleic acid molecule encoding a secretable immunomodulatory protein, such as for expression and

secretion of the secretable immunomodulatory protein in an infected cell (e.g. tumor cell or APC, e.g. dendritic cell). Among such methods are methods carried out by delivery of a variant PD-L1 polypeptide in a soluble format. Exemplary soluble formats are described herein, including formats in which an extracellular portion of a variant PD-L1 polypeptide containing an affinity modified IgSF domain (e.g. IgV) is linked, directly or indirectly, to a multimerization domain, e.g. an Fc domain or region. In some embodiments, such a therapeutic agent is a variant PD-L1-Fc fusion protein.

[0419] The provided methods to modulate an immune response can be used to treat a disease or condition, such as a tumor or cancer. In some embodiments, the pharmaceutical composition can be used to inhibit growth of mammalian cancer cells (such as human cancer cells). A method of treating cancer can include administering an effective amount of any of the pharmaceutical compositions described herein to a subject with cancer. The effective amount of the pharmaceutical composition can be administered to inhibit, halt, or reverse progression of cancers, including cancers that are sensitive to modulation of immunological activity, such as by the provided variants or immunomodulatory proteins. Human cancer cells can be treated in vivo, or ex vivo. In ex vivo treatment of a human patient, tissue or fluids containing cancer cells are treated outside the body and then the tissue or fluids are reintroduced back into the patient. In some embodiments, the cancer is treated in a human patient in vivo by administration of the therapeutic composition into the patient. Thus, the present invention provides ex vivo and in vivo methods to inhibit, halt, or reverse progression of the tumor, or otherwise result in a statistically significant increase in progression-free survival (i.e., the length of time during and after treatment in which a patient is living with cancer that does not get worse), or overall survival (also called "survival rate;" i.e., the percentage of people in a study or treatment group who are alive for a certain period of time after they were diagnosed with or treated for cancer) relative to treatment with a control.

[0420] The cancers that can be treated by the pharmaceutical compositions and the treatment methods described herein include, but are not limited to, melanoma, bladder cancer, hematological malignancies (leukemia, lymphoma, myeloma), liver cancer, brain cancer, renal cancer, breast cancer, pancreatic cancer (adenocarcinoma), colorectal cancer, lung cancer (small cell lung cancer and non-small-cell lung cancer), spleen cancer, cancer of the thymus or blood cells (i.e., leukemia), prostate cancer, testicular cancer, ovarian cancer, uterine cancer, a musculoskeletal cancer, a head and neck cancer, a gastrointestinal cancer, a germ cell cancer, or

an endocrine and neuroendocrine cancer . In some embodiments, the cancer is Ewing's sarcoma. In some embodiments, the cancer is selected from melanoma, lung cancer, bladder cancer, and a hematological malignancy. In some embodiments, the cancer is a lymphoma, lymphoid leukemia, myeloid leukemia, cervical cancer, neuroblastoma, or multiple myeloma.

[0421] In some embodiments, the pharmaceutical composition is administered as a monotherapy (i.e., as a single agent) or as a combination therapy (i.e., in combination with one or more additional anticancer agents, such as a chemotherapeutic drug, a cancer vaccine, or an immune checkpoint inhibitor. In some embodiments, the pharmaceutical composition can also be administered with radiation therapy. In some aspects of the present disclosure, the immune checkpoint inhibitor is nivolumab, tremelimumab, pembrolizumab, ipilimumab, or the like.

[0422] In some embodiments, the pharmaceutical composition suppresses an immune response, which can be useful in the treatment of inflammatory or autoimmune disorders, or organ transplantation. In some embodiments, the pharmaceutical composition contains a variant PD-L1 polypeptide in a format that exhibits agonist activity of its cognate binding partner PD-1 and/or that stimulates inhibitory signaling via PD-1. In some aspects, the variant PD-L1 polypeptide stimulates an inhibitory signal through CD80, such as expressed on a lymphocyte or APC. Exemplary formats of a PD-L1 polypeptide for use in connection with such therapeutic applications include, for example, an immunomodulatory protein or "stack" of a variant PD-L1 polypeptide and an IgSF domain or variant thereof that localizes to a cell or tissue of an inflammatory environment, a conjugate containing a variant PD-L1 polypeptide linked to a moiety that localizes to a cell or tissue of an inflammatory environment, an engineered cell expressing a transmembrane immunomodulatory protein, or an infectious agent comprising a nucleic acid molecule encoding a transmembrane immunomodulatory protein, such as for expression of the transmembrane immunomodulatory protein in an infected cell.

[0423] The provided methods to modulate an immune response can be used to treat a disease or condition, such as an inflammatory or autoimmune disorder. In some embodiments, the inflammatory or autoimmune disorder is antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis, a vasculitis, an autoimmune skin disease, transplantation, a Rheumatic disease, an inflammatory gastrointestinal disease, an inflammatory eye disease, an inflammatory neurological disease, an inflammatory pulmonary disease, an inflammatory endocrine disease, or an autoimmune hematological disease.

[0424] In some embodiments, the inflammatory and autoimmune disorders that can be treated by the pharmaceutical composition described herein is Addison's Disease, allergies, alopecia areata, Alzheimer's, antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis, ankylosing spondylitis, antiphospholipid syndrome (Hughes Syndrome), asthma, atherosclerosis, rheumatoid arthritis, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune inner ear disease, autoimmune lymphoproliferative syndrome, autoimmune myocarditis, autoimmune oophoritis, autoimmune orchitis, azoospermia, Behcet's Disease, Berger's Disease, bullous pemphigoid, cardiomyopathy, cardiovascular disease, celiac Sprue/coeliac disease, chronic fatigue immune dysfunction syndrome (CFIDS), chronic idiopathic polyneuritis, chronic inflammatory demyelinating, polyradicalneuropathy (CIDP), chronic relapsing polyneuropathy (Guillain-Barré syndrome), Churg-Strauss Syndrome (CSS), cicatricial pemphigoid, cold agglutinin disease (CAD), COPD (chronic obstructive pulmonary disease), CREST syndrome, Crohn's disease, dermatitis, herpetiformus, dermatomyositis, diabetes, discoid lupus, eczema, epidermolysis bullosa acquisita, essential mixed cryoglobulinemia, Evan's Syndrome, exopthalmos, fibromyalgia, Goodpasture's Syndrome, Graves' Disease, Hashimoto's thyroiditis, idiopathic pulmonary fibrosis, idiopathic thrombocytopenia purpura (ITP), IgA nephropathy, immunoproliferative disease or disorder, inflammatory bowel disease (IBD), interstitial lung disease, juvenile arthritis, juvenile idiopathic arthritis (JIA), Kawasaki's Disease, Lambert-Eaton Myasthenic Syndrome, lichen planus, lupus nephritis, lymphocytic hypophysitis, Ménière's Disease, Miller Fish Syndrome/acute disseminated encephalomyeloradiculopathy, mixed connective tissue disease, multiple sclerosis (MS), muscular rheumatism, myalgic encephalomyelitis (ME), myasthenia gravis, ocular inflammation, pemphigus foliaceus, pemphigus vulgaris, pernicious anaemia, polyarteritis nodosa, polychondritis, polyglandular syndromes (Whitaker's syndrome), polymyalgia rheumatica, polymyositis, primary agammaglobulinemia, primary biliary cirrhosis/autoimmune cholangiopathy, psoriasis, psoriatic arthritis, Raynaud's Phenomenon, Reiter's Syndrome/reactive arthritis, restenosis, rheumatic fever, rheumatic disease, sarcoidosis, Schmidt's syndrome, scleroderma, Sjörgen's Syndrome, stiff-man syndrome, systemic lupus erythematosus (SLE), systemic scleroderma, Takayasu arteritis, temporal arteritis/giant cell arteritis, thyroiditis, Type 1 diabetes, ulcerative colitis, uveitis, vasculitis, vitiligo, interstitial bowel disease or Wegener's Granulomatosis. In some embodiments, the inflammatory or

autoimmune disorder is selected from interstitial bowel disease, transplant, Crohn's disease, ulcerative colitis, multiple sclerosis, asthma, rheumatoid arthritis, and psoriasis.

[0425] In some embodiments, the pharmaceutical composition is administered to modulate an autoimmune condition. For example, suppressing an immune response can be beneficial in methods for inhibiting rejection of a tissue, cell, or organ transplant from a donor by a recipient. Accordingly, in some embodiments, the pharmaceutical compositions described herein are used to limit or prevent graft-related or transplant related diseases or disorders, such as graft versus host disease (GVHD). In some embodiments, the pharmaceutical compositions are used to suppress autoimmune rejection of transplanted or grafted bone marrow, organs, skin, muscle, neurons, islets, or parenchymal cells.

[0426] Pharmaceutical compositions comprising engineered cells and the methods described herein can be used in adoptive cell transfer applications. In some embodiments, cell compositions comprising engineered cells can be used in associated methods to, for example, modulate immunological activity in an immunotherapy approach to the treatment of, for example, a mammalian cancer or, in other embodiments the treatment of autoimmune disorders. The methods employed generally comprise a method of contacting a TIP of the present invention with a mammalian cell under conditions that are permissive to specific binding of the affinity modified IgSF domain and modulation of the immunological activity of the mammalian cell. In some embodiments, immune cells (such as tumor infiltrating lymphocytes (TILs), T-cells (including CD8+ or CD4+ T-cells), or APCs) are engineered to express as a membrane protein and/or as a soluble variant PD-L1 polypeptide, immunomodulatory protein, or conjugate as described herein. The engineered cells can then be contact a mammalian cell, such as an APC, a second lymphocyte or tumor cell in which modulation of immunological activity is desired under conditions that are permissive of specific binding of the affinity modified IgSF domain to a counter-structure on the mammalian cell such that immunological activity can be modulated in the mammalian cell. Cells can be contacted in vivo or ex vivo.

[0427] In some embodiments, the engineered cells are autologous cells. In other embodiments, the cells are allogeneic. In some embodiments, the cells are autologous engineered cells reinfused into the mammal from which it was isolated. In some embodiments, the cells are allogenic engineered cells infused into the mammal. In some embodiments, the cells are harvested from a patient's blood or tumor, engineered to express a polypeptide (such as the variant PD-L1polypeptide, immunomodulatory protein, or conjugate as described herein),

expanded in an in vitro culture system (for example, by stimulating the cells), and reinfused into the patient to mediate tumor destruction. In some embodiments, the methods is conducted by adoptive cell transfer wherein cells expressing the TIP (e.g., a T-cell) are infused back into the patient. In some embodiments, the therapeutic compositions and methods of the invention are used in the treatment of a mammalian patient of cancers such as lymphoma, lymphoid leukemia, myeloid leukemia, cervical cancer, neuroblastoma, or multiple myeloma.

[0428] In some embodiments, the pharmaceutical composition is administered to a subject. In some embodiments, the subject is a human patient. Generally, dosages and routes of administration of the pharmaceutical composition are determined according to the size and condition of the subject, according to standard pharmaceutical practice. For example, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models such as mice, rats, rabbits, dogs, pigs, or monkeys. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans. The exact dosage will be determined in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active compound or to maintain the desired effect. Factors that may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy.

[0429] Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation. The frequency of dosing will depend upon the pharmacokinetic parameters of the molecule in the formulation used. Typically, a composition is administered until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose, or as multiple doses (at the same or different concentrations/dosages) over time, or as a continuous infusion. Further refinement of the appropriate dosage is routinely made. Appropriate dosages may be ascertained through use of appropriate dose-response data. A number of biomarkers or physiological markers for therapeutic effect can be monitored including T cell activation or proliferation, cytokine synthesis or production (e.g., production of TNF-α, IFN-γ, IL-2), induction of various activation markers (e.g., CD25, IL-2 receptor), inflammation, joint swelling or tenderness, serum level of C-reactive protein, anti-collagen antibody production, and/or T cell-dependent antibody response(s).

[0430] In some embodiments, the pharmaceutical composition is administered to a subject through any route, including orally, transdermally, by inhalation, intravenously, intra-arterially, intramuscularly, direct application to a wound site, application to a surgical site, intraperitoneally, by suppository, subcutaneously, intradermally, transcutaneously, by nebulization, intrapleurally, intraventricularly, intra-articularly, intraocularly, or intraspinally.

[0431] In some embodiments, the dosage of the pharmaceutical composition is a single dose or a repeated dose. In some embodiments, the doses are given to a subject once per day, twice per day, three times per day, or four or more times per day. In some embodiments, about 1 or more (such as about 2 or more, about 3 or more, about 4 or more, about 5 or more, about 6 or more, or about 7 or more) doses are given in a week. In some embodiments, multiple doses are given over the course of days, weeks, months, or years. In some embodiments, a course of treatment is about 1 or more doses (such as about 2 or more does, about 3 or more doses, about 4 or more doses, about 5 or more doses, about 7 or more doses, about 10 or more doses, about 15 or more doses, about 25 or more doses, about 40 or more doses, about 50 or more doses, or about 100 or more doses).

[0432] In some embodiments, an administered dose of the pharmaceutical composition is about 1 μg of protein per kg subject body mass or more (such as about 2 μg of protein per kg subject body mass or more, about 5 μg of protein per kg subject body mass or more, about 10 μg of protein per kg subject body mass or more, about 25 μg of protein per kg subject body mass or more, about 50 μg of protein per kg subject body mass or more, about 100 μg of protein per kg subject body mass or more, about 250 μg of protein per kg subject body mass or more, about 500 μg of protein per kg subject body mass or more, about 1 mg of protein per kg subject body mass or more, about 2 mg of protein per kg subject body mass or more, or about 5 mg of protein per kg subject body mass or more).

[0433] In some embodiments, a therapeutic amount of a cell composition is administered. Typically, precise amount of the compositions of the present invention to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical composition comprising engineered cells, e.g. T cells, as described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, such as 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. Engineered cell compositions, such as T cell compositions, may also be administered multiple times at these dosages. The cells can

be administered by using infusion techniques that are commonly known in immunotherapy (see, e.g., Rosenberg et al, New Eng. J. of Med. 319: 1676, 1988). The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly.

[0434] In some embodiments, the pharmaceutical composition contains infectious agents containing nucleic acid sequences encoding the immunomodulatory variant polypeptides. In some embodiments, the pharmaceutical composition contains a dose of infectious agents suitable for administration to a subject that is suitable for treatment. In some embodiments, the pharmaceutical composition contains an infectious agent that is a virus, at a single or multiple dosage amount, of between about between or between about 1×10^5 and about 1×10^{12} plaque-forming units (pfu), 1×10^6 and 1×10^{10} pfu, or 1×10^7 and 1×10^{10} pfu, each inclusive, such as at least or at least about or at about 1×10^6, 1×10^7, 1×10^8, 1×10^9, 2×10^9, 3×10^9, 4×10^9, 5×10^9pfu or about 1×10^{10} pfu. In some embodiments, the pharmaceutical composition can contain a virus concentration of from or from about 10^5 to about 10^{10} pfu/mL, for example, 5×10^6 to 5×10^9 or 1×10^7 to 1×10^9 pfu/mL, such as at least or at least about or at about 10^6 pfu/mL, 10^7 pfu/mL, 10^8 pfu/mL or 10^9 pfu/mL. In some embodiments, the pharmaceutical composition contains an infectious agent that is a bacterium, at a single or multiple dosage amount, of between about between or between about 1×10^3 and about 1×10^9 colony-forming units (cfu), 1×10^4 and 1×10^9 cfu, or 1×10^5 and 1×10^7 cfu, each inclusive, such as at least or at least about or at about 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8 or 1×10^9 cfu. In some embodiments, the pharmaceutical composition can contain a bacterial concentration of from or from about 10^3 to about 10^8 cfu/mL, for example, 5×10^5 to 5×10^7 or 1×10^6 to 1×10^7 cfu/mL, such as at least or at least about or at about 10^5 cfu/mL, 10^6 cfu/mL, 10^7 cfu/mL or 10^8 cfu/mL.

[0435] A variety of means are known for determining if administration of a therapeutic composition of the invention sufficiently modulates immunological activity by eliminating, sequestering, or inactivating immune cells mediating or capable of mediating an undesired immune response; inducing, generating, or turning on immune cells that mediate or are capable of mediating a protective immune response; changing the physical or functional properties of immune cells; or a combination of these effects. Examples of measurements of the modulation of immunological activity include, but are not limited to, examination of the presence or absence of immune cell populations (using flow cytometry, immunohistochemistry, histology, electron microscopy, polymerase chain reaction (PCR)); measurement of the functional capacity of

immune cells including ability or resistance to proliferate or divide in response to a signal (such as using T-cell proliferation assays and pepscan analysis based on 3H-thymidine incorporation following stimulation with anti-CD3 antibody, anti-T-cell receptor antibody, anti-CD28 antibody, calcium ionophores, PMA (phorbol 12-myristate 13-acetate) antigen presenting cells loaded with a peptide or protein antigen; B cell proliferation assays); measurement of the ability to kill or lyse other cells (such as cytotoxic T cell assays); measurements of the cytokines, chemokines, cell surface molecules, antibodies and other products of the cells (e.g., by flow cytometry, enzyme-linked immunosorbent assays, Western blot analysis, protein microarray analysis, immunoprecipitation analysis); measurement of biochemical markers of activation of immune cells or signaling pathways within immune cells (e.g., Western blot and immunoprecipitation analysis of tyrosine, serine or threonine phosphorylation, polypeptide cleavage, and formation or dissociation of protein complexes; protein array analysis; DNA transcriptional, profiling using DNA arrays or subtractive hybridization); measurements of cell death by apoptosis, necrosis, or other mechanisms (e.g., annexin V staining, TUNEL assays, gel electrophoresis to measure DNA laddering, histology; fluorogenic caspase assays, Western blot analysis of caspase substrates); measurement of the genes, proteins, and other molecules produced by immune cells (e.g., Northern blot analysis, polymerase chain reaction, DNA microarrays, protein microarrays, 2-dimensional gel electrophoresis, Western blot analysis, enzyme linked immunosorbent assays, flow cytometry); and measurement of clinical symptoms or outcomes such as improvement of autoimmune, neurodegenerative, and other diseases involving self-proteins or self-polypeptides (clinical scores, requirements for use of additional therapies, functional status, imaging studies) for example, by measuring relapse rate or disease severity (using clinical scores known to the ordinarily skilled artisan) in the case of multiple sclerosis, measuring blood glucose in the case of type I diabetes, or joint inflammation in the case of rheumatoid arthritis.

VIII. EXEMPLARY EMBODIMENTS

[0436] Among the provided embodiments are:

1. A variant PD-L1 polypeptide, comprising an ECD or IgV domain or a specific binding fragment thereof, an IgC domain or a specific binding fragment thereof, or both, wherein the variant PD-L1 polypeptide comprises one or more amino acid modifications in an unmodified PD-L1 or a specific binding fragment thereof corresponding to position(s) selected from 6, 10, 11, 14, 15, 16, 17, 18, 19, 20, 22, 23, 26, 27, 28, 33, 35, 36, 40, 41, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 60, 64, 65, 68, 71, 72, 73, 74, 75, 78, 79, 83, 85, 89, 90, 93, 97, 98, 99,

101, 102, 103, 104, 106, 110, 111, 112, 113, 117, 119, 120, 121, 124, 129, 130, 131, 134, 137, 138, 144, 148, 149, 150, 155, 158, 160, 163, 165, 167, 170, 171, 173, 175, 176, 177, 179, 180, 183, 185, 188, 189, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 207, 213, or 221, with reference to the numbering of SEQ ID NO:30 or 1728.

2. The variant PD-L1 polypeptide of embodiment 1, wherein the amino acid modification is an amino acid substitution, insertion or deletion.

3. The variant PD-L1 polypeptide of embodiment 1 or embodiment 2, wherein the unmodified PD-L1 is a mammalian PD-L1 or a specific binding fragment thereof.

4. The variant PD-L1 polypeptide of embodiment 3, wherein the unmodified PD-L1 is a human PD-L1 or a specific binding fragment thereof.

5. The variant PD-L1 polypeptide of any one of embodiments 1-4, wherein the unmodified PD-L1 comprises (i) the sequence of amino acids set forth in SEQ ID NO:30 or 1728, (ii) a sequence of amino acids that has at least 95% sequence identity to SEQ ID NO:30 or 1728; or (iii) a portion thereof comprising an IgV domain or IgC domain or specific binding fragments thereof or both.

6. The variant PD-L1 polypeptide of any one of embodiments 1-5, wherein:

the specific binding fragment of the IgV domain or IgC domain has a length of at least 50, 60, 70, 80, 90, 100, 110 or more amino acids; or

the specific binding fragment of the IgV domain comprises a length that is at least 80% of the length of the IgV domain set for as amino acids 24-130 of SEQ ID NO:3 and/or the specific binding fragment of the IgC domain comprises a length that is at least 80% of the length of the IgC domain set forth as amino acids 133-225 of SEQ ID NO:3.

7. The variant PD-L1 polypeptide of any one of embodiments 1-6, wherein:

the variant PD-L1 comprises up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid modifications, optionally amino acid substitutions, insertions and/or deletions; or

the variant PD-L1 polypeptide comprises a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:30 or 1728 or a specific binding fragment thereof.

8. The variant PD-L1 polypeptide of any of embodiments 1-7, wherein the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of PD-1 or CD80 compared to the unmodified PD-L1.

9. The variant PD-L1 polypeptide of any of embodiments 1-8, wherein:

the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of PD-1 compared to the binding of the unmodified PD-L1 to the ectodomain of PD-1; and/or

the variant PD-L1 polypeptide exhibits altered binding to the ectodomain of CD80 compared to the binding of the unmodified PD-L1 to the ectodomain of CD80.

10. The variant PD-L1 polypeptide of embodiment 8 or embodiment 9, wherein the altered binding is altered binding affinity and/or altered binding selectivity.

11. The variant PD-L1 polypeptide of any of embodiments 1-10, wherein the one or more amino acid modifications are selected from P6S, Y10F, V11A, V11E, Y14S, G15A, S16G, N17D, M18I, M18T, M18V, T19A, T19I, I20L, C22R, K23E, K23N, K23R, E26A, E27D, E27G, K28E, K28I, K28R, K28N, A33D, L35P, I36S, I36T, E40G, M41K, M41V, D43G, D43V, K44E, N45D, N45I, N45T, I47T, I46V, F49S, V50A, H51N, H51R, H51Y, G52R, G52V, E53G, E53V, E54G, D55G, D55N, D55S, D55V, L56Q, K57E, K57R, V58A, V58D,H60R, S75P, R64S, Q65L, R68L, K71E, D72G, Q73R, L74P, S75P, N78I, N78S, A79T, I83T, D85E, Q89R, D90G, V93E, M97I, M97K, M97L, I98L, I98T, I98V, S99G, G101D. G101G-ins (G101GG), G102D, A103V,D104G, K106E, K106R, V110M, K111E, K111T, V112A, N113Y, N117S, I119T, N120S, Q121L, L124S, V129A, V129D, T130A, S131F, E134G, C137R, Q138R, K144E, K144Q, I148V, W149R, T150A, Q155H, S158G, K160M, T163I, K163N, N165Y, K167R, K167T, E170G, K171R, F173I, F173L, K173Y, V175A, T176N, S177C, L179P, R180S, T183A, T183I, T185A, I188V, F189L, F189S, T192S, F193S, R194G, R194W, R195G, R195S, R195T, L196S, D197G, P198S, P198T, E199G, E200K, E200N, N201D, N201Y, H202Q, T203A, A204T, L206F, V207A, L213P, T221L or a conservative amino acid substitution thereof.

12. The variant PD-L1 polypeptide of any of embodiments 1-11, wherein the one or more amino acid modifications are selected from among K28N/M41V/N45T/H51N/K57E I20L/I36T/N45D/I47T, I20L/M41K/K44E, P6S/N45T/N78I/I83T, N78I, M41K/N78I, N45T/N78I, I20L/N45T, N45T, M41K, I20L/I36T/N45D, N17D/N47T/V50A/D72G, I20L/F49S, N45T/V50A, I20L/N45T/N78I, I20L/N45T/V50A, M41V/N45T, M41K/N45T, A33D/S75P/D85E, M18I/M41K/D43G/H51R/N78I, V11E/I20L/I36T/N45D/H60R/S75P, A33D/V50A, S16G/A33D/K71E/S75P, E27G/N45T/M97I, E27G/N45T/K57R, A33D/E53V, D43G/N45D/V58A, E40G/D43V/N45T/V50A, Y14S/K28E/N45T, A33D/N78S, A33D/N78I, A33D/N45T, A33D/N45T/N78I, E27G/N45T/V50A, N45T/V50A/N78S, I20L/N45T/V110M,

I20L/I36T/N45T/V50A, N45T/L74P/S75P, N45T/S75P, S75P/K106R, S75P, A33D/S75P, A33D/S75P/D104G, A33D/S75P, I20L/E27G/N45T/V50A, I20L/E27G/D43G/N45D/V58A/N78I, I20L/D43G/N45D/V58A/N78I, I20L/A33D/D43G/N45D/V58A/N78I, I20L/D43G/N45D/N78I, E27G/N45T/V50A/N78I, N45T/V50A/N78I, V11A/I20L/E27G/D43G/N45D/H51Y/S99G, I20L/E27G/D43G/N45T/V50A, I20L/K28E/D43G/N45D/V58A/Q89R, I20L/I36T/N45D, I20L/K28E/D43G/N45D/E53G/V58A/N78I, A33D/D43G/N45D/V58A/S75P, K23R/D43G/N45D, I20L/D43G/N45D/V58A/N78I/D90G/G101D, D43G/N45D/L56Q/V58A/G101G-ins (G101GG), I20L/K23E/D43G/N45D/V58A/N78I, I20L/K23E/D43G/N45D/V50A/N78I, T19I/E27G/N45I/V50A/N78I/M97K, I20L/M41K/D43G/N45D, K23R/N45T/N78I, I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG), K57R/S99G, K57R/S99G/F189L, M18V/M97L/F193S/R195G/E200K/H202Q, I36S/M41K/M97L/K144Q/R195G/E200K/H202Q/L206F, C22R/Q65L/L124S/K144Q/R195G/E200N/H202Q/T221L, M18V/I98L/L124S/P198T/L206F, S99G/N117S/I148V/K171R/R180S, I36T/M97L/A103V/Q155H, K28I/S99G, R195S, A79T/S99G/T185A/R195G/E200K/H202Q/L206F, K57R/S99G/L124S/K144Q, K57R/S99G/R195G, D55V/M97L/S99G, E27G/I36T/D55N/M97L/K111E, E54G/M97L/S99G, G15A/I36T/M97L/K111E/H202Q, G15A/I36T/V129D, G15A/I36T/V129D/R195G, G15A/V129D, I36S/M97L, I36T/D55N/M97L/K111E/A204T, I36T/D55N/M97L/K111E/V129A/F173L, I36T/D55S/M97L/K111E/I148V/R180S, I36T/G52R/M97L/V112A/K144E/V175A/P198T, I36T/I46V/D55G/M97L/K106E/K144E/T185A/R195G, I36T/I83T/M97L/K144E/P198T, I36T/M97L/K111E, I36T/M97L/K144E/P198T, I36T/M97L/Q155H/F193S/N201Y, I36T/M97L/V129D, L35P/I36S/M97L/K111E, M18I/I36T/E53G/M97L/K144E/E199G/V207A, M18T/I36T/D55N/M97L/K111E, M18V/M97L/T176N/R195G, M97L/S99G, N17D/M97L/S99G, S99G/T185A/R195G/P198T, V129D/H202Q, V129D/P198T, V129D/T150A, V93E/V129D, Y10F/M18V/S99G/Q138R/T203A, N45D, K160M/R195G, N45D/K144E, N45D/P198S, N45D/P198T, N45D/R195G, N45D/R195S, N45D/S131F, N45D/V58D, V129D/R195S, I98T/F173Y/L196S, N45D/E134G/L213P, N45D/F173I/S177C, N45D/I148V/R195G, N45D/K111T/R195G, N45D/N113Y/R195S, N45D/N165Y/E170G, N45D/Q89R/I98V, N45D/S131F/P198S, N45D/S75P/P198S, N45D/V50A/R195T, E27D/N45D/T183A/I188V, F173Y/T183I/L196S/T203A, K23N/N45D/S75P/N120S,

N45D/G102D/R194W/R195G, N45D/G52V/Q121L/P198S, N45D/I148V/R195G/N201D, N45D/K111T/T183A/I188V, N45D/Q89R/F189S/P198S, N45D/S99G/C137R/V207A, N45D/T163I/K167R/R195G, N45D/T183A/T192S/R194G, N45D/V50A/I119T/K144E, T19A/N45D/K144E/R195G, V11E/N45D/T130A/P198T, V26A/N45D/T163I/T185A, K23N/N45D/L124S/K167T/R195G, K23N/N45D/Q73R/T163I, K28E/N45D/W149R/S158G/P198T, K28R/N45D/K57E/I98V/R195S, K28R/N45D/V129D/T163N/R195T, M41K/D43G/N45D/R64S/R195G, M41K/D43G/N45D/R64S/S99G, N45D/R68L/F173L/D197G/P198S, N45D/V50A/I148V/R195G/N201D, M41K/D43G/K44E/N45D/R195G/N201D, or N45D/V50A/L124S/K144E/L179P/R195G.

13. The variant PD-L1 polypeptide of any of embodiments 1-13, wherein the one or more amino acid modifications correspond to position(s) selected from 20, 27, 28, 33, 36, 41, 43, 45, 50, 58, 71, 75, 78, 97, 99, or 195, optionally wherein the one or more amino acid substitutions are selected from I20L, E27G, K28E, A33D, I36T, M41K, D43G, N45D, N45T, V50A, V58A, K71E, S75P, N78I, M97L, S99G, or R195G, or a conservative amino acid substitution thereof.

14. The variant PD-L1 polypeptide of any of embodiments 1-13, wherein the one or more amino acid modifications correspond to position(s) selected from 20, 27, 33, 36, 43, 45, 50, 58, 75 or 78, optionally wherein the one or more amino acid substitutions are selected from I20L, E27G, A33D, I36T, D43G, N45D, N45T, V50A, V58A, S75P, N78I, or a conservative amino acid substitution thereof.

15. The variant PD-L1 polypeptide of any of claims 1-14, wherein the variant PD-L1 polypeptide comprises amino acid modifications I20L/I36T, I20L/D43G, I20L/N45D, I20L/N45T, I20L/N45T, I20L/V50A, I20L/V58A, I20L/S75P, I20L/N78I, I36T/D43G, I36T/N45D, I36T/N45T, I36T/V50A, I36T/V58A, I36T/S75P, I36T/N78I, D43G/N45D, D43G/N45T, D43G/V50A, D43G/V58A, D43G/S75P, D43G/N78I, N45D/V50A, N45D/V58A, N45D/S75P, N45D/N78I, N45T/V50A, N45T/V58A, N45T/S75P, N45T/N78I, V50A/V58A, V50A/S75P, V50A/N78I, V58A/S75P, V58A/N78I, or S75P/N78I.

16. The variant PD-L1 polypeptide of any of claims 1-15, wherein the variant PD-L1 polypeptide comprises amino acid modifications D43G/N45D/V58A.

17. The variant PD-L1 polypeptide of any of claims 1-16, wherein the variant PD-L1 polypeptide comprises amino acid modifications D43G/N45D/L56Q/V58A/G101G-ins (G101GG) or I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG).

18. The variant PD-L1 polypeptide of any of embodiments 1-17, wherein:

the variant PD-L1 polypeptide comprises or consists of the extracellular domain (ECD); and/ or

the variant PD-L1 polypeptide comprises or consists of the IgV domain or a specific fragment thereof and the IgC domain or a specific fragment thereof.

19. The variant PD-L1 polypeptide of any of embodiments 1-18, comprising or consisting of the sequence of amino acids set forth in any of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008 or a specific binding fragment thereof, or a sequence of amino acids that exhibits at least 95% sequence identity to any of SEQ ID NOS: 56-120, 1725, 1729-1818, 1819-1907, 1943-2008 or a specific binding fragment thereof and that contains the one or more of the amino acid substitutions.

20. The variant PD-L1 polypeptide of any of embodiments 1-19, wherein the variant PD-L1 polypeptide comprises or consists of the ECD or IgV domain or a specific binding fragment thereof.

21. The variant PD-L1 polypeptide of any of embodiments 1-20, wherein the IgV domain or specific binding fragment thereof is the only PD-L1 portion of the variant PD-L1 polypeptide.

22. The variant PD-L1 polypeptide of any of embodiments 1-21, comprising or consisting of the sequence of amino acids set forth in any of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937 or a specific binding fragment thereof, a sequence of amino acids that exhibits at least 95% sequence identity to any of SEQ ID NOS: 121-185, 244-308, 1726-1727, 1908-1937 or a specific binding fragment thereof and that contains the one or more of the amino acid substitutions.

23. The variant PD-L1 polypeptide of any of embodiments 1-17, wherein the IgC domain or specific binding fragment thereof is the only PD-L1 portion of the variant PD-L1 polypeptide.

24. The variant PD-L1 polypeptide of any of embodiments 1-23, wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 or CD80 with increased affinity compared to the unmodified PD-L1.

25. The variant PD-L1 polypeptide of any of embodiments 1-24, wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity compared to the unmodified PD-L1.

26. The variant PD-L1 polypeptide of any of embodiments 1-25, wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 and the ectodomain of CD80 each with increased affinity compared to the unmodified PD-L1.

27. The variant PD-L1 polypeptide of any of embodiments 1-24, wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity and specifically binds to the ectodomain of CD80 with decreased affinity compared to the unmodified PD-L1.

28. The variant PD-L1 polypeptide of any of embodiments 24-27, wherein the increased affinity to the ectodomain of PD-1 is increased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold , 50-fold or 60-fold compared to the unmodified PD-L1.

29. The variant PD-L1 polypeptide of embodiment 24 or embodiment 26, wherein the increased affinity to the ectodomain of CD80 is increased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold or 60-fold compared to the unmodified PD-L1.

30. The variant PD-L1 polypeptide of embodiment 27, wherein the decreased affinity to the ectodomain of CD80 is decreased more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold , 50-fold or 60-fold compared to the unmodified PD-L1.

31. The variant PD-L1 polypeptide of any of embodiments 1-30, wherein the variant polypeptide specifically binds to the ectodomain of PD-1 with increased selectivity compared to the unmodified PD-L1.

32. The variant PD-L1 polypeptide of embodiment 31, wherein the increased selectivity comprises a greater ratio of binding of the variant polypeptide for PD-1 versus CD80 compared to the ratio of binding of the unmodified PD-L1 polypeptide for PD-1 versus CD80.

33. The variant PD-L1 polypeptide of embodiment 32, wherein the ratio is greater by at least or at least about 1.5-fold, 2.0-fold, 3.0-fold, 4.0-fold, 5-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold or more.

34. The variant PD-L1 polypeptide of any of embodiments 9-33, wherein the PD-1 is a human PD-1.

35. The variant PD-L1 polypeptide of any of embodiments 9-34, wherein the CD80 is a human CD80.

36. The variant PD-L1 polypeptide of any of embodiments 1-35, wherein the binding activity is altered (increased or decreased) more than 1.2-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold 40-fold or 50-fold compared to the unmodified PD-L1.

37. The variant PD-L1 polypeptide of any of embodiments 1-36 that is a soluble protein.

38. The variant PD-L1 polypeptide of any of embodiments 1-37, wherein the variant PD-L1 polypeptide is linked to a multimerization domain.

39. The variant PD-L1 polypeptide of embodiment38, wherein the multimerization domain is an Fc domain or a variant thereof with reduced effector function.

40. The variant PD-L1 polypeptide of any of embodiments 1-39, wherein the variant PD-L1 polypeptide is linked to a moiety that increases biological half-life of the polypeptide.

41. The variant PD-L1 polypeptide of any of embodiments 1-40, wherein the variant PD-L1 polypeptide is linked to an Fc domain or a variant thereof with reduced effector function.

42. The variant PD-L1 polypeptide of any of embodiments 39-41, wherein:

the Fc domain is mammalian, optionally human; or

the variant Fc domain comprises one or more amino acid modifications compared to an unmodified Fc domain that is mammalian, optionally human.

43. The variant PD-L1 polypeptide of any one of embodiments 39, 41 and 42, wherein the Fc domain or variant thereof comprises the sequence of amino acids set forth in SEQ ID NO:187 or SEQ ID NO:188 or a sequence of amino acids that exhibits at least 85% sequence identity to SEQ ID NO:187 or SEQ ID NO:188.

44. The variant PD-L1 polypeptide of any of embodiments39 and 41-43, wherein the Fc domain comprises one or more amino acid modifications selected from among E233P, L234A, L234V, L235A, L235E, G236del, G237A, S267K, N297G, R292C, V302C, and K447del each by EU numbering.

45. The variant PD-L1 polypeptide of any of embodiments 39 and 41-44, wherein the Fc domain comprises the amino acid modification C220S by EU numbering.

46. The variant PD-L1 polypeptide of any of embodiments 39 and 41-45, wherein the Fc domain comprises the sequence of amino acids set forth in any of SEQ ID NOS: 1155, 1157, 1158, 1159, 1715, 1938, 1939, and 1940 or a sequence of amino acids that exhibits at least 85% sequence identity to any of SEQ ID NOS:1155, 1157, 1158, 1159, 1715, 1938, 1939, and 1940, and exhibits reduced effector function.

47. The variant PD-L1 polypeptide of any of embodiments 38-46, wherein the variant PD-L1 polypetide is linked indirectly via a linker, optionally a G4S linker.

48. The variant PD-L1 polypeptide of any of embodiments 1-47, that is a transmembrane immunomodulatory protein further comprising a transmembrane domain linked to the extracellular domain (ECD) or specific binding fragment thereof of the variant PD-L1 polypeptide.

49. The variant PD-L1 polypeptide of embodiment 48, wherein the transmembrane domain comprises the sequence of amino acids set forth as residues 239-259 of SEQ ID NO:3 or a functional variant thereof that exhibits at least 85% sequence identity to residues 239-259 of SEQ ID NO:3.

50. The variant PD-L1 polypeptide of embodiment 48 or embodiment 49, further comprising a cytoplasmic signaling domain linked to the transmembrane domain.

51. The variant PD-L1 polypeptide of embodiment 50, wherein the cytoplasmic signaling domain comprises the sequence of amino acids set forth as residues 260-290 of SEQ ID NO:3 or a functional variant thereof that exhibits at least 85% sequence identity to residues 260-290 of SEQ ID NO:3.

52. The variant PD-L1 polypeptide of any of embodiments 1-51, wherein the variant PD-L1 increases IFN-gamma (interferon-gamma) expression relative to the unmodified PD-L1 in an *in vitro* T-cell assay.

53. The variant PD-L1 polypeptide of any of embodiments 1-52, wherein the variant PD-L1 decreases IFN-gamma (interferon-gamma) expression relative to the unmodified PD-L1 in an *in vitro* T-cell assay.

54. The variant PD-L1 polypeptide of any of embodiments 1-55 that is deglycosylated.

55. An immunomodulatory protein, comprising the variant PD-L1 polypeptide of any of embodiments 1-54 and a second polypeptide comprising an immunoglobulin superfamily (IgSF) domain of an IgSF family member or an affinity-modified IgSF domain thereof, said

affinity-modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member.

56. The immunomodulatory protein of embodiment 55, wherein the variant CD112 polypeptide and the second polypeptide are linked directly or are linked indirectly via a linker.

57. The immunomodulatory protein of embodiment 55 or embodiment 56, wherein the IgSF domain is affinity modified and exhibits altered binding to one or more of its cognate binding partner(s) compared to the unmodified or wild-type IgSF domain of the IgSF family member.

58. The immunomodulatory protein of embodiment 57, wherein the IgSF domain exhibits increased binding to one or more of its cognate binding partner(s) compared to the unmodified or wild-type IgSF domain of the IgSF family member.

59. The immunomodulatory protein of any one of embodiments 58-58, wherein the variant PD-L1 polypeptide is a first PD-L1 variant and the IgSF domain of the second polypeptide is an IgSF domain from a second variant PD-L1 polypeptde of any of embodiments 1-58, wherein the first and second variant PD-L1 polypeptides are the same or different.

60. The immunomodulatory protein of any one of embodiments 58-59, wherein the variant PD-L1 polypeptide is capable of specifically binding to PD-1 or CD80 and the IgSF domain of the second polypeptide is capable of binding to a cognate binding partner other than one specifically bound by the PD-L1 variant polypeptide.

61. The immunomodulatory protein of any of embodiments 58-60, wherein the IgSF domain is from a member of the B7 family.

62. The immunomodulatory protein of any of embodiments 58-61, wherein the IgSF domain is a tumor-localizing moiety that binds to a ligand expressed on a tumor or to an inflammatory-localizing moiety that binds to a cell or tissue associated with an inflammatory environment.

63. The immunomodulatory protein of embodiment 62, wherein the ligand is B7H6.

64. The immunomodulatory protein of embodiment 62 or embodiment 63, wherein the IgSF domain is from NKp30.

65. The immunomodulatory protein of any embodiments 55-64, wherein the IgSF domain of the second polypeptide is an IgSF domain of a ligand that binds to an inhibitory receptor, or is an affinity-modified IgSF domain thereof, optionally wherein the affinity-modified

IgSF domain exhibits increased binding affinity and/or binding selectivity for the inhibitory receptor compared to binding of the unmodified IgSF domain to the inhibitory receptor.

66. The immunomodulatory protein of embodiment 65, wherein:

the inhibitory receptor is TIGIT, PD-1, or CTLA-4; or

the ligand of the inhibitory receptor is PD-L2, CD155, CD112 or CD80.

67. The immunomodulatory protein of any of embodiments 55-66, wherein the second polypeptide is selected from:

(i) a wildtype CD155 comprising an IgSF set forth in any of SEQ ID NOS: 47, 310, or 353, or a variant CD155 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS:311-352, 354-665, 1505-1576, 1551-1714;

(ii) a wildtype CD112 comprising an IgSF domain set forth in any of SEQ ID NOS: 48, 666, or 761, or a variant CD112 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 667-760, 762-931, 1433-1504;

(iii) a wildtype CD80 comprising an IgSF domain set forth in any of SEQ ID NOS: 28, 1005, or 2030, or a variant CD80 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 932-964, 966-1038, 1040-1078, 1080-1112, 1114-1152;

(iv) a wildtype PD-L2 comprising an IgSF domain set forth in any of SEQ ID NOS: 31, 1203, or 1263, or a variant PD-L2 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 1204-1254, 1256-1331, 1333-1407, 1409-1432;

(v) a sequence of amino acids that exhibits at least 95% sequence identity to any of the SEQ ID NOSs in (i)-(iv) and that comprises the amino acid substitution; or

(vi) a specific binding fragment of any of (i)-(v).

68. The immunomodulatory protein of any of embodiments 55-67, further comprising a third polypeptide comprising an IgSF domain of an IgSF family member or an affinity-modified IgSF domain thereof, said affinity-modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member, wherein:

the third polypeptide is the same as the first and/or second polypeptide; or

the third polypeptide is different from the first and/or second polypeptide..

69. The immunomodulatory protein of embodiment 68, wherein the third polypeptide is selected from:

(i) a wildtype CD155 comprising an IgSF set forth in any of SEQ ID NOS: 47, 310, or 353, or a variant CD155 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS:311-352, 354-665, 1505-1576, 1551-1714;

(ii) a wildtype CD112 comprising an IgSF domain set forth in any of SEQ ID NOS: 48, 666, or 761, or a variant CD112 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 667-760, 762-931, 1433-1504;

(iii) a wildtype CD80 comprising an IgSF domain set forth in any of SEQ ID NOS: 28, 1005, or 2030, or a variant CD80 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 932-964, 966-1038, 1040-1078, 1080-1112, 1114-1152;

(iv) a wildtype PD-L2 comprising an IgSF domain set forth in any of SEQ ID NOS: 31, 1203, or 1263, or a variant PD-L2 polypeptide comprising an IgSF domain set forth in any of SEQ ID NOS: 1204-1254, 1256-1331, 1333-1407, 1409-1432;

(v) a sequence of amino acids that exhibits at least 95% sequence identity to any of the SEQ ID NOSs in (i)-(iv) and that comprises the amino acid substitution; or

(vi) a specific binding fragment of any of (i)-(v).

70. The immunomodulatory protein of any of embodiments 55-69, wherein the IgSF domain or affinity-modified IgSF domain thereof, optionally of the second or third polypeptide, is or comprises an IgV domain.

71. The immunomodulatory protein of any of embodiments 55-70, wherein the variant PD-L1 polypeptide is or comprises an IgV domain.

72. The immunomodulatory protein of any of embodiments 55-71, further comprising at least one additional polypeptide comprising an IgSF domain of an IgSF family member or an affinity-modified IgSF domain thereof, said affinity-modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild-type IgSF domain of the IgSF family member.

73. The immunomodulatory protein of any of embodiments 55-67, wherein the immunomodulatory protein further comprises a multimerization domain linked to at least one of the variant PD-L1 polypeptide, or the second polypeptide.

74. The immunomodulatory protein of any of embodiments 55-73, wherein the immunomodulatory protein further comprises a multimerization domain linked to at least one of the variant PD-L1 polypeptide, the second polypeptide and/or the third polypeptide, optionally

wherin the multimerization domain is an Fc domain or a variant thereof with reduced effector function.

75. The immunomodulatory protein of any of embodiments 68-75, wherein the multimerization domain promotes heterodimer formation.

76. An immunomodulatory protein comprising a first variant PD-L1 polypeptide of any of embodiments 38-47 in which the multimerization domain is a first multimerization domain and a second variant PD-L1 polypeptide of any of embodiments 38-47 in which the multimerization domain is a second multimerization domain, wherein the first and second multimerization domains interact to form a multimer containing the first and second variant PD-L1 polypeptide, optionally wherein the first and second variant PD-L1 polypeptide are the same.

77. An immunomodulatory protein comprising the immunomodulatory protein of any of embodiments 73-75, wherein the multimerization domain is a first multimerization domain and interacts with a second multimerization domain to form a multimer comprising the immunomodulatory protein.

78. The immunomodulatory protein of embodiment 77, wherein the immunomodulatory protein is a first immunomodulatory protein and a second immunomodulatory protein is linked directly or indirectly via a linker to the second multimerization domain, wherein the multimer comprises the first and second immunomodulatory protein, optionally wherein the second immunomodulatory protein is an immunomodulatory protein of any of claims 68-70 in which the multimerization domain is the second multimerization domain.

79. The immunomodulatory protein of any of embodiments 76-78, wherein the multimer is a dimer.

80. The immunomodulatory protein of any of embodiments 76-79 that is a homodimer, optionally wherein the first and second multimerization domain is the same.

81. The immunomodulatory protein of any of claims 77-80, wherein:

the second polypeptide is a variant CD155 polypeptide and the first and/or second immunomodulatory protein comprises the sequence set forth in any of SEQ ID NOS: 1716-1721, or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of SEQ ID NOS: 1716-1721; or

the second polypeptide is CD112 or CD155 and the third polypeptide is the other of CD112 or CD155 and the first and/or second immunomodulatory portin comprise the sequence set forth in any of SEQ ID NOS: 1722-1724, or a sequence of amino acids that exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of SEQ ID NOS: 1716-1721.

82. The immunomodulatory protein of any of embodiments 76-79 that is a heterodimer, optionally wherein the first and second multimerization domain are different and/or are capable of interacting to mediate heterodimer formation.

83. The immunomodulatory protein of any of embodiments 76-82, wherein the first and/or second multimerization domain is an Fc domain or a variant thereof with reduced effector function, optionally wherein:

the Fc domain is of an immunoglobulin protein that is human and/or the Fc region is human, optionally wherein the Fc region is of an immunoglobulin G1 (IgG1) or an immunoglobulin G2 (IgG2), optionally set forth in SEQ ID NO:187 or SEQ ID NO:188, optionally wherein the Fc region exhibits one or more effector functions; or

the variant Fc domain comprises one or more amino acid substitutions in a wildtype Fc region, optionally wherein the reduced effector function is reduced compared to a wildtype Fc region, optionally wherein the wildtype human Fc is of human IgG1.

84. The immunomodulatory protein of any of embodiments76-83, wherein the first and second multimerization domain is the same or different.

85. The immunomodulatory protein of any of embodiments 74, 75, 83 and 84, wherein the variant Fc region comprises:

the amino acid substitutions E233P, L234A, L234V, L235A, L235E, G236del, G237A, S267K, or N297G, with residue numbering according to the EU index of Kabat; or

the amino acid substitutions R292C/N297G/V302C or L234A/L235E/G237A, with residue numbering according to the EU index of Kabat.

86. The immunomodulatory protein of any of embodiments 74, 75 and 83-85, wherein the Fc region or variant Fc region comprises the amino acid substitution C220S, with residue numbering according to the EU index of Kabat.

87. The immunomodulatory protein of any of embodiments 74, 75 and 83-86, wherein the Fc region or variant Fc region comprises K447del, with residue numbering according to the EU index of Kabat.

88. A conjugate, comprising a variant PD-L1 of any of embodiments 1-54, or an immunomodulatory protein of any of embodiments 55-87 linked to a moiety.

89. The conjugate of embodiment 88, wherein the moiety is a targeting moiety that specifically binds to a molecule on the surface of a cell.

90. The conjugate of embodiment 89, wherein the targeting moiety specifically binds to a molecule on the surface of an immune cell, optionally wherein the immune cell is an antigen presenting cell or a lymphocyte.

91. The conjugate of embodiment 89, wherein the targeting moiety is a tumor-localizing moiety that binds to a molecule on the surface of a tumor.

92. The conjugate of any of embodiments 88-91, wherein the moiety is a protein, a peptide, nucleic acid, small molecule or nanoparticle.

93. The conjugate of any of embodiments 88-93, wherein the moiety is an antibody or antigen-binding fragment.

94. The conjugate of any of embodiments 88-94, wherein the conjugate is divalent, tetravalent, hexavalent or octavalent.

95. The conjugate of any of embodiments 88-94 that is a fusion protein.

96. A nucleic acid molecule, encoding a variant PD-L1 polypeptide of any of embodiments 1-54, an immunomodulatory protein of any of embodiments 55-87 or a conjugate that is a fusion protein of any of embodiments 88-95.

97. The nucleic acid molecule of embodiment 96 that is synthetic nucleic acid.

98. The nucleic acid molecule of embodiment 96 or embodiment 97 that is cDNA.

99. A vector, comprising the nucleic acid molecule of any of embodiments 96-98.

100. The vector of embodiment 99 that is an expression vector.

101. The vector of embodiment 99 or embodiment 100, wherein the vector is a mammalian expression vector or a viral vector.

102. A cell, comprising the vector of embodiment 100 or embodiment 101.

103. The cell of embodiment 102 that is a mammalian cell.

104. The cell of embodiment 102 or embodiment 103 that is a human cell.

105. A method of producing a variant PD-L1 polypeptide or an immunomodulatory protein, comprising introducing the nucleic acid molecule of any of embodiments 96-98 or vector of any of embodiments 99-101 into a host cell under conditions to express the protein in the cell.

106. The method of embodiment 105, further comprising isolating or purifying the variant PD-L1 polypeptide or immunomodulatory protein from the cell.

107. A method of engineering a cell expressing a variant PD-L1 variant polypeptide, comprising introducing a nucleic acid molecule encoding the variant PD-L1 polypeptide of any of embodiments 1-54 into a host cell under conditions in which the polypeptide is expressed in the cell.

108. An engineered cell, expressing the variant PD-L1 polypeptide of any of embodiments 1-54, the immunomodulatory protein of any of embodiments 55-87, a conjugate that is a fusion protein of any of claims 88-95, the nucleic acid molecule of any of embodiments 96-98 or the vector of any of embodiments 99-101.

109. The engineered cell of embodiment 108, wherein the variant PD-L1 polypeptide or immunomodulatory protein is encoded by a nucleic acid comprising a sequence of nucleotides encoding comprises a signal peptide.

110. The engineered cell of embodiment 108 or embodiment 109, wherein the variant PD-L1 polypeptide or immunomodulatory protein does not comprise a transmembrane domain and/or is not expressed on the surface of the cell.

111. The engineered cell of any of embodiments 108-110, wherein the variant PD-L1 polypeptide or immunomodulatory protein is secreted from the engineered cell.

112. The engineered cell of embodiment 108 or embodiment 110, wherein the engineered cell comprises a variant PD-L1 polypeptide that comprises a transmembrane domain and/or is the transmembrane immunomodulatory protein of any of embodiments 48-54.

113. The engineered cell of any of embodiments 108, 110 and 112, wherein the variant PD-L1 polypeptide is expressed on the surface of the cell.

114. The engineered cell of any of embodiments 108-113, wherein the cell is an immune cell.

115. The engineered cell of embodiment 114, wherein the immune cell is an antigen presenting cell (APC) or a lymphocyte.

116. The engineered cell of any of embodiments 108-115 that is a primary cell.

117. The engineered cell of any of embodiments 108-116, wherein the cell is a mammalian cell.

118. The engineered cell of any of embodiments 108-117, wherein the cell is a human cell.

119. The engineered cell of any of embodiments 108-118, wherein the cell is a lymphocyte and the lymphocyte is a T cell.

120. The engineered cell of embodiment 115, wherein the cell is an APC and the APC is an artificial APC.

121. The engineered cell of any of embodiments 108-120, further comprising a chimeric antigen receptor (CAR) or an engineered T-cell receptor.

122. An infectious agent, comprising a nucleic acid molecule encoding a variant PD-L1 polypeptide of any of embodiments 1-54 or an immunomodulatory protein of any of embodiments 55-84 or a conjugate that is a fusion protein of any of claims 88-95.

123. The infectious agent of embodiment 122, wherein the encoded variant PD-L1 polypeptide or immunomodulatory protein does not comprise a transmembrane domain and/or is not expressed on the surface of a cell in which it is expressed.

124. The infectious agent of embodiment 122 or embodiment 123, wherein the encoded variant PD-L1 polypeptide or immunomodulatory protein is secreted from a cell in which it is expressed.

125. The infectious agent of embodiment 122, wherein the encoded variant PD-L1 polypeptide comprises a transmembrane domain.

126. The infectious agent of embodiment 122 or embodiment 125, wherein the encoded variant PD-L1 polypeptide is expressed on the surface of a cell in which it is expressed.

127. The infectious agent of any of embodiments 122-126, wherein the infectious agent is a bacterium or a virus.

128. The infectious agent of embodiment 127, wherein the infectious agent is a virus and the virus is an oncolytic virus.

129. The infectious agent of embodiment 128, wherein the oncolytic virus is an adenovirus, adeno-associated virus, herpes virus, Herpes Simplex Virus, Vesticular Stomatic virus, Reovirus, Newcastle Disease virus, parvovirus, measles virus, vesticular stomatitis virus (VSV), Coxsackie virus or a Vaccinia virus.

130. The infectious agent of embodiment 129, wherein the virus specifically targets dendritic cells (DCs) and/or is dendritic cell-tropic.

131. The infectious agent of embodiment 130, wherein the virus is a lentiviral vector that is pseudotyped with a modified Sindbis virus envelope product.

132. The infectious agent of any of embodiments 122-131, further comprising a nucleic acid molecule encoding a further gene product that results in death of a target cell or that can augment or boost an immune response.

133. The infectious agent of embodiment 132, wherein the further gene product is selected from an anticancer agent, anti-metastatic agent, an antiangiogenic agent, an immunomodulatory molecule, an immune checkpoint inhibitor, an antibody, a cytokine, a growth factor, an antigen, a cytotoxic gene product, a pro-apoptotic gene product, an anti-apoptotic gene product, a cell matrix degradative gene, genes for tissue regeneration or reprogramming human somatic cells to pluripotency.

134. A pharmaceutical composition, comprising the variant PD-L1 polypeptide of any of embodiments 1-47 and 48-54, an immunomodulatory protein of any of embodiments 55-87, a conjugate of any of embodiments 88-95 or an engineered cell of any of embodiments 108-121 or an infectious agent of any of embodiments 122-133.

135. The pharmaceutical composition of embodiment 134, comprising a pharmaceutically acceptable excipient.

136. The pharmaceutical composition of embodiment 134 or embodiment 135, wherein the pharmaceutical composition is sterile.

137. An article of manufacture comprising the pharmaceutical composition of any of embodiments 134-136 in a vial.

138. The article of manufacture of embodiment 137, wherein the vial is sealed.

139. A kit comprising the pharmaceutical composition of any of embodiments 134-136, and instructions for use.

140. A kit comprising the article of manufacture of embodiment 137 or embodiment 138, and instructions for use.

141. A method of modulating an immune response in a subject, comprising administering the pharmaceutical composition of any of embodiments 123-125 to the subject.

142. A method of modulating an immune response in a subject, comprising administering the engineered cells of any of embodiments 108-121 to the subject.

143. The method of embodiment 142, wherein the engineered cells are autologous to the subject.

144. The method of embodiment 142, wherein the engineered cells are allogenic to the subject.

145. The method of any of embodiments 141-144, wherein modulating the immune response treats a disease or condition in the subject.

146. The method of any of embodiments 141-145, wherein the immune response is increased.

147. The method of any of embodiments 141-146, wherein a variant PD-L1 polypeptide or immunomodulatory protein that is soluble is administered to the subject.

148. The method of any of embodiments 141-147, wherein the variant PD-L1 polypeptide or immunomodulatory protein is an Fc fusion protein.

149. The method of any of embodiments 142-148, wherein a variant PD-L1 polypeptide of any of embodiments 1-47 and 52-54, the immunomodulatory protein of any of embodiments 55-87, or the conjugate of 88-95 is administered to the subject.

150. The method of any of embodiments 142-146, wherein an engineered cell comprising a secretable variant PD-L1 polypeptide is administered to the subject.

151. The method of any of embodiments 142-146 and 150, wherein an engineered cell of any of embodiments 97-100 and 103-110 is administered to the subject.

152. The method of any of embodiments 141, 145 and 146, wherein an infectious agent encoding a variant PD-L1 polypeptide that is a secretable immunomodulatory protein is administered to the subject, optionally under conditions in which the infectious agent infects a tumor cell or immune cell and the secretable immunomodulatory protein is secreted from the infected cell.

153. The method of any of embodiments 141-152, wherein the disease or condition is a tumor or cancer.

154. The method of any one of embodiments 141-153, wherein the disease or condition is selected from melanoma, lung cancer, bladder cancer, a hematological malignancy, liver cancer, brain cancer, renal cancer, breast cancer, pancreatic cancer, colorectal cancer, spleen cancer, prostate cancer, testicular cancer, ovarian cancer, uterine cancer, gastric carcinoma, a musculoskeletal cancer, a head and neck cancer, a gastrointestinal cancer, a germ cell cancer, or an endocrine and neuroendocrine cancer.

155. The method of any of embodiments 141-145, wherein the immune response is decreased.

156. The method of any of embodiments 141, 145 and 155, wherein an immunomodulatory protein or conjugate comprising a variant PD-L1 polypeptide linked to an

IgSF domain or a moiety that localizes to a cell or tissue of an inflammatory environment is administered to the subject.

157. The method of embodiment 156, wherein the binding molecule comprises an antibody or an antigen-binding fragment thereof or comprises a wild-type IgSF domain or variant thereof.

158. The method of any of embodiments 141-145 and 155-157, wherein the immunomodulatory protein of any of embodiments 57-76 or the conjugate of any of embodiments 77-84 is administered to the subject.

159. The method of any of embodiments 141-145 and 155, wherein a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein is administered to the subject.

160. The method of any of embodiments 142-145 and 155-159, wherein the engineered cell comprising a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein of any of embodiments 48-87 is administered to the subject.

161. The method of any of embodiments 141, 145 and 155, wherein an infectious agent encoding a variant PD-L1 polypeptide that is a transmembrane immunomodulatory protein is administered to the subject, optionally under conditions in which the infectious agent infects a tumor cell or immune cell and the transmembrane immunomodulatory protein is expressed on the surface of the infected cell.

162. The method of any of embodiments 141-145 and 155-161, wherein the disease or condition is an inflammatory or autoimmune disease or condition.

163. The method of any of embodiments 141-145 and 155-162, wherein the disease or condition is an antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis, a vasculitis, an autoimmune skin disease, transplantation, a Rheumatic disease, an inflammatory gastrointestinal disease, an inflammatory eye disease, an inflammatory neurological disease, an inflammatory pulmonary disease, an inflammatory endocrine disease, or an autoimmune hematological disease.

164. The method of embodiment 162 or embodiment 163, wherein the disease or condition is selected from inflammatory bowel disease, transplant, Crohn's disease, ulcerative colitis, multiple sclerosis, asthma, rheumatoid arthritis, or psoriasis.

IX. EXAMPLES

[0437] The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

EXAMPLE 1

Generation of Mutant DNA Constructs of IgSF Domains

[0438] Example 1 describes the generation of mutant DNA constructs of human PD-L1 IgSF domains for translation and expression on the surface of yeast as yeast display libraries.

A. Degenerate Libraries

[0439] Constructs were generated based on a wildtype human PD-L1 sequence set forth in SEQ ID NO:309 containing the immunoglobulin-like V-type (IgV) IgV domain as follows:

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDL
KVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKV
NA

[0440] For libraries that target specific residues for complete or partial randomization with degenerate codons, degenerate codons, such as specific mixed base sets to code for various amino acid substitutions, were generated using an algorithm at the URL: rosettadesign.med.unc.edu/SwiftLib/.

[0441] In general, positions to mutate were chosen from direct crystal structure information for PDL1::PD1 complex (eg PDB: 4ZQK). Alternatively, a homology models may be generated if structures of homologous protein complexes are available. Using the structural information, a structure viewer (available at the URL: spdbv.vital-it.ch) was used to identify contact or non-contact interface residues for mutagenesis with degenerate codons.

[0442] The next step in library design was the alignment of human, mouse, rat, and monkey PD-L1 sequences to identify which of the residues chosen for mutagenesis are conserved residues. Based on this analysis, conserved target residues were mutated with degenerate codons that only specified conservative amino acid changes plus the wild-type residue. Residues that were not conserved, were mutated more aggressively, but also including the wild-type residue. Degenerate codons that also encoded the wild-type residue were deployed to avoid excessive mutagenesis of target protein. For the same reason, only up to 20 positions were targeted for mutagenesis for each library. Mutational analysis was focused on contact and non-contact interfacial residues that were within 6 Å of the binding surface with their side chains directed toward the ligand/counter structure.To generate DNA encoding the targeted library, overlapping oligos of up to 80 nucleotides in length and containing degenerate codons at the residue positions

targeted for mutagenesis, were ordered from Integrated DNA Technologies (Coralville, USA). The oligonucleotides were dissolved in sterile water, mixed in equimolar ratios, heated to 95°C for five minutes and slowly cooled to room temperature for annealing. IgV domain-specific oligonucleotide primers that anneal to the start and end of the IgV domain gene sequence were then used to generate a first PCR product. IgV domain-specific oligonucleotides which overlap by 40bp with pBYDS03 cloning vector (Life Technologies USA), beyond and including the BamHI and KpnI cloning sites, were then used to amplify 100ng of PCR product from the prior step to generate a total of at least 12 μg of DNA for every elextroproation. Both PCR's were by polymerase chain reaction (PCR) using OneTaq 2x PCR master mix (New England Biolabs, USA). The second PCR products were purified using a PCR purification kit (Qiagen, Germany) and resuspended in sterile deionized water. Alternatively, Ultramers (Integrated DNA Technologies) of up to 200 bp in length were used in conjunction with megaprimer PCR (URL: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC146891/pdf/253371.pdf) to generate larger stretches of degenerate codons that could not be as easily generated using multiple small overlapping primers. Following the generation of full length product using megaprimer PCR, the mutant IgV domain library was PCR amplified again using DNA primers containing 40 bp overlap region with the modified pBYDS03 cloning variant for homologous recombination into yeast.

[0443] To prepare for library insertion, pBYDS03 vector was digested with BamHI and KpnI restriction enzymes (New England Biolabs, USA) and the large vector fragment was gel-purified and dissolved in sterile, deionized water. Electroporation-ready DNA for the next step was generated by mixing 12 μg of library DNA insert with 4 μg of linearized vector in a total volume of 50 μl deionized and sterile water. An alternative method to generate targeted libraries, is to carry out site-directed mutagenesis (Multisite kit, Agilent, USA) of the target IgV domain with oligonucleotides containing degenerate codons. This approach was used to generate sublibraries that only target a few specific stretches of DNA for mutagenesis. In these cases, sublibraries were mixed before proceeding to the selection steps. In general, library sizes are in the range of 10E7 (10^7) to 10E8 (10^8) clones, except that sublibraries are only in the range of 10E4 (10^4) to 10E5 (10^5).

B. Random Libraries

[0444] Random libraries were also constructed to identify variants of the IgV domain of PD-L1 set forth in SEQ ID NO:309 (containing the PD-L1 IgV domain corresponding to residues 19-132 as set forth in UniProt Accession No. Q9NZQ7 flanked by adjacent N- and C-terminal residues of the wildtype sequence). DNA encoding the wild-type IgV domain was cloned between the BamHI and KpnI sites of the yeast display vector pBYDS03. The DNA was then mutagenized with the Genemorph II Kit (Agilent, USA) so as to generate an average of three to five amino acid changes per library variant. Mutagenized DNA was then amplified by the two-step PCR and further processed as described above for targeted libraries.

EXAMPLE 2

Introduction of DNA Libraries into Yeast

[0445] Example 2 describes the introduction of PD-L1 DNA libraries into yeast.

[0446] To introduce degenerate and random library DNA into yeast, electroporation-competent cells of yeast strain BJ5464 (ATCC.org; ATCC number 208288) were prepared and electroporated on a Gene Pulser II (Biorad, USA) with the electroporation-ready DNA from the steps above essentially as described (Colby, D.W. et al. 2004 Methods Enzymology 388, 348-358). The only exception is that transformed cells were grown in non-inducing minimal selective SCD-Leu medium to accommodate the LEU2 selective marker carried by modified plasmid pBYDS03. One liter of SCD-Leu media consists of 14.7 grams sodium citrate, 4.29 grams citric acid monohydrate, 20 grams dextrose, 6.7 grams yeast nitrogen base, and 1.6 grams yeast synthetic drop-out media supplement without leucine. The medium was filter sterilized before use using a 0.22 μm vacuum filter device.

[0447] Library size was determined by plating serial dilutions of freshly recovered cells on SCD-Leu agar plates and then extrapolating library size from the number of single colonies from plating that generated at least 50 colonies per plate. The remainder of the electroporated culture was grown to saturation and cells from this culture were subcultured 1/100 into the same medium once more and grown to saturation to minimize the fraction of untransformed cells and to allow for segregation of plasmid from cells that may contain two or more library variants. To maintain library diversity, this subculturing step was carried out using an inoculum that contained at least 10x more cells than the calculated library size. Cells from the second saturated culture were

resuspended in fresh medium containing sterile 25% (weight/volume) glycerol to a density of 10E10/mL and frozen and stored at -80°C (frozen library stock).

EXAMPLE 3

Yeast Selection

[0448] Example 3 describes the selection of yeast cells expressing affinity-modified variants of PD-L1.

[0449] A number of cells equal to at least 10 times the estimated library size were thawed from individual library stocks, suspended to 0.1 x 10E6 cells/mL in non-inducing SCD-Leu medium, and grown overnight. The next day, a number of cells equal to 10 times the library size were centrifuged at 2000 RPM for two minutes and resuspended to 0.5 x 10E6 cells/mL in inducing SCDG-Leu media. One liter of SCDG-Leu induction media consists of 5.4 grams Na_2HPO_4, 8.56 grams $NaH_2PO_4 \cdot H_20$, 20 grams galactose, 2.0 grams dextrose, 6.7 grams yeast nitrogen base, and 1.6 grams yeast synthetic drop out media supplement without leucine dissolved in water and sterilized through a 0.22 μm membrane filter device. The culture was grown in induction medium for 1 day at room temperature to induce expression of library proteins on the yeast cell surface.

[0450] Cells were sorted two to three times using Protein A magnetic beads (New England Biolabs, USA) loaded with cognate ligand to reduce non-binders and enrich for all variant PD-L1 variants with the ability to bind their exogenous recombinant counter-structure proteins. This was then followed by one to two rounds of fluorescence activated cell sorting (FACS) using exogenous counter-structure protein staining to enrich the fraction of yeast cells that displays improved binders. Magnetic bead enrichment and selections by flow cytometry were carried out essentially as described in Miller K.D. et al., Current Protocols in Cytometry 4.7.1-4.7.30, July 2008.

[0451] With PD-L1 libraries, target ligand proteins were human rPD-1.Fc (i.e., recombinant PD-1-Fc fusion protein from R&D Systems, USA). Magnetic Protein A beads were obtained from New England Biolabs, USA. For two-color, flow cytometric sorting, a Bio-Rad S3e sorter was used. PD-L1 display levels were monitored with an anti-hemagglutinin antibody labeled with Alexafluor 488 (Life Technologies, USA). Ligand binding of Fc fusion protein to rPD-1.Fc, was detected with PE conjugated human Ig specific goat Fab (Jackson ImmunoResearch, USA). Doublet yeast were gated out using forward scatter (FSC) / side scatter (SSC) parameters, and

sort gates were based upon higher ligand binding detected in FL2 that possessed more limited tag expression binding in FL1. Alternatively, selections were performed with human rCD80.Fc (i.e., human recombinant CD80 Fc fusion protein from R&D Systems, USA). Selections were carried out largely as described for PD-1 above.

[0452] Yeast outputs from the flow cytometric sorts were assayed for higher specific binding affinity. Sort output yeast were expanded and re-induced to express the particular IgSF affinity modified domain variants they encode. This population then can be compared to the parental, wild-type yeast strain, or any other selected outputs, such as the bead output yeast population, by flow cytometry.

[0453] For PD-L1, the second round FACS outputs (F2) were compared to parental for binding rPD-1.Fc or rCD80.Fc by double staining each population with anti-HA (hemagglutinin) tag expression and the anti-human Fc secondary to detect ligand binding.

[0454] Selected variant PD-L1 IgV domains were further formatted as fusion proteins and tested for binding and functional activity as described below.

EXAMPLE 4

Reformatting Selection Outputs as Fc-Fusions and in Various Immunomodulatory Protein Types

[0455] Example 4 describes reformatting of selection outputs identified in Example 3 as immunomodulatory proteins containing an affinity modified (variant) immunoglobulin-like V-type (IgV) domain of PD-L1 fused to an Fc molecule (variant IgV domain -Fc fusion molecules).

[0456] Output cell pools from final flow cytometric PD-L1 sorts were grown to terminal density in SCD-Leu medium. Plasmid DNA from each output was isolated using a yeast plasmid DNA isolation kit (Zymoresearch, USA). For Fc fusions, PCR primers with added restriction sites suitable for cloning into the Fc fusion vector of choice were used to batch-amplify from the plasmid DNA preps the coding DNA for the mutant target IgV domains. After restriction digestion, the PCR products were ligated into Fc fusion vector followed by heat shock transformation into *E. coli* strain XL1 Blue (Agilent, USA) or NEB5alpha (New England Biolabs, USA) as directed by supplier. Alternatively, the outputs were PCR amplified with primers containing 40 bp overlap regions on either end with Fc fusion vector to carry out in vitro recombination using Gibson Assembly Mastermix (New England Biolabs), which was

subsequently used in heat shock transformation into E. Coli strain NEB5alpha. Exemplary of an Fc fusion vector is pFUSE-hIgG1-Fc2 (Invivogen, USA).

[0457] Dilutions of transformation reactions were plated on LB-agar containing 100 μg/mL carbenicillin (Teknova, USA) to isolate single colonies for selection. Up to 96 colonies from each transformation were then grown in 96 well plates to saturation overnight at 37°C in LB-broth containing 100 μg/mL carbenicillin (Teknova cat # L8112) and a small aliquot from each well was submitted for DNA sequencing of the IgV domain insert in order to identify mutation(s) in all clones. Sample preparation for DNA sequencing was carried out using protocols provided by the service provider (Genewiz; South Plainfield, NJ). After removal of sample for DNA sequencing, glycerol was then added to the remaining cultures for a final glycerol content of 25% and plates were stored at -20°C for future use as master plates (see below). Alternatively, samples for DNA sequencing were generated by replica plating from grown liquid cultures to solid agar plates using a disposable 96 well replicator (VWR, USA). These plates were incubated overnight to generate growth patches and the plates were submitted to Genewiz as specified by Genewiz.

[0458] After identification of clones of interest from analysis of Genewiz-generated DNA sequencing data, clones of interest were recovered from master plates and individually grown to density in liquid LB-broth containing 100 μg/mL carbenicillin (Teknova, USA) and cultures were then used for preparation of plasmid DNA of each clone using a standard kit such as the PureYield Plasmid Miniprep System (Promega, USA) or the MidiPlus kit (Qiagen). Identification of clones of interest from Genewiz sequencing data generally involved the following steps. First, DNA sequence data files were downloaded from the Genewiz website. All sequences were then manually curated so that they start at the beginning of the IgV domain coding region. The curated sequences were then batch-translated using a suitable program available at the URL: www.ebi.ac.uk/Tools/st/emboss_transeq/. The translated sequences were then aligned using a suitable program available at the URL: multalin.toulouse.inra.fr/multalin/multalin.html. Alternatively, Genewiz sequences were processed to generate alignments using Ugene software (http://ugene.net).

[0459] Clones of interest were then identified from alignments using the following criteria: 1.) identical clone occurs at least two times in the alignment and 2.) a mutation occurs at least two times in the alignment and preferably in distinct clones. Clones that meet at least one of these

criteria were assumed to be clones that have been enriched by the sorting process due to improved binding.

[0460] To generate recombinant immunomodulatory proteins that are Fc fusion proteins containing an affinity-modified variant of the PD-L1 IgV domain (e.g. variant PD-L1 IgV-Fc), the encoding DNA was generated to encode a protein as follows: variant (mutant) IgV domain followed by a linker of three alanines (AAA) followed by a human IgG1 Fc set forth in SEQ ID NO: 1157 containing the mutations R292C, N297G and V302C by EU numbering (corresponding to R77C, N82G and V87C with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 187). Since the construct does not include any antibody light chains that can form a covalent bond with a cysteine, the human IgG1 Fc also contains replacement of the cysteine residues to a serine residue at position 220 (C220S) by EU numbering (corresponding to position 5 (C5S) with reference to the wild-type or unmodified Fc set forth in SEQ ID NO: 187.

EXAMPLE 5

Expression and Purification of Fc-Fusions

[0461] Example 5 describes the high throughput expression and purification of Fc-fusion proteins containing variant IgV PD-L1 as described in the above Examples.

[0462] Recombinant variant Fc fusion proteins were produced from suspension-adapted human embryonic kidney (HEK) 293 cells using the with Expi293 expression system (Invitrogen, USA). 4μg of each plasmid DNA from the previous step was added to 200μL Opti-MEM (Invitrogen, USA) at the same time as 10.8μL ExpiFectamine was separately added to another 200μL Opti-MEM. After 5 minutes, the 200μL of plasmid DNA was mixed with the 200μL of ExpiFectamine and was further incubated for an additional 20 minutes before adding this mixture to cells. Ten million Expi293 cells were dispensed into separate wells of a sterile 10ml, conical bottom, deep 24 well growth plate (Thomson Instrument Company, USA) in a volume 4mL Expi293 media (Invitrogen, USA). Plates were shaken for 5 days at 120 RPM in a mammalian cell culture incubator set to 95% humidity and 8% CO_2. Following a 5 day incubation, cells were pelleted and culture supernatants were retained.

[0463] Proteins were purified from supernatants using a high throughput 96 well Filter Plate (Thomson Catalog number931919), each well loaded with 60μL of Mab SelectSure settled bead(GE Healthcare cat. no.17543801). Protein was eluted with four consecutive 200μL fractions, of 50mM Acetate pH3.3. Each fraction's pH was adjusted to above pH 5.0 with 4μL

2M Tris pH 8.0. Fractions were pooled and quantitated using 280nm absorbance measured by Nanodrop instrument (Thermo Fisher Scientific, USA), and protein purity was assessed by loading 5 μg of protein on NUPAGE pre-cast, polyacrylamide gels (Life Technologies, USA) under denaturing and non-reducing conditions and subsequent gel electrophoresis. Proteins were visualized in gel using standard Coomassie staining.

EXAMPLE 6

Assessment of Binding of Affinity-Matured IgSF Domain-Containing Molecules

A. Binding to Cell-Expressed Counter Structure

[0464] This Example describes Fc-fusion binding studies of purified proteins from the above Examples to assess specificity and affinity of PD-L1 domain variant immunomodulatory proteins for a cognate binding partner.

[0465] Binding studies were carried out using Jurkat/IL-2 reporter cells (purchased from Promega Corp. USA) that were then transduced to stably express human PD-1 (Jurkat/PD-1 cells). For staining by flow cytometry, 100,000 Jurkat/PD-1 cells or negative control (Jurkat only) were plated in 96 well round bottom plates. Cells were spun down and resuspended in staining buffer (PBS (phosphate buffered saline), 1% BSA (bovine serum albumin), and 0.1% sodium azide) for 20 minutes to block non-specific binding. Afterwards, cells were centrifuged again and resuspended in 50μL staining buffer containing 100 nM to 46pM of each candidate PD-L1 variant Fc fusion protein. As controls, a full extracellular domain of wild-type PD-L1 (composed of one IgV and one IgC domain) fused to Fc ("Full length ECD of PD-L1") and a IgV domain of wild-type PD-L1 ("wild type PD-L1 IgV") were tested. Primary staining was performed on ice for 45 minutes, before washing cells twice in 150μL staining buffer. PE-conjugated anti-human Fc (Jackson ImmunoResearch, USA) was diluted 1:150 in 50 μL staining buffer and added to cells and incubated another 30 minutes on ice. Secondary antibody was washed out twice, cells were fixed in 4% formaldehyde/PBS, and samples were analyzed on Intellicyt flow cytometer (Intellicyt Corp,, USA).

[0466] Mean Fluorescence Intensity (MFI) was calculated and compared to wildtype PD-L1 IgV as control with FlowJo Version 10 (FlowJo Version 10, USA). Results for the binding studies for exemplary tested variant PD-L1 IgV-Fc fusion molecules are shown in Table 10.

Table 10 also indicates amino acid substitutions (replacements or insertions designated by "ins") in the IgV of the variant PD-L1 selected in the screen described above. In the Table, the exemplary amino acid substitutions and insertions in the IgV domain are designated by amino acid position number corresponding to amino acid positions in the respective reference unmodified mature PD-L1 extracellular domain (ECD) sequence set forth in SEQ ID NO:30 or 1728. The amino acid position is indicated in the middle, with the corresponding unmodified (e.g. wild-type) amino acid listed before the number and the identified variant amino acid substitution (or inserted designated by "ins") listed after the number. Column 2 sets forth the SEQ ID NO identifier for each variant IgV domain contained in the variant IgV-Fc fusion molecule.

[0467] Also shown is the binding activity as measured by the Mean Fluorescence Intensity (MFI) value for binding of 50 nM of each variant Fc-fusion molecule to Jurkat/PD-1 cells and the ratio of the MFI compared to the binding of the corresponding unmodified (wildtype) IgV-Fc fusion molecule not containing the amino acid substitution(s) to PD-1. As shown in Table 10, the selections resulted in the identification of a number of PD-L1 IgSF (e.g. IgV) domain variants that were affinity-modified to exhibit increased binding for PD-1.

TABLE 10: Selected PD-L1 variants and binding data.

PD-L1 Mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells	
		MFI at 50nM	Fold increase over wildtype PD-L1 IgV-Fc
K28N, M41V, N45T, H51N, K57E	244	12585	2.4
I20L, I36T, N45D, I47T	245	3119	0.6
I20L, M41K, K44E	246	9206	1.8
P6S, N45T, N78I, I83T	247	419	0.1
N78I	248	2249	0.4
M41K, N78I	249	Little or no protein produced	
N17D, N45T, V50A, D72G	255	Little or no protein produced	
N45T, V50A	257	23887	4.6
I20L, N45T, N78I	258	29104	5.6
N45T, N78I	250	24865	4.7
I20L, N45T	251	24279	4.6
I20L, N45T, V50A	259	34158	6.5
N45T	252	6687	1.3
M41K	253	5079	1.0
M41V, N45T	260	Little or no protein produced	
M41K, N45T	261	Little or no protein produced	
A33D, S75P, D85E	262	685	0.1

TABLE 10: Selected PD-L1 variants and binding data.			
PD-L1 Mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells	
		MFI at 50nM	Fold increase over wildtype PD-L1 IgV-Fc
M18I, M41K, D43G, H51R, N78I	263	20731	4.0
V11E, I20L, I36T, N45D, H60R, S75P	264	3313	0.6
A33D, V50A		Little or no protein produced	
S16G, A33D, K71E, S75P	266	Little or no protein produced	
E27G, N45T, M97I	267	881	0.2
E27G, N45T, K57R	268	5022	1.0
A33D, E53V	269	650	0.1
D43G, N45D, V58A	270	63960	12.2
E40G, D43V, N45T, V50A	271	809	0.2
Y14S, K28E, N45T	272	16232	3.1
A33D, N78S	273	1725	0.3
A33D, N78I	274	8482	1.6
A33D, N45T	275	17220	3.3
E27G, N45T, V50A	277	25267	4.8
N45T, V50A, N78S	278	28572	5.4
N45T, V50A	257	18717	3.6
I20L, N45T, V110M	279	464	0.1
I20L, I36T, N45T, V50A	280	7658	1.5
N45T, L74P, S75P	281	5251	1.0
N45T, S75P	282	12200	2.3
S75P, K106R	283	388	0.1
S75P	284	1230	0.2
A33D, S75P	285	306	0.1
A33D, S75P, D104G	286	251	0.0
A33D, S75P	287	1786	0.3
I20L, E27G, N45T, V50A	288	29843	5.7
I20L, E27G, D43G, N45D, V58A, N78I	289	69486	13.3
I20L, D43G, N45D, V58A, N78I	290	72738	13.9
I20L, A33D, D43G, N45D, V58A, N78I	291	80205	15.3
I20L, D43G, N45D, N78I	292	67018	12.8
E27G, N45T, V50A, N78I	293	30677	5.9
N45T, V50A, N78I	294	32165	6.1
V11A, I20L, E27G, D43G, N45D, H51Y, S99G	295	73727	14.1
I20L, E27G, D43G, N45T, V50A	296	36739	7.0
I20L, K28E, D43G, N45D, V58A, Q89R, G101G-ins (G101GG)	1727	80549	15.4

TABLE 10: Selected PD-L1 variants and binding data.			
PD-L1 Mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells	
		MFI at 50nM	Fold increase over wildtype PD-L1 IgV-Fc
I20L, I36T, N45D	298	16870	3.2
I20L, K28E, D43G, N45D, E53G, V58A, N78I	299	139	0.0
A33D, D43G, N45D, V58A, S75P	300	58484	11.2
K23R, D43G, N45D	301	67559	12.9
I20L, D43G, N45D, V58A, N78I, D90G, G101D	302	259	0.0
D43G, N45D, L56Q, V58A, G101G-ins (G101GG)	303	88277	16.8
I20L, K23E, D43G, N45D, V58A, N78I	304	89608	17.1
I20L, K23E, D43G, N45D, V50A, N78I	305	88829	16.9
T19I, E27G, N45I, V50A, N78I, M97K	306	25496	4.9
I20L, M41K, D43G, N45D	307	599	0.1
K23R, N45T, N78I	308	84980	16.2
Full length ECD PD-L1	-	18465	3.5
Wild type PD-L1 IgV	309	5243	1.0
Anti-PD-1 monoclonal antibody (nivolumab)	-	79787	15.2
Human IgG	-	198	0.0

B. ForteBio Octet Binding Assay

[0468] Protein-protein interactions between PD-L1 domain variant immunomodulatory proteins and the binding partners PD-1 and CD80 were assessed using Fortebio binding assays. PD-1 or CD80 were loaded individually onto anti-human capture sensors (ForteBio Octet AHC) and Fc fusions of full length wildtype (unmodified) ECD of PD-L1, wildtype (unmodified) PD-L1 IgV-Fc fusion molecule, or variant PD-L1 IgV-Fc fusion molecules were bound to the receptors at a single concentration of 100nM.

[0469] Loading response of anti-human capture sensors of each binding protein being tested with the variant IgV-Fc fusion molecule was determined and compared to the response of wildtype PD-L1 IgV-Fc. A ratio between the response of each variant PD-L1 IgV-Fc fusion molecule to PD-1 and CD80 was also determined as set forth in Table 11A-B. In each of the Tables below, Column 2 sets forth the SEQ ID NO identifier for each variant IgV domain contained in the tested variant IgV-Fc fusion molecule.

[0470] As shown in Table 11A-B, the selections resulted in the identification of a number of PD-L1 IgSF (e.g. IgV) domain variants that were affinity-modified to exhibit altered binding for PD-1 and/or CD80.

TABLE 11A: ForteBio Binding Data.

PD-L1 Mutation(s)	SEQ ID NO (IgV)	PD-1: Fc Response	Fold over WT PD-L1 IgV-Fc	CD80:Fc Response	Fold over WT PD-L1 IgV-Fc	PD-1: CD80 ratio
K28N, M41V, N45T, H51N, K57E	244	1.16	0.8	0.49	0.6	2.4
I20L, I36T, N45D, I47T	245	0.73	0.5	0.52	0.7	1.4
I20L, I36T, N45D	254	1.25	0.9	0.61	0.8	2.0
I20L, M41K, K44E	246	2.26	1.6	1.67	2.1	1.4
P6S, N45T, N78I, I83T	247	0.27	0.2	0.23	0.3	1.2
I20L, F49S	256	0.79	0.6	0.58	0.7	1.4
N78L	248	2.23	1.6	1.55	2.0	1.4
N45T, V50A	257	1.90	1.4	0.79	1.0	2.4
I20L, N45T, N78I	258	2.34	1.7	1.85	2.3	1.3
N45T, N78I	250	2.38	1.7	1.73	2.2	1.4
I20L, N45T	251	2.30	1.7	1.58	2.0	1.5
I20L, N45T, V50A	259	2.32	1.7	1.22	1.5	1.9
N45T	252	1.34	1.0	0.65	0.8	2.0
M41k	253	2.25	1.6	1.70	2.2	1.3
A33D, S75P, D85E	262	0.84	0.6	0.55	0.7	1.5
M18I, M41K, D43G, H51R, N78I	263	2.33	1.7	2.14	2.7	1.1
V11E, I20L, I36T, N45D, H60R, S75P	264	0.93	0.7	0.56	0.7	1.7
E27G, N45T, M97I	267	2.10	1.5	1.05	1.3	2.0
E27G, N45T, K57R	268	2.31	1.7	1.57	2.0	1.5
A33D, E53V	269	1.09	0.8	0.62	0.8	1.7
D43G, N45D, V58A	270	1.55	1.1	0.71	0.9	2.2
Y14S, K28E, N45T	272	2.28	1.7	1.18	1.5	1.9
A33D, N78S	273	1.61	1.2	0.79	1.0	2.0
A33D, N78I	274	2.35	1.7	1.57	2.0	1.5
A33D, N45T	275	1.90	1.4	0.80	1.0	2.4
A33D, N45T, N78I	276	2.34	1.7	1.59	2.0	1.5
E27G, N45T, V50A	277	2.26	1.6	1.22	1.5	1.9
N45T, V50A, N78S	278	2.23	1.6	0.88	1.1	2.5
N45T, V50A	257	1.79	1.3	0.63	0.8	2.8
I20L, N45T, V110M	279	0.38	0.3	0.27	0.3	1.4
I20L, I36T, N45T, V50A	280	2.27	1.7	0.96	1.2	2.4
N45T, L74P, S75P	281	0.90	0.7	0.44	0.6	2.0

TABLE 11A: ForteBio Binding Data.

PD-L1 Mutation(s)	SEQ ID NO (IgV)	PD-1: Fc Response	Fold over WT PD-L1 IgV-Fc	CD80:Fc Response	Fold over WT PD-L1 IgV-Fc	PD-1: CD80 ratio
N45T, S75P	282	2.31	1.7	1.24	1.6	1.9
S75P, K106R	283	0.84	0.6	0.45	0.6	1.9
S75P	284	2.09	1.5	1.09	1.4	1.9
A33D, S75P	285	0.72	0.5	0.43	0.5	1.7
A33D, S75P, D104G	286	0.71	0.5	0.66	0.8	1.1
A33D, S75P	287	2.07	1.5	0.93	1.2	2.2
Full length ECD PD-L1	-	2.53	1.8	1.46	1.8	1.7
Wild type PD-L1 IgV	309	1.37	1.0	0.79	1.0	1.7

TABLE 11B. ForteBio Binding Data.

PD-L1 Mutation(s)	SEQ ID NO (IgV)	PD-1: Fc Response	Fold over WT PD-L1 IgV	CD80:Fc Response	Fold over WT PD-L1 IgV	PD-1: CD80 ratio
I20L, E27G, N45T, V50A	288	1.08	2.0	0.39	3.2	2.7
I20L, E27G, D43G, N45D, V58A, N78I	289	1.20	2.2	0.62	5.1	1.9
I20L, D43G, N45D, V58A, N78I	290	1.27	2.4	0.54	4.5	2.3
I20L, A33D, D43G, N45D, V58A, N78I	291	1.22	2.3	0.47	3.9	2.6
I20L, D43G, N45D, N78I	292	1.25	2.3	0.49	4.0	2.6
E27G, N45T, V50A, N78I	293	1.12	2.1	0.48	3.9	2.4
N45T, V50A, N78I	294	1.24	2.3	0.31	2.5	4.0
V11A, I20L, E27G, D43G, N45D, H51Y, S99G	295	1.20	2.2	0.28	2.3	4.3
I20L, E27G, D43G, N45T, V50A	296	1.10	2.1	0.55	4.5	2.0
I20L, K28E, D43G, N45D, V58A, Q89R, G101G-ins (G101GG)	1727	1.20	2.2	0.06	0.5	18.9
I20L, I36T, N45D	298	0.72	1.3	0.10	0.8	7.2
A33D, D43G, N45D, V58A, S75P	300	0.67	1.2	0.09	0.7	7.5
K23R, D43G, N45D	301	1.08	2.0	0.27	2.2	4.1
I20L, D43G, N45D, V58A, N78I, D90G, G101D	302	-0.02	0.0	-0.04	-0.3	0.5
D43G, N45D, L56Q, V58A, G101G-ins (G101GG)	303	1.24	2.3	0.07	0.6	18.4
I20L, K23E, D43G, N45D, V58A, N78I	304	1.20	2.2	0.37	3.0	3.3
I20L, K23E, D43G, N45D,	305	1.14	2.1	0.21	1.7	5.4

TABLE 11B. ForteBio Binding Data.						
PD-L1 Mutation(s)	**SEQ ID NO (IgV)**	**PD-1: Fc Response**	**Fold over WT PD-L1 IgV**	**CD80:Fc Response**	**Fold over WT PD-L1 IgV**	**PD-1: CD80 ratio**
V50A, N78I						
T19I, E27G, N45I, V50A, N78I, M97K	306	1.12	2.1	0.72	5.9	1.6
I20L, M41K, D43G, N45D	307	0.01	0.0	0.02	0.2	0.6
K23R, N45T, N78I	308	1.19	2.2	0.53	4.3	2.3
Full length ECD PD-L1	-	1.44	-	0.80	-	-
Wild type PD-L1 IgV	309	0.54	1.0	0.12	1.0	4.4

EXAMPLE 7

Assessment of Bioactivity of Affinity-Matured IgSF Domain-Containing Molecules Using Jurkat/IL2/PD-1 Reporter Assay

[0471] This Example describes a Jurkat/IL2/PD-1 reporter assay to assess bioactivity of PD-L1 domain variant immunomodulatory proteins for blockade of PD-1.

[0472] Jurkat effector cells expressing an IL-2-luciferase reporter and PD-1 on its surface were suspended in Jurkat Assay buffer (RPMI1640 + 5%FBS) at $2x10^6$ cells/mL and 2 µg/mL anti-CD28 was added. Jurkat cells were then plated at 50 µL/well for a total of 100,000 cells per well.

[0473] Variant PD-L1 IgV-Fc fusion molecules and control proteins (full length PD-L1-Fc, wild type PD-L1 IgV-Fc) or anti-PD-1 monoclonal antibody (nivolumab) were diluted to 200nM and 25 µL of each protein was added to the plated Jurkat cells. The Jurkat cells with PD-L1 variant IgV-Fc fusion molecules or control proteins were incubated for 15 minutes at room temperature. K562 derived artificial antigen presenting cells (aAPC) cells displaying cell surface anti-CD3 single chain Fv (OKT3) and PD-L1were brought to $0.67x10^6$ cells/mL and 25 µL was added to each well bringing the final volume of each well to 100 µL. Each well had a final ratio of 6:1 Jurkat:K562 cells, 1ug/mL anti-CD28 and test protein concentration of 50nM. Jurkat cells and K562 cells were incubated for 5-6 hours at 37 degrees Celsius in a humidified 5% CO_2 incubation chamber. Plates were then removed from the incubator and acclimated to room temperature for 15 minutes. 100 µL of a cell lysis and luciferase substrate solution (BioGlo®, Promega Corp, USA) was added to each well and the plates were placed on an orbital

shaker for 10 minutes at room temperature. Luminescence was measured with a 1 second per well integration time using a BioTek Cytation luminometer (BioTek Corp., USA).

[0474] An average relative luminescence value was determined for each variant PD-L1 IgV Fc and a fold increase in IL-2 reporter signal was calculated for each variant compared to wildtype PD-L1 IgV-Fc variant protein.

[0475] As shown in Table 12, luciferase activity of Jurkat effector cells expressing PD-1 and IL-2-luciferase reporter co-cultured with anti-CD3/PD-L1 aAPC and variant PD-L1 IgV-Fc molecules were altered (increased and decreased). The differences in luminescence values demonstrates variant PD-L1 IgV-Fc molecule binding to PD-1 and ability to block the interaction of PD-1 and PD-L1. Higher values are indicative of increased blockade of PD-1-mediated inhibition. In the Table, Column 2 sets forth the SEQ ID NO identifier for each variant IgV domain contained in the tested variant IgV-Fc fusion molecule.

TABLE 12. Jurkat/IL2/PD-1 Reporter Assay

PD-L1 Mutation(s)	SEQ ID NO (IgV)	Average Relative Luminescence Units	Fold increase in IL2 reporter signal
K28N, M41V, N45T, H51N, K57E	244	2348.00	1.05
I20L, I36T, N45D, I47T	245	2249.50	1.01
I20L, I36T, N45D	254	2109.50	0.95
I20L, M41K, K44E	246	2220.50	1.00
P6S, N45T, N78I, I83T	247	2246.00	1.01
I20L, F49S	256	2226.50	1.00
N78L	248	2243.50	1.01
N45T, V50A	257	2076.50	0.93
I20L, N45T, N78I	258	2066.00	0.93
N45T, N78I	250	2179.50	0.98
I20L, N45T	251	2176.50	0.98
I20L, N45T, V50A	259	2226.50	1.00
N45T	252	2193.00	0.98
M41K	253	2154.00	0.97
A33D, S75P, D85E	262	2217.50	0.99
M18I, M41K, D43G, H51R, N78I	263	2124.50	0.95
V11E, I20L, I36T, N45D, H60R, S75P	264	2283.00	1.02
E27G, N45T, M97I	267	1971.00	0.88
E27G, N45T, K57R	268	2034.00	0.91

TABLE 12. Jurkat/IL2/PD-1 Reporter Assay

PD-L1 Mutation(s)	SEQ ID NO (IgV)	Average Relative Luminescence Units	Fold increase in IL2 reporter signal
A33D, E53V	269	2142.00	0.96
D43G, D45D, V58A	270	2464.00	1.11
E40G, D43V, N45T, V50A	271	2216.00	0.99
Y14S, K28E, N45T	272	2151.50	0.97
A33D, N78S	273	2056.50	0.92
A33D, N78I	274	2057.00	0.92
A33D, N45T	275	1995.00	0.90
A33D, N45T, N78I	276	1973.00	0.89
E27G, N45T, V50A	277	2004.00	0.90
N45T, V50A, N78S	278	2224.50	1.00
N45T, V50A	257	2201.50	0.99
I20L, N45T, V110M	279	2210.00	0.99
I20L, I36T, N45T, V50A	280	2157.50	0.97
N45T, L74P, S75P	281	2031.00	0.91
N45T, S75P	282	1963.50	0.88
A33D, V50A	265	2251.50	1.01
S75P, K106R	283	2127.50	0.95
S75P	284	2233.50	1.00
A33D, S75P	285	2168.50	0.97
A33D, S75P, D104G	286	2168.50	0.97
A33D, S75P	287	2044.50	0.92
I20L, E27G, N45T, V50A	288	1804.50	0.81
I20L, E27G, D43G, N45D, V58A, N78I	289	4588.50	2.06
I20L, D43G, N45D, V58A, N78I	290	4191.50	1.88
I20L, A33D, D43G, N45D, V58A, N78I	291	4384.50	1.97
I20L, D43G, N45D, N78I	292	3471.50	1.56
E27G, N45T, V50A, N78I	293	1960.00	0.88
N45T, V50A, N78I	294	1899.00	0.85
V11A, I20L, E27G, D43G, N45D, H51Y, S99G	295	3381.50	1.52
I20L, E27G, D43G, N45T, V50A	296	2013.50	0.90
I20L, K28E, D43G, N45D, V58A, Q89R, G101G-ins (G101GG)	1727	4294.00	1.93
I20L, I36T, N45D,	298	2210.50	0.99
A33D, D43G, N45D, V58A, S75P	300	2312.50	1.04

TABLE 12. Jurkat/IL2/PD-1 Reporter Assay			
PD-L1 Mutation(s)	**SEQ ID NO (IgV)**	**Average Relative Luminescence Units**	**Fold increase in IL2 reporter signal**
K23R, D43G, N45D	301	2361.00	1.06
I20L, D43G, N45D, V58A, N78I, D90G, G101D	302	1998.50	0.90
D43G, N45D, L56Q, V58A, G101G-ins (G101GG)	303	3926.00	1.76
I20L, K23E, D43G, N45D, V58A, N78I	304	3506.00	1.57
I20L, K23E, D43G, N45D, V50A, N78I	305	3586.00	1.61
T19I, E27G, N45I, V50A, N78I, M97K	306	2047.00	0.92
I20L, M41K, D43G, N45D	307	2109.50	0.95
K23R, N45T, N78I	308	2690.50	1.21
Full length PD-L1 Fc	-	1945.00	0.87
Wild type PD-L1 IgV	309	2229.00	1.00
Anti-PD-1 monoclonal antibody (nivolumab)	-	8892.00	3.99

EXAMPLE 8

Additional Affinity Modified IgSF Domains

[0476] This examples describe the design, creation, and screening of additional affinity modified CD80 (B7-1), PD-L2, CD155 and CD112, and CD86 (B7-2) immunomodulatory proteins, which are other components of the immune synapse (IS) that have a demonstrated dual role in both immune activation and inhibition. Affinity-modified NKp30 variants also were generated and screened. These examples demonstrate that affinity modification of IgSF domains yields proteins that can act to both increase and decrease immunological activity. Various combinations of those domains can be fused in pairs (i.e., stacked) with a variant affinity modified PD-L1 to form a Type II immunomodulatory protein to achieve immunomodulatory activity.

[0477] Mutant DNA constructs encoding a variant of the IgV domain of human CD80, or IgV domains of PD-L2, CD155 and CD112 for translation and expression as yeast display libraries were generated substantially as described in Example 1. Target libraries that target specific residues for complete or partial randomization with degenerate codons and/or random libraries were constructed to identify variants of the IgV of CD80 (SEQ ID NO:2030), variants of the IgV of PD-L2 (SEQ ID NO: 1263), variants of the IgV of CD155 (SEQ ID NO:353), and

variants of the IgV of CD112 (SEQ ID NO:761) substantially as described in Example 1. Similar methods also were used to generate libraries of the IgC-like domain of NKp30 (SEQ ID NO:1190).

[0478] The degenerate or random library DNA was introduced into yeast substantially as described in Example 2 to generate yeast libraries. The libraries were used to select yeast expressing affinity modified variants of CD80, PD-L2, CD155, CD112, CD86 (B7-2), and NKp30 substantially as described in Example 3. Cells were processed to reduce non-binders and to enrich for CD80, PD-L2, CD155 or CD112, CD86 (B7-2), and NKp30 variants with the ability to bind their exogenous recombinant counter-structure proteins substantially as described in Example 3.

[0479] With CD80, CD86 and NKp30 libraries, target ligand proteins were sourced from R&D Systems (USA) as follows: human rCD28.Fc (i.e., recombinant CD28-Fc fusion protein), rPDL1.Fc, rCTLA4.Fc, and rB7H6.Fc. Two-color flow cytometry was performed substantially as described in Example 3. Yeast outputs from the flow cytometric sorts were assayed for higher specific binding affinity. Sort output yeast were expanded and re-induced to express the particular IgSF affinity modified domain variants they encode. This population then can be compared to the parental, wild-type yeast strain, or any other selected outputs, such as the bead output yeast population, by flow cytometry.

[0480] In the case of NKp30 yeast variants selected for binding to B7-H6, the F2 sort outputs gave MFI values of 533 when stained with 16.6nM rB7H6.Fc, whereas the parental NKp30 strain MFI was measured at 90 when stained with the same concentration of rB7H6.Fc (6-fold improvement).

[0481] Among the NKp30 variants that were identified, was a variant that contained mutations L30V/A60V/S64P/S86G with reference to positions in the NKp30 extracellular domain corresponding to positions set forth in SEQ ID NO: 54.

[0482] For CD80 variants provided in Table 13A-B, CD80 libraries consisted of positive selection with the desired counter structure CTLA4 and negative selection with the counter structure CD28.

[0483] For CD155 variants provided in Table 14A, CD155 libraries were selected against each of TIGIT, CD96, and CD226, separately. For CD155 variants provided in Table 14B-F, selection involved two positive selections with the desired counter structures TIGIT and CD96 followed by one negative selection with the counter structure CD226 to select away from CD226

and improve binding specificity of the variant CD155. Selection was performed essentially as described in Example 3 above except the concentrations of the counter structures (TIGIT/CD96) and selection stringency of the positive sorts were varied to optimize lead identification. The concentration of CD226 for the negative selection was kept at 100 nM.

[0484] For CD112 variants provided in Table 15A, CD112 libraries were selected against each of TIGIT, CD112R, and CD226, separately. For additional CD112 variants provided in Table 15B-15C, selection involved two positive selections with the desired counter structures TIGIT and CD112R followed by one negative selection with the counter structure CD226 to select away from CD226 and improve binding specificity of the variant CD112. Selection was performed essentially as described in Example 3 above except the concentrations of the counter structures (TIGIT/CD112R) and selection stringency of the positive sorts were varied to optimize lead identification. The concentration of CD226 for the negative selection was kept at 100 nM.

[0485] For PD-L2 variants provided in Table 16A-B, yeast display targeted or random PD-L2 libraries were selected against PD-1. This was then followed by two to three rounds of flow cytometry sorting using exogenous counter-structure protein staining to enrich the fraction of yeast cells that displays improved binders. Magnetic bead enrichment and selections by flow cytometry are essentially as described in Miller K.D. et al., Current Protocols in Cytometry 4.7.1-4.7.30, July 2008.

[0486] Exemplary selection outputs were reformatted as immunomodulatory proteins containing an affinity modified (variant) IgV of CD80, variant IgV of PD-L2, variant IgV of CD155, variant IgV of CD112, each fused to an Fc molecule (variant ECD-Fc fusion molecules or variant IgV-Fc fusion molecules) substantially as described in Example 4 and the Fc-fusion protein was expressed and purified substantially as described in Example 5.

[0487] Binding of exemplary IgSF domain variants to cell-expressed counter structures was then assessed substantially as described in Example 6. Cells expressing cognate binding partners were produced and binding studies and flow cytometry were carried out substantially as described in Example 6. In addition, the bioactivity of the Fc-fusion variant protein was characterized by either mixed lymphocyte reaction (MLR) or anti-CD3 coimmobilization assay substantially as described in Example 6.

[0488] As above, for each Table, the exemplary amino acid substitutions are designated by amino acid position number corresponding to the respective reference unmodified ECD sequence (Table 2). The amino acid position is indicated in the middle, with the corresponding unmodified

(e.g. wild-type) amino acid listed before the number and the identified variant amino acid substitution listed (or inserted designated by a) after the number.

[0489] Also shown is the binding activity as measured by the Mean Fluorescence Intensity (MFI) value for binding of each variant Fc-fusion molecule to cells engineered to express the cognate counter structure ligand and the ratio of the MFI compared to the binding of the corresponding unmodified Fc fusion molecule not containing the amino acid substitution(s) to the same cell-expressed counter structure ligand. The functional activity of the variant Fc-fusion molecules to modulate the activity of T cells also is shown based on the calculated levels of IFN-gamma in culture supernatants (pg/mL) generated either i) with the indicated variant Fc fusion molecule coimmoblized with anti-CD3 or ii) with the indicated variant Fc fusion molecule in an MLR assay. The Tables also depict the ratio of IFN-gamma produced by each variant ECD-Fc or IgV-Fc compared to the corresponding unmodified ECD-Fc or IgV-Fc in the functional assays.

[0490] As shown in Tables 13A-16F, the selections resulted in the identification of a number of PD-L2, CD155, CD112, and CD80 IgSF domain variants that were affinity-modified to exhibit increased binding for at least one, and in some cases more than one, cognate counter structure ligand. In addition, the results showed that affinity modification of the variant molecules also exhibited improved activities to both increase and decrease immunological activity depending on the format of the molecule.

TABLE 13A: Variant CD80 Binding to HEK293 Cells Transfected with CTLA4, CD28 or PD-L1

CD80 mutation(s)	SEQ ID NO (IgV)	CTLA4		CD28		PD-L1		
		MFI at 66.6 nM	Fold change to WT	MFI at 66.6 nM	Fold change to WT	MFI at 22.2 nM	Fold change to WT	Ratio of CTLA4: CD28
L70P	1080	Not tested						
I30F/L70P	1081	Not tested						
Q27H/T41S/A71D	1082	368176	2.3	25051	1.01	24181	N/A	14.7
I30T/L70R	1083	2234	0.0	2596	0.10	5163	N/A	0.9
T13R/C16R/L70Q/A71D	1084	197357	1.2	16082	0.65	9516	N/A	12.3
T57I	1085	393810	2.4	23569	0.95	3375	N/A	16.7
M43I/C82R	1086	3638	0.0	3078	0.12	7405	N/A	1.2
V22L/M38V/M47T/A71D/ L85M	1087	175235	1.1	3027	0.12	6144	N/A	57.9
I30V/T57I/L70P/A71D/ A91T	1088	116085	0.7	10129	0.41	5886	N/A	11.5
V22I/L70M/A71D	1089	163825	1.0	22843	0.92	33404	N/A	7.2
N55D/L70P/E77G	1090	Not tested						

TABLE 13A: Variant CD80 Binding to HEK293 Cells Transfected with CTLA4, CD28 or PD-L1								
	SEQ ID NO (IgV)	CTLA4		CD28		PD-L1		
CD80 mutation(s)		MFI at 66.6 nM	Fold change to WT	MFI at 66.6 nM	Fold change to WT	MFI at 22.2 nM	Fold change to WT	Ratio of CTLA4: CD28
T57A/I69T	1091	Not tested						
N55D/K86M	1092	3539	0.0	3119	0.13	5091	N/A	1.1
L72P/T79I	1093	50176	0.3	3397	0.14	6023	N/A	14.8
L70P/F92S	1094	4035	0.0	2948	0.12	6173	N/A	1.4
T79P	1095	2005	0.0	2665	0.11	4412	N/A	0.8
E35D/M47I/L65P/D90N	1096	4411	0.0	2526	0.10	4034	N/A	1.7
L25S/E35D/M47I/D90N	1097	61265	0.4	4845	0.20	20902	N/A	12.6
Q27X*/S44P/I67T/P74S/ E81G/E95D	1098	195637	1.2	17524	0.71	17509	N/A	11.2
A71D	1099	220090	1.4	16785	0.68	29642	N/A	13.1
T13A/Q27X*/I61N/A71D	1100	195061	1.2	17519	0.71	21717	N/A	11.1
E81K/A91S	1101	98467	0.6	3309	0.13	44557	N/A	29.8
A12V/M47V/L70M	1102	81616	0.5	7400	0.30	31077	N/A	11.0
K34E/T41A/L72V	1103	88982	0.6	3755	0.15	35293	N/A	23.7
T41S/A71D/V84A	1104	103010	0.6	5573	0.22	83541	N/A	18.5
E35D/A71D	1105	106069	0.7	18206	0.73	40151	N/A	5.8
E35D/M47I	1106	353590	2.2	14350	0.58	149916	N/A	24.6
K36R/G78A	1107	11937	0.1	2611	0.11	5715	N/A	4.6
Q33E/T41A	1108	8292	0.1	2442	0.10	3958	N/A	3.4
M47V/N48H	1109	207012	1.3	14623	0.59	145529	N/A	14.2
M47L/V68A	1110	74238	0.5	13259	0.53	11223	N/A	5.6
S44P/A71D	1111	8839	0.1	2744	0.11	6309	N/A	3.2
Q27H/M43I/A71D/R73S	1112	136251	0.8	12391	0.50	8242	N/A	11.0
E35D/T57I/L70Q/A71D	1114	121901	0.8	21284	0.86	2419	N/A	5.7
M47I/E88D	1115	105192	0.7	7337	0.30	97695	N/A	14.3
M42I/I61V/A71D	1116	54478	0.3	6074	0.24	4226	N/A	9.0
P51A/A71D	1117	67256	0.4	4262	0.17	5532	N/A	15.8
H18Y/M47I/T57I/A71G	1118	136455	0.8	20081	0.81	13749	N/A	6.8
V20I/M47V/T57I/V84I	1119	183516	1.1	26922	1.08	3583	N/A	6.8
WT	2030	161423	1.0	24836	1.00	Not tested	N/A	6.5

*Stop codon at indicated position

TABLE 13B: Variant CD80 Binding to HEK293 Cells Transfected with CTLA4, CD28 or PD-L1								
	SEQ ID NO (IgV)	CTLA4		CD28		PD-L1		
CD80 mutation(s)		MFI at 66.6 nM	Fold change to WT	MFI at 66.6 nM	Fold change to WT	MFI at 22.2 nM	Fold change to WT	Ratio of CTLA4: CD28
V20I/M47V/A71D	1120	149937	7.23	15090	9.33	9710	5.48	9.9
A71D/L72V/E95K	1121	140306	6.77	6314	3.90	8417	4.75	22.2
V22L/E35G/A71D/L72P	1122	152588	7.36	8150	5.04	1403	0.79	18.7
E35D/A71D	1123	150330	7.25	14982	9.26	13781	7.77	10.0

TABLE 13B: Variant CD80 Binding to HEK293 Cells Transfected with CTLA4, CD28 or PD-L1								
	SEQ ID NO (IgV)	CTLA4		CD28		PD-L1		
CD80 mutation(s)		MFI at 66.6 nM	Fold change to WT	MFI at 66.6 nM	Fold change to WT	MFI at 22.2 nM	Fold change to WT	Ratio of CTLA4: CD28
E35D/I67L/A71D	1124	146087	7.04	11175	6.91	9354	5.28	13.1
T13R/M42V/M47I/A71D	1126	108900	5.25	16713	10.33	1869	1.05	6.5
E35D	1127	116494	5.62	3453	2.13	25492	14.38	33.7
E35D/M47I/L70M	1128	116531	5.62	14395	8.90	49131	27.71	8.1
E35D/A71/L72V	1129	134252	6.47	11634	7.19	13125	7.40	11.5
E35D/M43L/L70M	1130	102499	4.94	3112	1.92	40632	22.92	32.9
A26P/E35D/M43I/L85Q/ E88D	1131	83139	4.01	5406	3.34	9506	5.36	15.4
E35D/D46V/L85Q	1132	85989	4.15	7510	4.64	38133	21.51	11.4
Q27L/E35D/M47I/T57I/ L70Q/E88D	1133	59793	2.88	14011	8.66	1050	0.59	4.3
Q27H/E35G/A71D/L72P/ T79I	1125	85117	4.10	10317	6.38	1452	0.82	8.3
M47V/I69F/A71D/V83I	1134	76944	3.71	15906	9.83	3399	1.92	4.8
E35D/T57A/A71D/L85Q	1135	85724	4.13	3383	2.09	1764	0.99	25.3
H18Y/A26T/E35D/A71D/ L85Q	1136	70878	3.42	6487	4.01	8026	4.53	10.9
E35D/M47L	1137	82410	3.97	11508	7.11	58645	33.08	7.2
E23D/M42V/M43I/I58V/ L70R	1138	37331	1.80	10910	6.74	2251	1.27	3.4
V68M/L70M/A71D/E95K	1139	56479	2.72	10541	6.51	38182	21.53	5.4
N55I/T57I/I69F	1140	2855	0.14	1901	1.17	14759	8.32	1.5
E35D/M43I/A71D	1141	63789	3.08	6369	3.94	27290	15.39	10.0
T41S/T57I/L70R	1142	59844	2.89	4902	3.03	19527	11.01	12.2
H18Y/A71D/L72P/E88V	1143	68391	3.30	8862	5.48	1085	0.61	7.7
V20I/A71D	1144	60323	2.91	10500	6.49	3551	2.00	5.7
E23G/A26S/E35D/T62N/ A71D/L72V/L85M	1145	59025	2.85	5484	3.39	10662	6.01	10.8
A12T/E24D/E35D/D46V/ I61V/L72P/E95V	1146	63738	3.07	7411	4.58	1221	0.69	8.6
V22L/E35D/M43L/A71G/ D76H	1147	2970	0.14	1498	0.93	1851	1.04	2.0
E35G/K54E/A71D/L72P	1148	71899	3.47	3697	2.29	1575	0.89	19.4
L70Q/A71D	1149	45012	2.17	18615	11.50	1692	0.95	2.4
A26E/E35D/M47L/L85Q	1150	40325	1.94	2266	1.40	55548	31.33	17.8
D46E/A71D	1151	69674	3.36	16770	10.36	22777	12.85	4.2
Y31H/E35D/T41S/V68L/ K93R/R94W	1152	3379	0.16	2446	1.51	18863	10.64	1.4
WT CD80 IgV Fc	2030 (IgV)	20739	1.00	1618	1.00	1773	1.00	12.8
WT CD80 ECD Fc	-	72506	3.50	3072	1.90	4418	2.49	23.6

TABLE 14A: Variant CD155 selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.

CD155 mutations	SEQ ID NO (IgV)	CD226 tfxn MFI (CD226 MFI parental ratio)	TIGIT tfxn MFI (TIGIT MFI parental ratio)	CD96 MFI (CD96 MFI parental ratio)	Mock Expi293 MFI (Mock MFI parental ratio)	Anti-CD3 IFN-gamma (pg/mL) (Anti-CD3 IFN-gamma parental ratio)
P18S, P64S, F91S	354	497825 (133.7)	247219 (91.1)	140065 (45.4)	3528 (1.2)	270.1 (0.7)
P18S, F91S, L104P	355	26210 (7.0)	75176 (27.7)	10867 (3.5)	2130 (0.7)	364.2 (0.9)
L44P	356	581289 (156.1)	261931 (96.5)	152252 (49.4)	3414 (1.2)	277.6 (0.7)
A56V	357	455297 (122.3)	280265 (103.2)	161162 (52.2)	2601 (0.9)	548.2 (1.4)
P18L, L79V, F91S	358	5135 (1.4)	4073 (1.5)	3279 (1.1)	2719 (0.9)	1241.5 (3.2)
P18S, F91S	359	408623 (109.8)	284190 (104.7)	147463 (47.8)	3348 (1.1)	760.6 (2.0)
P18T, F91S	360	401283 (107.8)	223985 (82.5)	157644 (51.1)	3065 (1.1)	814.7 (2.1)
P18T, S42P, F91S	361	554105 (148.8)	223887 (82.5)	135395 (43.9)	3796 (1.3)	539.7 (1.4)
G7E, P18T, Y30C, F91S	362	12903 (3.5)	12984 (4.8)	7906 (2.6)	2671 (0.9)	275.9 (0.7)
P18T, F91S, G111D	363	438327 (117.7)	287315 (105.8)	167583 (54.3)	4012 (1.4)	307.2 (0.8)
P18S, F91P	364	4154 (1.1)	3220 (1.2)	2678 (0.9)	2816 (1.0)	365.7 (0.9)
P18T, F91S, F108L	365	394546 (106.0)	298680 (110.0)	193122 (62.6)	2926 (1.0)	775.4 (2.0)
P18T, T45A, F91S	366	435847 (117.1)	222044 (81.8)	191026 (61.9)	2948 (1.0)	1546.8 (4.0)
P18T, F91S, R94H	367	3589 (1.0)	2942 (1.1)	2509 (0.8)	2390 (0.8)	1273.2 (3.3)
P18S, Y30C, F91S	368	382352 (102.7)	276358 (101.8)	56934 (18.5)	3540 (1.2)	426.5 (1.1)
A81V, L83P	369	4169 (1.1)	2912 (1.1)	2616 (0.8)	2993 (1.0)	339.7 (0.9)
L88P	370	65120 (17.5)	74845 (27.6)	35280 (11.4)	2140 (0.7)	969.2 (2.5)
Wild type	353	3723 (1.0)	2715 (1.0)	3085 (1.0)	2913 (1.0)	389.6 (1.0)
R94H	371	18905 (5.1)	104013 (38.3)	11727 (3.8)	1663 (0.6)	372.6 (1.0)
A13E, P18S, A56V, F91S	372	357808 (96.1)	179060 (66.0)	118570 (38.4)	2844 (1.0)	349.2 (0.9)
P18T, F91S, V115A	373	38487 (10.3)	46313 (17.1)	22718 (7.4)	2070 (0.7)	1574.5 (4.0)
P18T, Q60K	374	238266 (64.0)	173730 (64.0)	154448 (50.1)	4778 (1.6)	427.2 (1.1)

TABLE 14B: Additional CD155 Variants and Binding Data.					
CD155 Mutation(s)	SEQ	TIGIT	CD226	CD112R	CD96

	ID NO (IgV)	MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD
S52M	569	1865.3	0.00	1901.0	0.01	1553.4	0.87	1609.8	0.02
T45Q, S52L, L104E, G111R	570	2287.0	0.01	2390.4	0.01	1735.1	0.97	1575.1	0.02
S42G	571	4837.5	0.01	2448.1	0.01	1815.4	1.02	1699.6	0.02
Q62F	572	2209.5	0.01	2572.1	0.01	2706.5	1.52	2760.7	0.03
S52Q	573	2288.1	0.01	2022.3	0.01	1790.1	1.00	1822.3	0.02
S42A, L104Q, G111R	574	1923.7	0.00	1901.7	0.01	1815.1	1.02	1703.8	0.02
S42A, S52Q, L104Q, G111R	575	1807.5	0.00	2157.2	0.01	1894.4	1.06	1644.0	0.02
S52W, L104E	576	1938.2	0.00	1905.6	0.01	2070.6	1.16	1629.5	0.02
S42C	577	1914.0	0.00	2096.1	0.01	1685.0	0.95	1592.4	0.02
S52W	578	1991.6	0.00	2037.3	0.01	1612.8	0.90	1712.9	0.02
S52M, L104Q	579	2666.6	0.01	2252.2	0.01	1706.0	0.96	1633.1	0.02
S42L, S52L, Q62F, L104Q	580	2021.4	0.00	2643.8	0.02	1730.1	0.97	2318.7	0.02
S42W	581	2434.5	0.01	2133.4	0.01	2325.7	1.30	2555.4	0.03
S42Q	582	2073.5	0.00	2225.9	0.01	1905.1	1.07	2143.1	0.02
S52L	583	2224.8	0.01	2676.3	0.02	2038.6	1.14	2043.2	0.02
S52R	584	4395.4	0.01	3964.4	0.02	2741.7	1.54	4846.9	0.05
L104E	585	3135.4	0.01	2264.2	0.01	1803.5	1.01	1556.7	0.02
G111R	586	2082.7	0.00	2791.3	0.02	2470.9	1.39	3317.1	0.03
S52E	587	2655.4	0.01	2599.8	0.02	1904.9	1.07	1799.0	0.02
Q62Y	588	2528.6	0.01	2621.4	0.02	1918.4	1.08	1827.5	0.02
T45Q, S52M, L104E	589	79498.2	0.19	143238.5	0.83	2600.6	1.46	6310.4	0.06
S42N, L104Q, G111R	590	2432.1	0.01	2311.3	0.01	1847.4	1.04	1958.3	0.02
S52M, V57L	591	1760.7	0.00	2431.6	0.01	2006.9	1.13	1858.7	0.02
S42N, S52Q, Q62F	592	2402.7	0.01	2152.0	0.01	1855.0	1.04	1737.6	0.02
S42A, S52L, L104E, G111R	593	2262.7	0.01	1889.4	0.01	1783.2	1.00	1606.2	0.02
S42W, S52Q, V57L, Q62Y	594	1961.4	0.00	2138.3	0.01	1844.9	1.03	1699.6	0.02
L104Q	595	10314.4	0.02	3791.4	0.02	2119.9	1.19	1542.6	0.02
S42L, S52Q, L104E	596	1946.9	0.00	6474.3	0.04	1749.0	0.98	1702.2	0.02
S42C, S52L	597	1762.5	0.00	2147.3	0.01	1663.4	0.93	1484.7	0.01
S42W, S52R, Q62Y, L104Q	598	1918.8	0.00	2300.1	0.01	1824.6	1.02	1756.0	0.02
T45Q, S52R, L104E	599	121636.9	0.29	142381.2	0.82	2617.9	1.47	3748.2	0.04
S52R, Q62F, L104Q, G111R	600	2969.2	0.01	3171.6	0.02	1725.4	0.97	2362.3	0.02
T45Q, S52L, V57L, L104E	601	2857.7	0.01	5943.5	0.03	1496.8	0.84	1533.3	0.02
S52M, Q62Y	602	1926.6	0.00	2000.3	0.01	1771.6	0.99	1651.1	0.02

TABLE 14B: Additional CD155 Variants and Binding Data.									
CD155 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD	MFI at 100nM	Fold ↑ to WT ECD
Q62F, L104E, G111R	603	1966.4	0.00	2043.5	0.01	1701.9	0.95	1524.8	0.02
T45Q, S52Q	604	4812.8	0.01	5787.5	0.03	1765.6	0.99	2451.3	0.02
S52L, L104E	605	4317.8	0.01	2213.9	0.01	1756.9	0.99	1829.3	0.02
S42V, S52E	606	2055.0	0.00	2272.6	0.01	1808.0	1.01	2530.2	0.03
T45Q, S52R, G111R	607	4092.3	0.01	2075.2	0.01	1793.6	1.01	2336.6	0.02
S42G, S52Q, L104E, G111R	608	2010.1	0.00	2019.2	0.01	1706.4	0.96	1707.6	0.02
S42N, S52E, V57L, L104E	609	1784.2	0.00	1743.6	0.01	1690.1	0.95	1538.7	0.02
Wildtype	353	1964.7	0.00	2317.1	0.01	2169.6	1.22	1893.4	0.02
S42C, S52M, Q62F	610	1861.0	0.00	2084.2	0.01	1592.3	0.89	1481.3	0.01
S42L	611	1930.4	0.00	2187.2	0.01	1743.2	0.98	1618.4	0.02
Wildtype	353	2182.6	0.01	2374.5	0.01	1743.1	0.98	1680.4	0.02
S42A	612	1929.2	0.00	2188.6	0.01	1733.7	0.97	1623.6	0.02
S42G, S52L, Q62F, L104Q	613	1924.3	0.00	2157.6	0.01	1661.3	0.93	1642.1	0.02
S42N	614	1817.4	0.00	1910.9	0.01	1699.7	0.95	1691.5	0.02
CD155 IgV Fc	353 (IgV)	4690	0.01	4690	0.03	2941	1.65	3272	0.03
Wildtype CD155 ECD-Fc	47 (ECD)	423797	1.00	172839	1.00	1783	1.00	99037	1.00
Anti-human Fc PE	-	1506.3	0.00	3774	0.02	1587	0.89	1618	0.02

TABLE 14C: Additional CD155 Variants and Binding Data.							
CD155 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD
P18T, S65A, S67V, F91S	615	297843	1.99	351195	3.22	128180	1.68
P18T, T45Q, T61R, S65N, S67L	617	224682	1.50	270175	2.48	22820	0.30
P18F, T39A, T45Q, T61R, S65N, S67L, E73G, R78G	616	Little to no protein produced					
P18F, S65A, S67V, F91S	618	534106	3.57	350410	3.21	144069	1.89
P18F, T45Q, T61R, S65N, S67L, F91S, L104P	619	Little to no protein produced					
P18S, L79P, L104M	620	342549	2.29	320823	2.94	107532	1.41
P18S, L104M	621	449066	3.00	295126	2.70	121266	1.59
L79P, L104M	622	3210	0.02	8323	0.08	2894	0.04

TABLE 14C: Additional CD155 Variants and Binding Data.							
CD155 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD
P18T, T45Q, L79P	623	542878	3.63	371498	3.40	193719	2.55
P18T, T45Q, T61R, S65H, S67H	624	312337	2.09	225439	2.07	152903	2.01
P18T, A81E	625	Little to no protein produced					
P18S, D23Y, E37P, S52G, Q62M, G80S, A81P, G99Y, S112N	626	Little to no protein produced					
A13R, D23Y, E37P, S42P, Q62Y, A81E	627	4161	0.03	11673	0.11	5762	0.08
A13R, D23Y, E37P, G99Y, S112N	627	Little to no protein produced					
A13R, D23Y, E37P, Q62M, A77V, G80S, A81P, G99Y	629	Little to no protein produced					
P18L, E37S, Q62M, G80S, A81P, G99Y, S112N	630	5900	0.04	14642	0.13	3345	0.04
P18S, L104T	631	321741	2.15	367470	3.37	108569	1.43
P18S, Q62H, L79Q, F91S	632	283357	1.89	324877	2.98	125541	1.65
P18S, F91S	359	222780	1.49	300049	2.75	48542	0.64
T45Q, S52K, Q62F, L104Q, G111R	633	Little to no protein produced					
T45Q, S52Q, Q62Y, L104Q, G111R	634	Little to no protein produced					
T45Q, S52Q, Q62Y, L104E, G111R	635	Little to no protein produced					
V57A, T61M, S65W, S67A, E96D, L104T	636	Little to no protein produced					
P18L, V57T, T61S, S65Y, S67A, L104T	637	278178	1.86	276870	2.54	121499	1.60
P18T, T45Q	638	326769	2.18	357515	3.28	92389	1.21
P18L, V57A, T61M, S65W, S67A, L104T	639	Little to no protein produced					
T61M, S65W, S67A, L104T	640	360915	2.41	417897	3.83	148954	1.96
P18S, V41A, S42G, T45G, L104N	641	3821	0.03	11449	0.10	3087	0.04
P18H, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104N	642	5066	0.03	177351	1.63	3700	0.05
P18S, S42G, T45V, F58L, S67W, L104N	643	14137	0.09	15175	0.14	15324	0.20
P18S, T45I, L104N	644	141745	0.95	298011	2.73	97246	1.28
P18S, S42G, T45G, L104N, V106A	645	29387	0.20	117965	1.08	15884	0.21
P18H, H40R, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104Y, V106L, F108H	646	12335	0.08	14657	0.13	15779	0.21
E37V, S42G, T45G, L104N	647	Little to no protein produced					
P18S, T45Q, L79P, L104T	648	206674	1.38	285512	2.62	87790	1.15

TABLE 14C: Additional CD155 Variants and Binding Data.							
CD155 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD	MFI at 100nM	Fold Increase to WT ECD
P18L, Q62R	649	66939	0.45	25063	0.23	10928	0.14
A13R, D23Y, E37P, S42L, S52G, Q62Y, A81E	650	Little to no protein produced					
P18L, H49R, L104T, D116N	651	167980	1.12	214677	1.97	62451	0.82
A13R, D23Y, E37P, Q62M, G80S, A81P, L104T	652	Little to no protein produced					
S65T, L104T	653	205942	1.38	187147	1.71	65207	0.86
A13R, D23Y, E37P, S52G, V57A, Q62M, K70E, L104T	654	Little to no protein produced					
P18L, A47V, Q62Y, E73D, L104T	655	146142	0.98	248926	2.28	73956	0.97
H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, D97G, E98S, L104T, D116N	656	Little to no protein produced					
P18L, S42P, T45Q, T61G, S65H, S67E, L104T, D116N	657	153536	1.03	402503	3.69	53044	0.70
P18S, H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, L104M, V106A	658	Little to no protein produced					
H40T, V41M, A47V, S52Q, Q62L, S65T, E68G, E73R, D97G, E98S, L104T	659	Little to no protein produced					
T45Q, S52E, L104E	660	Little to no protein produced					
T45Q, S52E, Q62F, L104E	661	132850	0.89	276434	2.53	14558	0.19
Wildtype CD155 ECD-Fc	47 (ECD)	149692	1.00	109137	1.00	76083	1.00
Anti-human Fc PE	-	2287	0.02	4799	0.04	2061	0.03

TABLE 14D: Additional CD155 Variants and Binding Data.							
CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV
P18F, T26M, L44V, Q62K, L79P, F91S, L104M, G111D	662	117327	1.2	1613	0.1	1629	0.1
P18S, T45S, T61K, S65W, S67A, F91S, G111R	663	124936	1.3	2114	0.1	2223	0.1
P18S, L79P, L104M, T107M	664	110512	1.1	18337	0.9	22793	1.3

P18S, S65W, S67A, M90V, V95A, L104Q, G111R	665	101726	1.0	1605	0.1	2571	0.1
Wildtype CD155-ECD	47 (ECD)	98935	1.0	20029	1.0	17410	1.0

TABLE 14E: Additional CD155 Variants and Binding Data.

CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 11.1nM	Fold Change from CD155-ECD	MFI at 11.1nM	Fold Change from CD155-ECD	MFI at 11.1nM	Fold Change from CD155-ECD
P18S, A47G, L79P, F91S, L104M, T107A, R113W	1528	56,409	1.19	1,191	0.08	25,362	1.49
P18T, D23G, S24A, N35D, H49L, L79P, F91S, L104M, G111R	1529	128,536	2.72	987	0.06	3,497	0.20
V9L, P18S, Q60R, V75L, L79P, R89K, F91S, L104E, G111R	1530	125,329	2.65	986	0.06	959	0.06
P18S, H49R, E73D, L79P, N85D, F91S, V95A, L104M, G111R	1531	Little to no protein produced					
V11A, P18S, L79P, F91S, L104M, G111R	1532	48,246	1.02	974	0.06	923	0.05
V11A, P18S, S54R, Q60P, Q62K, L79P, N85D, F91S, T107M	1533	190,392	4.02	1,019	0.07	1,129	0.07
P18T, S52P, S65A, S67V, L79P, F91S, L104M, G111R	1534	121,611	2.57	986	0.06	16,507	0.97
P18T, M36T, L79P, F91S, G111R	1535	150,015	3.17	1,029	0.07	2,514	0.15
D8G, P18S, M36I, V38A, H49Q, A76E, F91S, L104M, T107A, R113W	1536	79,333	1.68	1,026	0.07	2,313	0.14
P18S, S52P, S65A, S67V, L79P, F91S, L104M, T107S, R113W	1537	23,766	0.50	1,004	0.07	1,080	0.06
T15I, P18T, L79P, F91S, L104M, G111R	1538	55,498	1.17	1,516	0.10	1,030	0.06
P18F, T26M, L44V, Q62K, L79P, E82D, F91S, L104M, G111D	1539	213,640	4.51	991	0.06	1,276	0.07
P18T, E37G, G53R, Q62K, L79P, F91S, E98D, L104M, T107M	1540	251,288	5.31	2,001	0.13	45,878	2.69

TABLE 14E: Additional CD155 Variants and Binding Data.

CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD96	
		MFI at 11.1nM	Fold Change from CD155-ECD	MFI at 11.1nM	Fold Change from CD155-ECD	MFI at 11.1nM	Fold Change from CD155-ECD
P18L, K70E, L79P, F91S, V95A, G111R	1541	62,608	1.32	1,117	0.07	973	0.06
V9I, Q12K, P18F, S65A, S67V, L79P, L104T, G111R, S112I	1542	81,932	1.73	803	0.05	68,295	4.00
P18F, S65A, S67V, F91S, L104M, G111R	1543	30,661	0.65	901	0.06	3,193	0.19
V9I, V10I, P18S, F20S, T45A, L79P, F91S, L104M, F108Y, G111R, S112V	1544	151,489	3.20	973	0.06	974	0.06
V9L, P18L, L79P, M90I, F91S, T102S, L104M, G111R	1545	155,279	3.28	910	0.06	10,568	0.62
P18C, T26M, L44V, M55I, Q62K, L79P, F91S, L104M, T107M	1546	137,521	2.91	973	0.06	111,085	6.51
V9I, P18T, D23G, L79P, F91S, G111R	1547	151,426	3.20	897	0.06	2,725	0.16
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1548	125,639	2.66	917	0.06	3,939	0.23
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1548	115,156	2.43	1,073	0.07	2,464	0.14
P18T, M36T, S65A, S67E, L79Q, A81T, F91S, G111R	1549	10,616	0.22	1,130	0.07	963	0.06
V9L, P18T, Q62R, L79P, F91S, L104M, G111R	1550	195,111	4.12	835	0.05	1,497	0.09
CD155-ECD-Fc	47 (ECD)	47,319	1.00	15,421	1.00	17,067	1.00
Fc Control	1155	2,298	0.05	1,133	0.07	996	0.06

TABLE 14F: Additional CD155 Variants and Binding Data.

CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI at 25nM	Fold Change from CD155-ECD	MFI at 25nM	Fold Change from CD155-ECD	MFI at 25nM	Fold Change from CD155-ECD	MFI at 25nM	Fold Change from CD155-ECD
P18T, G19D, M36T, S54N, L79P, L83Q, F91S, T107M, F108Y	1669	905	0.02	748	0.02	1276	1.56	726	0.01

TABLE 14F: Additional CD155 Variants and Binding Data.

CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD
V9L, P18L, M55V, S69L, L79P, A81E, F91S, T107M	1670	58656	1.34	11166	0.29	920	1.13	67364	1.39
P18F, H40Q, T61K, Q62K, L79P, F91S, L104M, T107V	1671	108441	2.48	853	0.02	918	1.13	8035	0.17
P18S, Q32R, Q62K, R78G, L79P, F91S, T107A, R113W	1672	5772	0.13	701	0.02	843	1.03	831	0.02
Q12H, P18T, L21S, G22S, V57A, Q62R, L79P, F91S, T107M	1673	1084	0.02	687	0.02	876	1.07	818	0.02
V9I, P18S, S24P, H49Q, F58Y, Q60R, Q62K, L79P, F91S, T107M	1674	69926	1.60	1089	0.03	1026	1.26	43856	0.90
P18T, W46C, H49R, S65A, S67V, A76T, L79P, S87T, L104M	1675	918	0.02	640	0.02	803	0.98	717	0.01
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1676	12630	0.29	707	0.02	857	1.05	1050	0.02
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1676	7476	0.17	851	0.02	935	1.15	924	0.02
V10F, T15S, P18L, R48Q, L79P, F91S, T107M, V115M	1677	1168	0.03	792	0.02	901	1.10	998	0.02
P18S, L21M, Y30F, N35D, R84W, F91S, T107M, D116G	1678	1377	0.03	743	0.02	946	1.16	1033	0.02
P18F, E51V, S54G, Q60R, L79Q, E82G, S87T, M90I, F91S, G92R, T107M	1679	46090	1.05	15701	0.41	1012	1.24	61814	1.27
Q16H, P18F, F91S, T107M	1680	Little to no protein produced							
P18T, D23G, Q60R, S67L, L79P, F91S, T107M, V115A	1681	64091	1.47	30931	0.81	874	1.07	108875	2.24
D8G, V9I, V11A, P18T, T26M, S52P, L79P, F91S, G92A, T107L, V115A	1682	52508	1.20	9483	0.25	817	1.00	97770	2.01
V9I, P18F, A47E, G50S, E68G, L79P, F91S, T107M	1683	55167	1.26	54341	1.43	752	0.92	102115	2.10
P18S, M55I, Q62K, S69P,	1684	Little to no protein produced							

TABLE 14F: Additional CD155 Variants and Binding Data.

CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD
L79P, F91S, T107M									
P18T, T39S, S52P, S54R, L79P, F91S, T107M	1685	45927	1.05	744	0.02	1038	1.27	1225	0.03
P18S, D23N, L79P, F91S, T107M, S114N	1686	Little to no protein produced							
P18S, P34S, E51V, L79P, F91S, G111R	1687	7917	0.18	769	0.02	853	1.04	892	0.02
P18S, H59N, V75A, L79P, A81T, F91S, L104M, T107M	1688	800	0.02	676	0.02	915	1.12	759	0.02
P18S, W46R, E68D, L79P, F91S, T107M, R113G	1689	1359	0.03	717	0.02	798	0.98	737	0.02
V9L, P18F, T45A, S65A, S67V, R78K, L79V, F91S, T107M, S114T	1690	130274	2.98	153569	4.04	812	1.00	85605	1.76
P18T, M55L, T61R, L79P, F91S, V106I, T107M	1691	133399	3.05	1906	0.05	827	1.01	57927	1.19
T15I, P18S, V33M, N35F, T39S, M55L, R78S, L79P, F91S, T107M	1692	7550	0.17	1015	0.03	789	0.97	2709	0.06
P18S, Q62K, K70E, L79P, F91S, G92E, R113W	1693	11173	0.26	691	0.02	735	0.90	1951	0.04
P18F, F20I, T26M, A47V, E51K, L79P, F91S	1694	136088	3.11	54026	1.42	1401	1.72	96629	1.99
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1695	43795	1.00	98241	2.58	888	1.09	70891	1.46
P18S, D23G, C29R, N35D, E37G, M55I, Q62K, S65A, S67G, R78G, L79P, F91S, L104M, T107M, Q110R	1696	1599	0.04	1030	0.03	1115	1.37	1944	0.04
A13E, P18S, M36R, Q62K, S67T, L79P, N85D, F91S, T107M	1697	Little to no protein produced							
V9I, P18T, H49R, L79P, N85D, F91S, L104T, T107M	1698	46375	1.06	76851	2.02	794	0.97	80210	1.65
V9A, P18F, T61S, Q62L, L79P, F91S, G111R	1699	26109	0.60	891	0.02	825	1.01	2633	0.05
D8E, P18T, T61A, L79P, F91S, T107M	1700	Little to no protein produced							
P18S, V41A, H49R, S54C, L79S, N85Y, L88P, F91S, L104M, T107M	1701	1098	0.03	830	0.02	876	1.07	1678	0.03

TABLE 14F: Additional CD155 Variants and Binding Data.									
CD155 Mutations	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD	MFI at 25nM	Fold Change from CD155 -ECD
V11E, P18H, F20Y, V25E, N35S, H49R, L79P, F91S, T107M, G111R	1702	979	0.02	846	0.02	844	1.03	928	0.02
V11A, P18F, D23A, L79P, G80D, V95A, T107M	1703	45249	1.04	913	0.02	830	1.02	33883	0.70
P18S, K70R, L79P, F91S, G111R	1704	16180	0.37	793	0.02	854	1.05	1182	0.02
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1695	175673	4.02	161958	4.26	879	1.08	50981	1.05
V9L, V11M, P18S, N35S, S54G, Q62K, L79P, L104M, T107M, V115M	1705	2999	0.07	2315	0.06	893	1.09	925	0.02
V9L, P18Y, V25A, V38G, M55V, A77T, L79P, M90I, F91S, L104M	1706	138011	3.16	26015	0.68	919	1.13	17970	0.37
V10G, P18T, L72Q, L79P, F91S, T107M	1707	4253	0.10	1584	0.04	863	1.06	3643	0.07
P18S, H59R, A76G, R78S, L79P	1708	130622	2.99	79435	2.09	1009	1.24	44493	0.91
V9A, P18S, M36T, S65G, L79P, F91S, L104T, G111R, S112I	1709	92503	2.12	989	0.03	886	1.09	7850	0.16
P18T, S52A, V57A, Q60R, Q62K, S65C, L79P, F91T, N100Y, T107M	1710	187338	4.29	10579	0.28	908	1.11	3791	0.08
V11A, P18F, N35D, A47E, Q62K, L79P, F91S, G99D, T107M, S114N	1711	Little to no protein produced							
V11A, P18T, N35S, L79P, S87T, F91S	1712	218660	5.00	273825	7.20	1269	1.56	69871	1.44
V9D, V11M, Q12L, P18S, E37V, M55I, Q60R, K70Q, L79P, F91S, L104M, T107M	1713	8693	0.20	790	0.02	852	1.04	1991	0.04
T15S, P18S, Y30H, Q32L, Q62R, L79P, F91S, T107M	1714	16213	0.37	2092	0.06	1056	1.29	6994	0.14
CD155-ECD-Fc	47 (ECD)	43704	1.00	38032	1.00	816	1.00	48638	1.00
CD112-IgV	761	1289		824		17819		1172	0.02

TABLE 15A: Variant CD112 selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.

CD112 mutation(s)	SEQ ID NO (IgV)	TIGIT tfxn MFI (TIGIT MFI parental ratio)	CD112R tfxn MFI (CD112R MFI parental ratio)	CD226 MFI (CD226 MFI parental ratio)	Mock Expi293 MFI (Mock MFI parental ratio)	Anti-CD3 IFN-gamma (pg/mL) (Anti-CD3 IFN-gamma parental ratio)
WT CD112	761	210829 (1.00)	1452 (1.00)	265392 (1.00)	1112 (1.00)	676.6 (1.00)
Y33H, A112V, G117D	762	12948 (0.06)	1552 (1.07)	1368 (0.01)	1241 (1.12)	164.8 (0.24)
V19A, Y33H, S64G, S80G, G98S, N106Y, A112V	763	48356 (0.23)	1709 (1.18)	2831 (0.01)	1098 (0.99)	
L32P, A112V	764	191432 (0.91)	1557 (1.07)	11095 (0.04)	1259 (1.13)	390.4 (0.58)
A95V, A112I	765	238418 (1.13)	1706 (1.17)	51944 (0.20)	1215 (1.09)	282.5 (0.42)
P28S, A112V	766	251116 (1.19)	1985 (1.37)	153382 (0.58)	1189 (1.07)	503.4 (0.74)
P27A, T38N, V101A, A112V	767	255803 (1.21)	2138 (1.47)	222822 (0.84)	1399 (1.26)	240.7 (0.36)
S118F	768	11356 (0.05)	5857 (4.03)	6938 (0.03)	1270 (1.14)	271.7 (0.40)
R12W, H48Y, F54S, S118F	769	10940 (0.05)	3474 (2.39)	5161 (0.02)	1069 (0.96)	
R12W, Q79R, S118F	770	2339 (0.01)	7370 (5.08)	1880 (0.01)	1338 (1.20)	447.4 (0.66)
T113S, S118Y	771	6212 (0.03)	6823 (4.70)	1554 (0.01)	1214 (1.09)	225.1 (0.33)
S118Y	772	2921 (0.01)	6535 (4.50)	2003 (0.01)	1463 (1.32)	190.4 (0.28)
N106I, S118Y	773	2750 (0.01)	7729 (5.32)	1815 (0.01)	1222 (1.10)	265.8 (0.39)
N106I, S118F	774	1841 (0.01)	9944 (6.85)	1529 (0.01)	1308 (1.18)	437.9 (0.65)
A95T, L96P, S118Y	775	2352 (0.01)	4493 (3.09)	1412 (0.01)	1329 (1.19)	292.4 (0.43)
Y33H, P67S, N106Y, A112V	776	225015 (1.07)	3259 (2.24)	204434 (0.77)	1296 (1.17)	618.8 (0.91)
N106Y, A112V	777	6036 (0.03)	1974 (1.36)	15334 (0.06)	1108 (1.00)	409.9 (0.61)
T18S, Y33H, A112V	778	252647 (1.20)	1347 (0.93)	183181 (0.69)	1412 (1.27)	601.8 (0.89)
P9S, Y33H, N47S, A112V	779	240467 (1.14)	1418 (0.98)	203608 (0.77)	1361 (1.22)	449.1 (0.66)
P42S, P67H, A112V	780	204484 (0.97)	1610 (1.11)	188647 (0.71)	1174 (1.06)	530.6 (0.78)
P27L, L32P, P42S, A112V	781	219883 (1.04)	1963 (1.35)	84319 (0.32)	1900 (1.71)	251.6 (0.37)
G98D, A112V	782	4879 (0.02)	2369 (1.63)	6100 (0.02)	1729 (1.55)	387.0 (0.57)
Y33H, S35P, N106Y, A112V	783	250724 (1.19)	1715 (1.18)	94373 (0.36)	1495 (1.34)	516.2 (0.76)
L32P, P42S, T100A, A112V	784	242675 (1.15)	1742 (1.20)	202567 (0.76)	1748 (1.57)	435.3 (0.64)
P27S, P45S, N106I, A112V	785	223557	1799	84836	1574	277.5

TABLE 15A: Variant CD112 selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.

CD112 mutation(s)	SEQ ID NO (IgV)	TIGIT tfxn MFI (TIGIT MFI parental ratio)	CD112R tfxn MFI (CD112R MFI parental ratio)	CD226 MFI (CD226 MFI parental ratio)	Mock Expi293 MFI (Mock MFI parental ratio)	Anti-CD3 IFN-gamma (pg/mL) (Anti-CD3 IFN-gamma parental ratio)
		(1.06)	(1.24)	(0.32)	(1.42)	(0.41)
Y33H, N47K, A112V	786	251339 (1.19)	1525 (1.05)	199601 (0.75)	1325 (1.19)	483.2 (0.71)
Y33H, N106Y, A112V	787	297169 (1.41)	1782 (1.23)	258315 (0.97)	1440 (1.30)	485.4 (0.72)
K78R, D84G, A112V, F114S	788	236662 (1.12)	1638 (1.13)	24850 (0.09)	1345 (1.21)	142.5 (0.21)
Y33H, N47K, F54L, A112V	789	14483 (0.07)	1617 (1.11)	2371 (0.01)	1353 (1.22)	352.8 (0.52)
Y33H, A112V	790	98954 (0.47)	1216 (0.84)	1726 (0.01)	1298 (1.17)	
A95V, A112V	791	168521 (0.80)	2021 (1.39)	200789 (0.76)	1459 (1.31)	412.9 (0.61)
R12W, A112V	792	135635 (0.64)	1582 (1.09)	23378 (0.09)	1412 (1.27)	165.8 (0.24)
A112V	798	213576 (1.01)	1986 (1.37)	151900 (0.57)	1409 (1.27)	211.4 (0.31)
Y33H, A112V	790	250667 (1.19)	1628 (1.12)	230578 (0.87)	1216 (1.09)	612.7 (0.91)
R12W, P27S, A112V	793	3653 (0.02)	1308 (0.90)	9105 (0.03)	1051 (0.94)	
Y33H, V51M, A112V	794	218698 (1.04)	1384 (0.95)	195450 (0.74)	1170 (1.05)	709.4 (1.05)
Y33H, A112V, S118T	795	219384 (1.04)	1566 (1.08)	192645 (0.73)	1313 (1.18)	396.3 (0.59)
Y33H, V101A, A112V, P115S	796	5605 (0.03)	1582 (1.09)	5079 (0.02)	1197 (1.08)	
H24R, T38N, D43G, A112V	797	227095 (1.08)	1537 (1.06)	229311 (0.86)	1336 (1.20)	858.6 (1.27)
A112V	798	4056 (0.02)	1356 (0.93)	10365 (0.04)	986 (0.89)	
P27A, A112V	799	193537 (0.92)	1531 (1.05)	230708 (0.87)	3084 (2.77)	355.1 (0.52)
A112V, S118T	800	233173 (1.11)	1659 (1.14)	121817 (0.46)	845 (0.76)	533.3 (0.79)
R12W, A112V, M122I	801	235935 (1.12)	1463 (1.01)	217748 (0.82)	1350 (1.21)	528.0 (0.78)
Q83K, N106Y, A112V	802	205948 (0.98)	2042 (1.41)	234958 (0.89)	1551 (1.39)	481.4 (0.71)
R12W, P27S, A112V, S118T	803	11985 (0.06)	2667 (1.84)	12756 (0.05)	1257 (1.13)	334.4 (0.49)
P28S, Y33H, A112V	804	4711 (0.02)	1412 (0.97)	3968 (0.01)	955 (0.86)	
P27S, Q90R, A112V	805	3295 (0.02)	1338 (0.92)	6755 (0.03)	1048 (0.94)	
L15V, P27A, A112V, S118T	806	209888 (1.00)	1489 (1.03)	84224 (0.32)	1251 (1.13)	512.3 0.76)

TABLE 15A: Variant CD112 selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.						
CD112 mutation(s)	**SEQ ID NO (IgV)**	**TIGIT tfxn MFI (TIGIT MFI parental ratio)**	**CD112R tfxn MFI (CD112R MFI parental ratio)**	**CD226 MFI (CD226 MFI parental ratio)**	**Mock Expi293 MFI (Mock MFI parental ratio)**	**Anti-CD3 IFN-gamma (pg/mL) (Anti-CD3 IFN-gamma parental ratio)**
Y33H, N106Y, T108I, A112V	807	Not tested				
Y33H, P56L, V75M, V101M, A112V	808	Not tested				

TABLE 15B: Additional CD112 Variants and Binding Data.									
CD112 Mutation(s)	**SEQ ID NO (IgV)**	**TIGIT**		**CD226**		**CD112R**		**CD96**	
		MFI 100nM	**Fold Increase to WT IgV**	**MFI at 100nM**	**Fold Increase to WT IgV**	**MFI at 100nM**	**Fold Increase to WT IgV**	**MFI at 100nM**	**Fold Increase to WT IgV**
S118F	768	1763	0.02	1645	0.08	2974	0.61	1659	0.19
N47K, Q79R, S118F	891	1738	0.02	1689	0.09	2637	0.54	1647	0.19
Q40R, P60T, A112V, S118T	892	4980	0.06	1608	0.08	2399	0.50	2724	0.32
F114Y, S118F	893	110506	1.34	7325	0.37	1502	0.31	1553	0.18
N106I, S118Y	773	1981	0.02	1700	0.09	2394	0.49	1582	0.19
S118Y	772	101296	1.23	9990	0.50	1429	0.30	1551	0.18
Y33H, K78R, S118Y	894	2276	0.03	2115	0.11	3429	0.71	2082	0.24
N106I, S118F	774	1875	0.02	1675	0.08	2365	0.49	1662	0.19
R12W, A46T, K66M, Q79R, N106I, T113A, S118F	895	3357	0.04	1808	0.09	1664	0.34	4057	0.48
Y33H, A112V, S118F	896	3376	0.04	2886	0.15	3574	0.74	3685	0.43
R12W, Y33H, N106I, S118F	897	100624	1.22	24513	1.24	1490	0.31	2060	0.24
L15V, Q90R, S118F	898	5791	0.07	4169	0.21	2752	0.57	4458	0.52
N47K, D84G, N106I, S118Y	899	3334	0.04	2819	0.14	2528	0.52	3498	0.41
L32P, S118F	900	3881	0.05	2506	0.13	2659	0.55	2518	0.29
Y33H, Q79R, A112V, S118Y	901	Low to no protein produced							
T18A, N106I, S118T	902	84035	1.02	10208	0.52	1585	0.33	1590	0.19
L15V, Y33H, N106Y, A112V, S118F	903	Low to no protein produced							
V37M, S118F	904	96986	1.18	2523	0.13	1985	0.41	1849	0.22

TABLE 15B: Additional CD112 Variants and Binding Data.									
CD112 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV
N47K, A112V, S118Y	905	1980	0.02	1859	0.09	2733	0.56	1825	0.21
A46T, A112V	906	4224	0.05	4685	0.24	3288	0.68	4273	0.50
P28S, Y33H, N106I, S118Y	907	6094	0.07	2181	0.11	1891	0.39	3021	0.35
P30S, Y33H, N47K, V75M, Q79R, N106I, S118Y	908	2247	0.03	2044	0.10	1796	0.37	2658	0.31
V19A, N47K, N106Y, K116E, S118Y	909	2504	0.03	2395	0.12	2174	0.45	2852	0.33
Q79R, T85A, A112V, S118Y	910	2192	0.03	1741	0.09	2367	0.49	1620	0.19
Y33H, A112V	790	20646	0.25	1465	0.07	1794	0.37	2589	0.30
V101M, N106I, S118Y	911	55274	0.67	6625	0.33	1357	0.28	1494	0.17
Y33H, Q79R, N106I, A112V, S118T	912	6095	0.07	1760	0.09	2393	0.49	3033	0.36
Q79R, A112V	913	1571	0.02	1490	0.08	2284	0.47	1326	0.16
Y33H, A46T, Q79R, N106I, S118F	914	90813	1.10	15626	0.79	1298	0.27	3571	0.42
A112V, G121S	915	95674	1.16	19992	1.01	1252	0.26	4005	0.47
Y33H, Q79R, N106I, S118Y	916	36246	0.44	2118	0.11	1970	0.41	3250	0.38
Y33H, N106I, A112V	917	47352	0.57	4217	0.21	2641	0.55	1488	0.17
Y33H, A46T, V101M, A112V, S118T	918	14413	0.17	1596	0.08	2335	0.48	1441	0.17
L32P, L99M, N106I, S118F	919	3056	0.04	1791	0.09	2210	0.46	2000	0.23
L32P, T108A, S118F	920	104685	1.27	4531	0.23	2308	0.48	1518	0.18
A112V	798	4937	0.06	1903	0.10	1646	0.34	3011	0.35
R12W, Q79R, A112V	921	55539	0.67	6918	0.35	1386	0.29	1740	0.20
Y33H, N106Y, E110G, A112V	922	2786	0.03	2517	0.13	1787	0.37	2023	0.24
Y33H, N106I, S118Y	923	1967	0.02	1579	0.08	2601	0.54	1517	0.18
Q79R, S118F	924	82055	1.00	7582	0.38	1298	0.27	1970	0.23
Y33H, Q79R, G98D, V101M,	925	21940	0.27	1632	0.08	1141	0.24	18423	2.16

TABLE 15B: Additional CD112 Variants and Binding Data.

CD112 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV	MFI at 100nM	Fold Increase to WT IgV
A112V									
N47K, T81S, V101M, A112V, S118F	926	6889	0.08	1311	0.07	1303	0.27	1145	0.13
G82S, S118Y	927	4267	0.05	1938	0.10	2140	0.44	2812	0.33
Y33H, A112V, S118Y	928	14450	0.18	1532	0.08	2353	0.49	3004	0.35
Y33H, N47K, Q79R, N106Y, A112V	929	70440	0.85	3557	0.18	1447	0.30	1679	0.20
Y33H, S118T	930	113896	1.38	17724	0.89	1252	0.26	5001	0.59
R12W, Y33H, Q79R, V101M, A112V	931	3376	0.04	2727	0.14	2047	0.42	2339	0.27
S118F	768	2685	0.03	1864	0.09	2520	0.52	1566	0.18
Wildtype CD112-IgV Fc	761 (IgV)	82414	1.00	19803	1.00	4842	1.00	8541	1.00
CD112 ECD-Fc	48 (ECD)	29157	0.35	8755	0.44	1107	0.23	1103	0.13
Anti-hFc PE	-	1383	0.02	1461	0.07	1358	0.28	1468	0.17

TABLE 15C: Additional CD112 Variants and Binding Data.

CD112 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV
N106I, S118Y	773	1288	0.04	1334	0.12	6920	4.16	1102	0.44
Y33H, Q83K, A112V, S118T	1481	115690	3.31	10046	0.93	1128	0.68	2053	0.82
R12W, Q79R, S118F	779	1436	0.04	1296	0.12	6546	3.93	1046	0.42
V29M, Y33H, N106I, S118F	1482	Not tested							
Y33H, A46T, A112V	1483	111256	3.18	14974	1.39	1148	0.69	3333	1.34
Y33H, Q79R, S118F	1484	1483	0.04	1326	0.12	7425	4.46	1138	0.46
Y33H, N47K, F74L, S118F	1485	1338	0.04	1159	0.11	1516	0.91	1140	0.46
R12W, V101M, N106I, S118Y	1486	1378	0.04	1249	0.12	5980	3.59	1182	0.47

TABLE 15C: Additional CD112 Variants and Binding Data.									
CD112 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV
A46T, V101A, N106I, S118Y	1487	1359	0.04	1199	0.11	6729	4.04	1173	0.47
Y33H, N106Y, A112V	787	113580	3.25	17771	1.65	1207	0.72	2476	0.99
N106Y, A112V, S118T	1488	Not tested							
S76P, T81I, V101M, N106Y, A112V, S118F	1489	Not tested							
N106Y, A112V	777	29015	0.83	2760	0.26	1159	0.70	1639	0.66
P9R, L21V, P22L, I34M, S69F, F74L, A87V, A112V, L125A	1490	1920	0.05	1218	0.11	1107	0.66	1074	0.43
Y33H, V101M, A112V	1491	126266	3.61	24408	2.27	1150	0.69	4535	1.82
N106I, S118F	774	1776	0.05	1385	0.13	9058	5.44	1370	0.55
V29A, L32P, S118F	1492	1265	0.04	1148	0.11	5057	3.04	1194	0.48
A112V	798	69673	1.99	6387	0.59	1140	0.68	1214	0.49
Y33H, V101M, A112V	1491	133815	3.83	24992	2.32	1184	0.71	6338	2.54
P28S, Y33H, N106I, S118Y	907	2745	0.08	1689	0.16	6625	3.98	1978	0.79
Y33H, V101M, N106I, A112V	1493	118654	3.40	21828	2.03	1253	0.75	3871	1.55
R12W, Y33H, N47K, Q79R, S118Y	1494	171390	4.91	5077	0.47	1124	0.68	2636	1.06
A112V, S118T	800	103203	2.95	15076	1.40	1155	0.69	1426	0.57
Y33H, A46T, A112V, S118T	1495	141859	4.06	29436	2.74	1184	0.71	5760	2.31
Y33H, A112V, F114L, S118T	1496	5161	0.15	1734	0.16	1184	0.71	1249	0.50
A112V	798	78902	2.26	6224	0.58	1114	0.67	1181	0.47
Y33H, T38A, A46T, V101M, A112V	1497	111293	3.19	25702	2.39	1192	0.72	99015	39.69
Q79R, A112V	913	96674	2.77	7264	0.67	1130	0.68	1216	0.49
Y33H, N106I, S118Y	923	5720	0.16	1453	0.14	6543	3.93	1248	0.50

TABLE 15C: Additional CD112 Variants and Binding Data.									
CD112 Mutation(s)	SEQ ID NO (IgV)	TIGIT		CD226		CD112R		CD96	
		MFI 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV	MFI at 20nM	Fold Increase to WT IgV
P28S, Y33H, S69P, N106I, A112V, S118Y	1498	22393	0.64	1378	0.13	1550	0.93	19174	7.68
Y33H, P42L, N47K, V101M, A112V	1499	214116	6.13	13878	1.29	1315	0.79	4753	1.91
Y33H, N47K, F74S, Q83K, N106I, F111L, A112V, S118T	1500	6719	0.19	1319	0.12	1305	0.78	1278	0.51
Y33H, A112V, S118T, V119A	1501	184794	5.29	10204	0.95	1269	0.76	4321	1.73
Y33H, N106I, A112V, S118F	1502	6872	0.20	1591	0.15	2308	1.39	2796	1.12
Y33H, K66M, S118F, W124L	1503	1724	0.05	1259	0.12	6782	4.07	1197	0.48
S118F	768	1325	0.04	1213	0.11	7029	4.22	1135	0.46
N106I, A112V	1504	111342	3.19	4241	0.39	1546	0.93	1178	0.47
Y33H, A112V	790	177926	5.09	13761	1.28	1152	0.69	3117	1.25
WT CD112 IgV	1367	34932	1.00	10762	1.00	1665	1.00	2495	1.00
WT CD112-Fc ECD	48 (ECD)	28277	0.81	8023	0.75	1253	0.75	1064	0.43
Anti-huFc PE	-	1138	0.03	1006	0.09	1010	0.61	1062	0.43

TABLE 16A: Variant PD-L2 selected against PD-1. Molecule sequence and binding data.				
PD-L2 mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells		Fortebio binding to PD-1-Fc Response Units
		MFI at 50nM	Fold increase over wildtype PD-L2 IgV-Fc	
H15Q	1357	15998	1.63	0.007
N24D	1358	1414	0.14	-0.039
E44D	1359	2928	0.3	-0.006
V89D	1360	3361	0.34	0.005
Q82R,V89D	1361	44977	4.57	1.111
E59G,Q82R	1362	12667	1.29	-0.028
S39I,V89D	1363	26130	2.65	0.26
S67L,V89D	1364	15991	1.62	0.608
S67L,I85F	1365	529	0.05	-0.005
S67L,I86T	1366	6833	0.69	0.141

TABLE 16A: Variant PD-L2 selected against PD-1. Molecule sequence and binding data.				
PD-L2 mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells		Fortebio binding to PD-1-Fc Response Units
		MFI at 50nM	Fold increase over wildtype PD-L2 IgV-Fc	
H15Q,K65R	1367	13497	1.37	-0.001
H15Q,Q72H,V89D	1368	12629	1.28	0.718
H15Q,S67L,R76G	1369	47201	4.8	0.418
H15Q,R76G,I85F	1370	2941	0.3	-0.038
H15Q,T47A,Q82R	1371	65174	6.62	0.194
H15Q,Q82R,V89D	1372	49652	5.04	1.198
H15Q,C23S,I86T	1373	830	0.08	-0.026
H15Q,S39I,I86T	1374	1027	0.1	0.309
H15Q,R76G,I85F	1375	1894	0.19	-0.006
E44D,V89D,W91R	1376	614	0.06	-0.048
I13V,S67L,V89D	1377	26200	2.66	1.42
H15Q,S67L,I86T	1378	15952	1.62	0.988
I13V,H15Q,S67L,I86T	1379	21570	2.19	1.391
I13V,H15Q,E44D,V89D	1380	23958	2.43	1.399
I13V,S39I,E44D,Q82R,V89D	1381	71423	7.26	0.697
I13V,E44D,Q82R,V89D	1382	45191	4.59	1.283
I13V,Q72H,R76G,I86T	1383	10429	1.06	0.733
I13V,H15Q,R76G,I85F	1384	4736	0.48	-0.04
H15Q,S67L,R76G,I85F	1386	2869	0.29	0.025
H15Q,S39I,R76G,V89D	1386	Little or no protein produced		
H15Q,T47A,Q72H,R76G,I86T	1387	32103	3.26	0.512
H15Q,T47A,Q72H,R76G	1388	16500	1.68	0.327
I13V,H15Q,T47A,Q72H,R76G	1389	73412	7.46	0.896
H15Q,E44D,R76G,I85F	1390	2885	0.29	-0.013
H15Q,S39I,S67L,V89D	1391	45502	4.62	1.174
H15Q,N32D,S67L,V89D	1392	25880	2.63	1.407
N32D,S67L,V89D	1393	31753	3.23	1.155
H15Q,S67L,Q72H,R76G,V89D	1394	40180	4.08	1.464
H15Q,Q72H,Q74R,R76G,I86T	1395	4049	0.41	0.093
G28V,Q72H,R76G,I86T	1396	5563	0.57	0.003
I13V,H15Q,S39I,E44D,S67L	1397	63508	6.45	0.889
E44D,S67L,Q72H,Q82R,V89D	1398	51467	5.23	1.061
H15Q,V89D	1399	17672	1.8	0.31
H15Q,T47A	1400	26578	2.7	0.016
I13V,H15Q,Q82R	1401	76146	7.74	0.655
I13V,H15Q,V89D	1402	28745	2.92	1.331
I13V,S67L,Q82R,V89D	1403	58992	5.99	1.391
I13V,H15Q,Q82R,V89D	1404	49523	5.03	1.419
H15Q,V31M,S67L,Q82R,V89D	1405	67401	6.85	1.37

TABLE 16A: Variant PD-L2 selected against PD-1. Molecule sequence and binding data.				
PD-L2 mutation(s)	SEQ ID NO (IgV)	Binding to Jurkat/PD-1 Cells		Fortebio binding to PD-1-Fc Response Units
		MFI at 50nM	Fold increase over wildtype PD-L2 IgV-Fc	
I13V,H15Q,T47A,Q82R	1406	89126	9.05	0.652
I13V,H15Q,V31A,N45S,Q82R,V89D	1407	68016	6.91	1.327
H15Q,T47A,H69L,Q82R,V89D	1409	65598	6.66	1.44
I13V,H15Q,T47A,H69L,R76G,V89D	1410	54340	5.52	1.719
I12V,I13V,H15Q,T47A,Q82R,V89D	1411	61207	6.22	1.453
I13V,H15Q,R76G,D77N,Q82R,V89D	1412	33079	3.36	0.065
I13V,H15Q,T47A,R76G,V89D	1413	53668	5.45	1.596
I13V,H15Q,T47A,Q82R,V89D	1414	63320	6.43	1.418
I13V,H15Q,T47A,Q82R,V89D	1414	60980	6.2	1.448
I13V,H15Q,I36V,T47A,S67L,V89D	1416	52835	5.37	1.627
H15Q,T47A,K65R,S67L,Q82R,V89D	1417	79692	8.1	1.453
H15Q,L33P,T47A,S67L,P71S,V89D	1418	45726	4.65	1.467
I13V,H15Q,Q72H,R76G,I86T	1419	24450	2.48	1.355
H15Q,T47A,S67L,Q82R,V89D	1420	67962	6.9	1.479
F2L,H15Q,D46E,T47A,Q72H,R76G,Q82R,V89D	1421	23039	2.34	1.045
I13V,H15Q,L33F,T47A,Q82R,V89D	1422	62254	6.32	1.379
H15Q,N24S,T47A,Q72H,R76G,V89D	1424	32077	3.26	0.4
I13V,H15Q,E44V,T47A,Q82R,V89D	1425	61005	6.2	1.329
H15Q,N18D,T47A,Q72H,V73A,R76G,I86T,V89D	1426	48317	4.91	0.475
I13V,H15Q,T37A,E44D,S48C,S67L,Q82R,V89D	1427	47605	4.84	1.255
H15Q,L33H,S67L,R76G,Q82R,V89D	1428	62326	6.33	1.507
I13V,H15Q,T47A,Q72H,R76G,I86T	1429	49016	4.98	1.477
H15Q,S39I,E44D,Q72H,V75G,R76G,Q82R,V89D	1430	43713	4.44	0.646
H15Q,T47A,S67L,R76G,Q82R,V89D	1431	71897	7.3	1.539
I13V,H15Q,T47A,S67L,Q72H,R76G,Q82R,V89D	1432	71755	7.29	1.536
Wild Type PD-L2 IgV	1263	9843	1	-0.024
Full length ECD of PD-L2	31	2145	0.22	0.071
Full length ECD of PD-L1 (R&D Systems)	30	23769	2.41	1.263
Anti-PD-1 monoclonal antibody (nivolumab)	-	87002	8.84	0.899

TABLE 16B: Bioactivity Data of PD-L2 variants selected against PD-1 in MLR.			
PD-L2 mutation(s)	SEQ ID NO (IgV)	IFN gamma levels pg/mL	Fold increase over wildtype PD-L2 IgV-Fc
H15Q	1357	1817.1	1.32

TABLE 16B: Bioactivity Data of PD-L2 variants selected against PD-1 in MLR.			
PD-L2 mutation(s)	**SEQ ID NO (IgV)**	**IFN gamma levels pg/mL**	**Fold increase over wildtype PD-L2 IgV-Fc**
N24D	1358	1976.3	1.44
E44D	1359	1499.4	1.09
V89D	1360	1168.1	0.85
Q82R,V89D	1361	1617	1.17
E59G,Q82R	1362	1511.3	1.1
S39I,V89D	1363	1314.5	0.95
S67L,V89D	1364	1230.1	0.89
S67L,I85F	1365	1281.9	0.93
S67L,I86T	1366	1020.4	0.74
H15Q,K65R	1367	1510.8	1.1
H15Q,Q72H,V89D	1368	1272.2	0.92
H15Q,S67L,R76G	1369	1426.2	1.04
H15Q,R76G,I85F	1370	1725.7	1.25
H15Q,T47A,Q82R	1371	1317.9	0.96
H15Q,Q82R,V89D	1372	1081.2	0.79
H15Q,C23S,I86T	1373	1847.2	1.34
H15Q,S39I,I86T	1374	1415.2	1.03
H15Q,R76G,I85F	1375	1437.8	1.04
E44D,V89D,W91R	1376	1560.1	1.13
I13V,S67L,V89D	1377	867.5	0.63
H15Q,S67L,I86T	1378	1034.2	0.75
I13V,H15Q,S67L,I86T	1379	1014.4	0.74
I13V,H15Q,E44D,V89D	1380	1384.2	1.01
I13V,S39I,E44D,Q82R,V89D	1381	935.6	0.68
I13V,E44D,Q82R,V89D	1382	1009.5	0.73
I13V,Q72H,R76G,I86T	1383	1953	1.42
I13V,H15Q,R76G,I85F	1384	1528.5	1.11
H15Q,S67L,R76G,I85F	1386	1318.7	0.96
H15Q,T47A,Q72H,R76G,I86T	1387	1599.6	1.16
H15Q,T47A,Q72H,R76G	1388	1462.5	1.06
I13V,H15Q,T47A,Q72H,R76G	1389	1469.8	1.07
H15Q,E44D,R76G,I85F	1390	1391.6	1.01
H15Q,S39I,S67L,V89D	1391	1227	0.89
H15Q,N32D,S67L,V89D	1392	1285.7	0.93
N32D,S67L,V89D	1393	1194	0.87
H15Q,S67L,Q72H,R76G,V89D	1394	1061.2	0.77
H15Q,Q72H,Q74R,R76G,I86T	1395	933.8	0.68
G28V,Q72H,R76G,I86T	1396	1781.6	1.29

TABLE 16B: Bioactivity Data of PD-L2 variants selected against PD-1 in MLR.			
PD-L2 mutation(s)	**SEQ ID NO (IgV)**	**IFN gamma levels pg/mL**	**Fold increase over wildtype PD-L2 IgV-Fc**
I13V,H15Q,S39I,E44D,S67L	1397	1256.9	0.91
E44D,S67L,Q72H,Q82R,V89D	1398	1281.4	0.93
H15Q,V89D	1399	1495.4	1.09
H15Q,T47A	1400	1637.2	1.19
I13V,H15Q,Q82R	1401	1432.9	1.04
I13V,H15Q,V89D	1402	1123	0.82
I13V,S67L,Q82R,V89D	1403	1372.8	1
I13V,H15Q,Q82R,V89D	1404	1596.6	1.16
H15Q,V31M,S67L,Q82R,V89D	1405	1206.5	0.88
I13V,H15Q,T47A,Q82R	1406	1703.3	1.24
I13V,H15Q,V31A,N45S,Q82R,V89D	1407	1723.1	1.25
H15Q,T47A,H69L,Q82R,V89D	1409	1732.5	1.26
I13V,H15Q,T47A,H69L,R76G,V89D	1410	1075.5	0.78
I12V,I13V,H15Q,T47A,Q82R,V89D	1411	1533.2	1.11
I13V,H15Q,R76G,D77N,Q82R,V89D	1412	1187.9	0.86
I13V,H15Q,T47A,R76G,V89D	1413	1253.7	0.91
I13V,H15Q,T47A,Q82R,V89D	1414	1445.5	1.05
I13V,H15Q,T47A,Q82R,V89D	1414	1737	1.26
I13V,H15Q,I36V,T47A,S67L,V89D	1416	1357.4	0.99
H15Q,T47A,K65R,S67L,Q82R,V89D	1417	1335.3	0.97
H15Q,L33P,T47A,S67L,P71S,V89D	1418	1289.1	0.94
I13V,H15Q,Q72H,R76G,I86T	1419	1221	0.89
H15Q,T47A,S67L,Q82R,V89D	1420	1197.1	0.87
F2L,H15Q,D46E,T47A,Q72H,R76G,Q82R,V89D	1421	1170.7	0.85
I13V,H15Q,L33F,T47A,Q82R,V89D	1422	1468.4	1.07
I13V,H15Q,T47A,E58G,S67L,Q82R,V89D	1423	836.1	0.61
H15Q,N24S,T47A,Q72H,R76G,V89D	1424	1091.8	0.79
I13V,H15Q,E44V,T47A,Q82R,V89D	1425	1270.5	0.92
H15Q,N18D,T47A,Q72H,V73A,R76G,I86T,V89D	1426	1065.8	0.77
I13V,H15Q,T37A,E44D,S48C,S67L,Q82R,V89D	1427	1751.7	1.27
H15Q,L33H,S67L,R76G,Q82R,V89D	1428	1502	1.09
I13V,H15Q,T47A,Q72H,R76G,I86T	1429	1088.1	0.79
H15Q,S39I,E44D,Q72H,V75G,R76G,Q82R,V89D	1430	940.9	0.68
H15Q,T47A,S67L,R76G,Q82R,V89D	1431	1097.8	0.8
I13V,H15Q,T47A,S67L,Q72H,R76G,Q82R,V89D	1432	1559.6	1.13
Wild Type PD-L2 IgV	1263	1376.8	1
Full length ECD of PD-L2	31	1173.2	0.85
Full length ECD of PD-L1	30	2190.9	1.59

TABLE 16B: Bioactivity Data of PD-L2 variants selected against PD-1 in MLR.			
PD-L2 mutation(s)	**SEQ ID NO (IgV)**	**IFN gamma levels pg/mL**	**Fold increase over wildtype PD-L2 IgV-Fc**
Nivolumab (anti-PD-1)	-	418.9	0.3

EXAMPLE 9

Assessment of Bioactivity of Affinity-Matured IgSF Domain-Containing Molecules Using Mixed Lymphocyte Reaction (MLR)

[0491] This Example describes Fc-fusion variant protein bioactivity characterization in human primary T cell in vitro assays.

[0492] Soluble variant PD-L1 IgV-Fc bioactivity was tested in a human Mixed Lymphocyte Reaction (MLR). Human primary dendritic cells (DC) were generated by culturing monocytes isolated from PBMC (BenTech Bio, USA) in vitro for 7 days with 50 ng/mL rIL-4 (R&D Systems, USA) and 80 ng/mL rGM-CSF (R&D Systems, USA) in Ex-Vivo 15 media (Lonza, Switzerland). To fully induce DC maturation, lipopolysaccharide (LPS) (InvivoGen Corp., USA) was added to the DC cultures on day 6 and cells were incubated for an additional 24 hours. Approximately, 10,000 matured DC and 100,000 purified allogeneic CD3+ T cells (BenTech Bio, USA) were co-cultured with several concentrations of variant PD-L1 IgV-Fc fusion proteins in 96 well round-bottom plates in 200 µl final volume of Ex-Vivo 15 media. Irrelevant human IgG or media only (designated "No Add") were used as negative controls. As positive controls, PDL1-Fc (full PD-L1 extracellular domain), wildtype PD-L1 IgV-Fc and or positive control anti-PD-1 monoclonal antibody (nivolumab) was assessed. Variant PD-L1 IgV-Fc fusion proteins were tested at various concentrations as indicated in FIG. 8 and 9. On day 5, IFN-gamma secretion in culture supernatants was analyzed using the Human IFN-gamma Duoset ELISA kit (R&D Systems, USA). Optical density was measured on a BioTek Cytation Multimode Microplate Reader (BioTek Corp., USA) and quantitated against titrated rIFN-gamma standard included in the IFN-gamma Duo-set kit (R&D Systems, USA).

[0493] Results for the bioactivity studies for exemplary tested variant PD-L1 IgV-Fc are shown in FIG. 8 and FIG. 9, which sets forth the calculated levels of IFN-gamma in culture supernatants (pg/mL) at the indicated concentration of variant IgV-Fc fusion molecule. The variants are identified with reference to the amino acid substitutions in the IgV of PD-L1 with

reference to positions corresponding to positions of the unmodified (wildtype) PD-L1 ECD sequence set forth in SEQ ID NO:30 or 1728. As shown in FIG. 8, exemplary variant PD-L1 IgV-Fc molecules exhibited improved activities to increase IFNg production in an MLR assay. As shown in FIG. 9, the exemplary variant PD-L1 IgV-Fc fusion molecules tested show comparable activity to nivolumab in an MLR assay.

EXAMPLE 10

Generation of Stacked Molecules Containing Different Affinity-Modified Domains

[0494] This Example describes immunomodulatory proteins that were generated as multi-domain stack constructs containing at least two different affinity modified IgV domains from identified variant PD-L1 polypeptides, identified variant CD112 polypeptides and identified variant CD155 polypeptides described above. Specifically, the exemplary variant PD-L1 IgV D43G/N45D/L56Q/V58A/ G101G-ins (G101GG) (SEQ ID NO: 303), CD112 IgV molecule S118F (SEQ ID NO: 768) and/or the exemplary variant CD155 IgV molecule P18S/S65W/S67A/L104Q/G111R (SEQ ID NO: 1576) were linked together and fused to an Fc in various configurations.

[0495] Homodimeric stacks were generated in various configurations as summarized in FIG. 5A and 5B and as follows. In the generated homodimeric stack constructs , the variant CD155 IgV variant, CD112 IgV and/or variant PD-L1 IgV were variously linked to the N- or C-terminus of a human IgG1 Fc region via a 2xGGGS (SEQ ID NO: 240) or 3x GGGGS (SEQ ID NO: 239) peptide linker. In this study, the exemplary IgG1 Fc region is set forth in SEQ ID NO:1155 and contained the mutations L234A, L235E, G237A, E356D and M358L by EU numbering (corresponding to L19A, L20E, G22A, E141D and M143L with reference to wild-type human IgG1 Fc set forth in SEQ ID NO:187). Further, the Fc region contained replacement of the cysteine residues to a serine residue at position 5 (C5S) compared to the wild-type or unmodified Fc set forth in SEQ ID NO: 187 (corresponding to C220S by EU numbering). In some examples, the Fc was further modified to remove the C-terminal lysine at position 232 of the wild-type or unmodified Fc set forth in SEQ ID NO: 197 (corresponding to K447del by EU numbering). The exemplary IgG1 Fc region comprising a lysine deletion is set forth in SEQ ID NO: 1715. Other Fc regions also are suitable for generation of stack molecules. Exemplary generated stacks are set forth below.

[0496] Expression constructs encoding Fc fusion proteins of interest were transiently expressed in Expi293 HEK293 cells from Invitrogen using the manufacturer's commercial

Expifectamine reagents and media. Supernatants were harvested and protein was captured and eluted from a Protein A column using an AKTA protein purification system. The eluted material was then separated by an additional preparative SEC step to generate monomeric, highly purified material. The purified proteins were formulated in 15mM acetate, 200mM NaCl, 9% sucrose, pH 5.0 (ASU5). The protein was vialed in a sterile biosafety cabinet and frozen at -80 C. A vial was thawed and assessed by analytical SEC to demonstrate the material was stable and predominantly monomeric after thaw.

[0497] For each stack, the encoding nucleic acid molecule was designed to produce homodimeric stacks in various configurations with sequences in the order shown:

A. Stack Constructs Containing PD-L1 and CD155

[0498] The encoding nucleic acid molecule were designed to generate homodimeric stacks in various configurations of sequences in the order shown:

- PD-L1/CD155 Stack 1 (SEQ ID NO: 1716): CD155 variant (SEQ ID NO: 1576) – 2xGGGS (SEQ ID NO: 240) – Fc (SEQ ID NO: 1155) – 3x GGGGS (SEQ ID NO: 239) – PD-L1 (SEQ ID NO: 303)
- PD-L1/CD155 Stack 2 (SEQ ID NO: 1717): PD-L1 (SEQ ID NO: 303) – 2xGGGS (SEQ ID NO: 240) – Fc (SEQ ID NO: 1155) – 3x GGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576)
- PD-L1/CD155 Stack 3 (SEQ ID NO: 1718): CD155 variant (SEQ ID NO: 1576) –3x GGGGS (SEQ ID NO: 239) – PD-L1 (SEQ ID NO: 303) – 2xGGGS (SEQ ID NO: 240) – Fc (SEQ ID NO: 1155)
- PD-L1/CD155 Stack 4 (SEQ ID NO: 1719): PD-L1 (SEQ ID NO: 303) – 3x GGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576) – 2xGGGS (SEQ ID NO: 240) –Fc (SEQ ID NO: 1155)
- PD-L1/CD155 Stack 5 (SEQ ID NO: 1720): N-terminal HMSSVSAQ set forth in SEQ ID NO: 1156 – Fc (SEQ ID NO: 1155) – 3x GGGGS (SEQ ID NO: 239) - CD155 variant (SEQ ID NO: 1576) – 3xGGGS (SEQ ID NO: 239) – PD-L1 (SEQ ID NO: 303)
- PD-L1/CD155 Stack 6 (SEQ ID NO: 1721): N-terminal HMSSVSAQ set forth in SEQ ID NO: 1156 – Fc (SEQ ID NO: 1155) – 3x GGGGS (SEQ ID NO: 239) – PD-

L1 (SEQ ID NO: 303) – 3xGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576)

B. Stack Constructs Containing PD-L1, CD112 and CD155

[0499] The encoding nucleic acid molecule were designed to generate homodimeric stacks in various configurations of sequences in the order shown:

- PD-L1/CD112/CD155 Stack 1 (SEQ ID NO: 1722): PD-L1 (SEQ ID NO: 303) – 3xGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576) – 2xGGGS (SEQ ID NO: 240) – Fc with lysine removed (SEQ ID NO: 1715) – 3x GGGGS (SEQ ID NO: 239) – CD112 (SEQ ID NO: 768)
- PD-L1/CD112/CD155 Stack 2 (SEQ ID NO: 1723): PD-L1 (SEQ ID NO: 303) – 3xGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576) – 3xGGGS (SEQ ID NO: 239) – CD112 (SEQ ID NO: 768) – 2xGGGS (SEQ ID NO: 240) – Fc (SEQ ID NO: 1155)
- PD-L1/CD112/CD155 Stack 3 (SEQ ID NO: 1724): PD-L1 (SEQ ID NO: 303) – 3xGGGS (SEQ ID NO: 239) – CD112 (SEQ ID NO: 768) – 3xGGGS (SEQ ID NO: 239) – CD155 variant (SEQ ID NO: 1576) – 2xGGGS (SEQ ID NO: 240) – Fc (SEQ ID NO: 1155)

EXAMPLE 11

Assessment of Binding and Bioactivity of PD-L1/CD155 Stacked Affinity-Matured IgSF Domain-Containing Molecules

[0500] This Example describes binding studies to assess specificity and affinity of exemplary PD-L1/CD155 variant IgV stack immunomodulatory proteins (PD-L1/CD155 stacked IgV-Fc), generated in Example 10, for binding to cognate binding partners. In addition, a Jurkat/IL2/PD1/TIGIT reporter assay was used to assess PD-1 and TIGIT blocking activity of PD-L1/CD155 stacked IgV-Fc molecules. As a control, binding and blocking activity also was assessed of the non-stack variant PD-L1 IgV-Fc or CD155 IgV-Fc fusion molecules containing the same variant PD-L1 IgV (SEQ ID NO:303) or variant CD155 IgV (SEQ ID NO:1576), respectively, used in the stacks. Wild-type CD155-ECD-Fc and wild-type PD-L1-ECD-Fc containing the wildtype CD155 ECD (SEQ ID NO:20) or the wildtype PD-L1 ECD (SEQ ID NO:3), respectively, also were assessed.

A. Binding to Cell-Expressed Counter Structure

[0501] Binding studies were carried out using Jurkat/IL-2 reporter cells (purchased from Promega Corp. USA) that were transduced to stably express human PD-1 (Jurkat/PD-1 cells), human TIGIT (Jurkat/TIGIT cells) or both PD-1 and TIGIT (Jurkat/PD-1/TIGIT cells). For staining by flow cytometry, 100,000 Jurkat/PD-1, Jurkat/TIGIT, Jurkat/PD-1/TIGIT cells or negative control (Jurkat only) were plated in 96-well round-bottom plates. Cells were spun down and resuspended in staining buffer (PBS (phosphate buffered saline), 1% BSA (bovine serum albumin), and 0.1% sodium azide) for 20 minutes to block non-specific binding. Afterwards, cells were centrifuged again and resuspended in 50 µL staining buffer containing 100 nM to 6 pM of each candidate Fc fusion protein, either variant PD-L1 IgV-Fc or CD155 IgV-Fc fusion molecules or PD-L1/CD155 stacked IgV-Fc fusion molecules described above. Primary staining was performed on ice for 90 minutes, before washing cells twice in 200 µL staining buffer. PE-conjugated anti-human Fc (Jackson ImmunoResearch, USA) was diluted 1:150 in 50 µL staining buffer and added to cells and incubated another 30 minutes on ice. Secondary antibody was washed out twice, cells were fixed in 4% formaldehyde/PBS, and samples were analyzed on Intellicyt flow cytometer (Intellicyt Corp., USA).

[0502] Mean Fluorescence Intensity (MFI) was calculated with FlowJo Version 10 software (FlowJo LLC, USA). Table 17 sets forth the binding activity as measured by the Mean Fluorescence Intensity (MFI) value for binding of 20 nM of each stack Fc-fusion molecule, non-stack variant PD-L1 IgV-Fc or CD155 IgV-Fc controls or wild-type ECD controls, to Jurkat/PD-1, Jurkat/TIGIT, and Jurkat/PD-1/TIGIT cells. As shown in Table 17, several stack proteins bound both PD-1 and TIGIT with high affinity. Studies were carried out substantially as described above to further assess binding of the stack proteins at various doses.

TABLE 17: Binding of Stacks to Cell-Expressed Counter Structure

		Flow Binding to Jurkat Cells Stably Expressing:		
SEQ ID NO	**Description**	**PD-1**	**TIGIT**	**PD-1 + TIGIT**
1716	(CD155 IgV) (G4S)2 Fc (G4S)3 (PD-L1 IgV)	61805	80658	35128
1717	(PD-L1 IgV) (G4S)2 Fc(G4S)3 (CD155 IgV)	69813	36485	52538
1718	(CD155 IgV) (G4S)3 (PD-L1 IgV) (G4S)2 Fc	47261	81840	32188

1719	(PD-L1 IgV) (G4S)3 (CD155 IgV) (G4S)2 Fc	77959	60515	51615
303	non-stack variant PD-L1 IgV-Fc control	111746	630	41390
1576	non-stack variant CD155 IgV-Fc control	460	79152	7910
20 (ECD)	CD155-ECD-Fc	511	28790	1196
3 (ECD)	PD-L1-ECD-Fc (R&D Systems)	35005	557	10358
1155	Fc Control (homodimer)	437	483	478
		MFI at 20nM	**MFI at 20nM**	**MFI at 20nM**

B. Assessment of Bioactivity of Affinity-Matured IgSF Domain-Containing Molecules

[0503] Jurkat effector cells expressing an IL-2-luciferase reporter and cell-surface PD-1 and TIGIT were suspended at $2x10^6$ cells/mL in Jurkat Assay buffer (RPMI1640 + 5%FBS) and anti-CD28 was added to a final concentration of 3 μg/mL. Jurkat cells were then plated at 50 μL/well for a total of 100,000 cells per well.

[0504] To each well, 25μL of PD-L1/CD155 stacked IgV-Fc test protein was added to the Jurkat cells. As a control, non-stack variant PD-L1 IgV-Fc or CD155 IgV-Fc fusion molecules, alone or in combination, also were assessed for comparison. Anti-TIGIT antibody (clone MBSA43), anti-PD-1 antibody (nivolumab) or an empty Fc molecule were also used as controls. All proteins were added at five concentrations: 400 nM, 100 nM, 25 nM, 6.25 nM, and 1.56 nM. The Jurkat cells with test or control proteins were incubated for 15 minutes at room temperature. CHO-derived artificial antigen presenting cells (aAPC) displaying transduced cell surface anti-CD3 single chain Fv (OKT3), PD-L1 and CD155 were brought to $0.8x10^6$ cells/mL and 25 μL of cells was added to each well bringing the final volume of each well to 100 μL. Each well had a final ratio of 5:1 Jurkat:CHO cells and a test protein concentration of 100, 25, 6.25, 1.56 or 0.47 nM and an anti-CD28 concentration of 1.5 μg/mL. Jurkat cells and CHO cells were incubated for 5 hours at 37 degrees Celsius in a humidified 5% CO_2 incubation chamber. Plates are then removed from the incubator and acclimated to room temperature for 15 minutes. 100 μL of a cell lysis and luciferase substrate solution (BioGlo luciferase reagent, Promega) was added to each well and the plates were incubated on an orbital shaker for 10 minutes. Luminescence was measured with a 1 second per well integration time using a BioTek Cytation luminometer.

[0505] An average relative luminescence value was determined for each test sample and a fold increase (or decrease) in IL-2 reporter signal was calculated for each stack molecule

compared to non-stack variant PD-L1 IgV-Fc and variant CD155 IgV-Fc proteins. Because the assay is a measure of blockade of inhibitory signals, an increase in luminescent signal compared to control indicates the presence of blocking activity.

[0506] As shown in Table 18, the luciferase activity of the Jurkat effector cells co-cultured with anti-CD3/PD-L1/CD155 aAPC and 100 nM PD-L1/CD155 stack Fc molecules was altered (increased) for each molecule tested compared to control. The differences in luminescence signals demonstrate the differences in binding of the PD-L1/CD155 stack-Fc molecules to PD-1 and TIGIT and the resulting co-blockade of inhibitory activity. In the Table, Column 1 sets forth the SEQ ID NO identifier for each PD-L1/CD155 stack-Fc variant tested. Studies were carried out substantially as described above to further assess binding of the stack proteins at various doses.

TABLE 18: Jurkat/IL2/PD1/TIGIT + CHO/OKT3/PD-L1/CD155 Reporter Assay Results

SEQ ID NO	Description	RLU	Fold Increase Compared to non-stack variant PD-L1 IgV-Fc control	Fold Increase Compared to non-stack variant CD155 IgV-Fc control	Fold Increase Compared to variant PD-L1 IgV-Fc and variant CD155 IgV-Fc
1716	(CD155 IgV) (G4S)2 Fc (G4S)3 (PD-L1 IgV)	573	0.6	1.7	0.8
1717	(PD-L1 IgV) (G4S)2 Fc(G4S)3 (CD155 IgV)	962	1.0	2.8	1.4
1718	(CD155 IgV) (G4S)3 (PD-L1 IgV) (G4S)2 Fc	434	0.5	1.3	0.6
1719	(PD-L1 IgV) (G4S)3 (CD155 IgV) (G4S)2 Fc	1923	2.0	5.6	2.7
303	non-stack variant PD-L1 IgV-Fc control	958	1.0	2.8	1.3
1576	non-stack variant CD155 IgV-Fc control	345	0.4	1.0	0.5
-	Anti-TIGIT antibody (clone MBSA43), anti-PD-1 antibody (nivolumab)	2192	2.3	6.4	3.1
303+1576	PD-L1 IgV + CD155 IgV	710	0.7	2.1	1.0
1715	Fc Control (homodimer)	235	0.2	0.7	0.3

EXAMPLE 12

Assessment of Binding and Bioactivity of PD-L1/CD112/CD155 Stacked Affinity-Matured IgSF Domain-Containing Molecules

[0507] This Example describes binding studies to assess specificity and affinity of PD-L1/CD112/CD155 stack immunomodulatory proteins (PD-L1/CD112/CD155 stacked IgV-Fc), generated in Example 10, for binding to cognate binding partners. In addition, a Jurkat/IL2/PD1/CD112R/TIGIT reporter assay was used to assess PD-1, CD112R, and TIGIT blocking activity of PD-L1/CD112/CD155 stacked IgV-Fc molecules. As a comparison, binding and blocking activity also was assessed of the non-stack variant PD-L1 IgV-Fc, CD112 IgV-Fc or CD155 IgV-Fc fusion molecules containing the same variant PD-L1 (SEQ ID NO:303), CD112 IgV (SEQ ID NO:768) or variant CD155 IgV (SEQ ID NO:1576), respectively, used in the stacks.

A. Binding to Cell-Expressed Counter Structure

[0508] Binding studies were carried out using Jurkat/IL-2 reporter cells which endogenously express CD112R (purchased from Promega Corp. USA) that were transduced to stably express human PD-1 (Jurkat/PD-1 cells), human TIGIT (Jurkat/TIGIT cells) or both PD-1 and TIGIT (Jurkat/PD-1/TIGIT cells). For staining by flow cytometry, 100,000 Jurkat parental (CD112R), Jurkat/PD-1, Jurkat/TIGIT, Jurkat/PD-1/TIGITcells were plated in 96-well round-bottom plates. Cells were spun down and resuspended in staining buffer (PBS (phosphate buffered saline), 1% BSA (bovine serum albumin), and 0.1% sodium azide) for 20 minutes to block non-specific binding. Afterwards, cells were centrifuged again and resuspended in 50 μL staining buffer containing 100 nM to 6 pM of each candidate Fc fusion protein. Primary staining was performed on ice for 90 minutes, before washing cells twice in 200 μL staining buffer. PE-conjugated anti-human Fc (Jackson ImmunoResearch, USA) was diluted 1:150 in 50 μL staining buffer and added to cells and incubated another 30 minutes on ice. Secondary antibody was washed out twice, cells were fixed in 4% formaldehyde/PBS, and samples were analyzed on an LSRII flow cytometer (Becton Dickinson Corp., USA).

[0509] Binding values, expressed as Mean Fluorescence Intensity (MFI), were determined for a 33.3 nM concentration of each stack Fc fusion protein and non-stack variant PD-L1 IgV-Fc, CD112-IgV-Fc and CD155-IgV-Fc proteins. Data was analyzed using FlowJo Version 10 software (FlowJo LLC, USA). Results for the binding studies for exemplary tested PD-

L1/CD112/CD155 stack Fc fusion molecules (tested at 33.3 nM) are shown in Table 19. As shown, several stack proteins bound PD-1, TIGIT and/or CD112R with high affinity.

TABLE 19: Binding of Stacks to Cell-Expressed Counter Structure

Category	Description	SEQ ID NO	Binding to Jurkat Transfectants			
			TIGIT	CD112R	PD1	TIGIT/ CD112R/ PD1
Stacks	(PD-L1 IgV) (G4S)3 (CD155 IgV) (G4S)3 (CD112 IgV) (G4S)2 Fc	1723	2457	969	16989	19041
	(PD-L1 IgV) (G4S)3 (CD112 IgV) (G4S)3 (CD155 IgV) (G4S)2 Fc	1724	1504	289	21968	18727
Controls	non-stack variant PD-L1 IgV-Fc control	303	101	100	20713	18468
	non-stack variant CD155 IgV-Fc control	1576	6294	55	31	961
	non-stack variant CD112 IgV-Fc control	768	358	516	459	477
	Fc Control	1155	23.3	27	22	35
			MFI at 33.3nM			

B. Assessment of Bioactivity of Affinity-Matured IgSF Domain-Containing Molecules

[0510] Jurkat effector cells expressing an IL-2-luciferase reporter and cell-surface PD-1, CD112R, and TIGIT were suspended at $2x10^6$ cells/mL in Jurkat Assay buffer (RPMI1640 + 5%FBS) and anti-CD28 was added to a final concentration of 3 μg/mL. Jurkat cells were then plated at 50 μL/well for a total of 100,000 cells per well.

[0511] To each well, 25μL of PD-L1/CD112/CD155 stacked IgV-Fc test protein was added to the Jurkat cells. As a control, non-stack variant PD-L1 IgV-Fc, CD112 IgV-Fc or CD155 IgV-Fc fusion molecules, alone or in combination, also were assessed for comparison. Anti-TIGIT antibody (clone MBSA43), anti-PD-1 antibody (nivolumab) or an empty Fc molecule are used as controls. All proteins were added at five concentrations: 400 nM, 100 nM, 25 nM, 6.25 nM, 1.56 nM, or 0.49 nM. The Jurkat cells with test or control proteins were incubated for 15 minutes at room temperature. CHO-derived artificial antigen presenting cells (aAPC) displaying transduced cell surface anti-CD3 single chain Fv (OKT3), PD-L1 and CD112 were brought to $0.8x10^6$ cells/mL and 25 μL of cells was added to each well bringing the final volume of each well to 100 μL. Each well had a final ratio of 5:1 Jurkat:CHO cells and a test protein concentration of 100,

25, 6.25, 1.56, 0.47 or 0.12 nM and an anti-CD28 concentration of 1.5 µg/mL. Jurkat cells and CHO cells were incubated for 5 hours at 37 degrees Celsius in a humidified 5% CO_2 incubation chamber. Plates are then removed from the incubator and acclimated to room temperature for 15 minutes. 100 µL of a cell lysis and luciferase substrate solution (BioGlo luciferase reagent, Promega) was added to each well and the plates were incubated on an orbital shaker for 10 minutes. Luminescence was measured with a 1 second per well integration time using a BioTek Cytation luminometer.

[0512] An average relative luminescence value (RLU) was determined for each test sample and a fold increase (or decrease) in IL-2 reporter signal was calculated for each stack molecule compared to non-stack variant PD-L1 IgV-Fc, variant CD112 IgV-Fc and variant CD155 IgV-Fc proteins. Because the assay is a measure of blockade of inhibitory signals, an increase in luminescent signal compared to control indicates the presence of blocking activity.

[0513] As shown in Table 20, the luciferase activity of the Jurkat effector cells co-cultured with anti-CD3/PD-L1/CD112 aAPC and the PD-L1/CD112/CD155 stack Fc molecules was altered (increased) for each molecule tested. The differences in luminescence signals demonstrate the differences in binding of the PD-L1/CD112/CD155 stack-Fc molecules to PD-1, CD112R and TIGIT and the resulting co-blockade of inhibitory activity. In the Table, Column 2 sets forth the SEQ ID NO identifier for each PD-L1/CD112/CD155 stack-Fc variant tested.

Table 20: Jurkat/IL2/TIGIT/PD1 Reporter Assay

Description	SEQ ID NO	RLU	Fold Increase compared to Fc Control	Fold Increase compared to PD-L1 IgV-Fc	Fold Increase compared to CD155 IgV-Fc	Fold Increase compared to CD112-IgV -Fc
(PD-L1 IgV) (G4S)3 (CD155 IgV) (G4S)3 (CD112 IgV) (G4S)2 Fc	1723	896	1.44	1.12	1.04	1.40
(PD-L1 IgV) (G4S)3 (CD112 IgV) (G4S)3 (CD155 IgV) (G4S)2 Fc	1724	961	1.54	1.20	1.12	1.50
non-stack variant PD-L1 IgV-Fc control	303	800	1.28	1.00	0.93	1.25
non-stack variant CD155 IgV-Fc control	1576	859	1.38	1.07	1.00	1.34
non-stack variant CD112 IgV-Fc control	768	640	1.03	0.80	0.75	1.00
Fc Control	1155	624	1.00	0.78	0.73	0.98

EXAMPLE 13

Assessment of Binding of Affinity-Matured IgSF Domain-Containing Molecules to Cell Expressed Counted Structure

[0514] This Example describes flow cytometry binding studies to assess specificity and affinity of PD-L1-extracellular domain (ECD) variant immunomodulatory proteins for cognate binding partners PD-1 and CD80 using the selection scheme as described in Example 3 for second round selection against rPD-1.Fc or rCD80.Fc, except that mutant constructs were generated based on a wildtype human PD-L1 sequence set forth in SEQ ID NO:1728 containing the full extracellular domain (IgV + IgC) as follows.

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLK VQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKVN APYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREE KLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERT (SEQ ID NO:1728)

[0515] To measure binding to PD-1, studies were carried out using Jurkat/IL-2 reporter cells (purchased from Promega Corp. USA) that were transduced to stably express human PD-1 (Jurkat/PD-1 cells). To measure binding to CD80, studies were carried out using Chinese Hamster Overy (CHO) cells that were transduced to stably express human CD80 (CHO/CD80). 100,000 cells per well of Jurkat/PD-1, CHO/CD80, Jurkat parental or CHO parental cells were plated into 96-well round-bottom plates. Cells were spun down and resuspended in staining buffer (PBS (phosphate buffered saline), 1% BSA (bovine serum albumin), and 0.1% sodium azide) for 20 minutes to block non-specific binding. Afterwards, cells were centrifuged again and resuspended in 50 μL staining buffer containing 100 nM to 3.7 nM of each candidate Fc fusion protein. Primary staining was performed on ice for 90 minutes, before washing cells twice in 200 μL staining buffer. APC-conjugated anti-human Fc (Jackson ImmunoResearch, USA) was diluted 1:150 in 50 μL staining buffer and added to cells and incubated another 30 minutes on ice. Secondary antibody was washed out twice, cells were fixed in 4% formaldehyde/PBS, and samples were analyzed on LSRII flow cytometer (Becton Dickinson Corp., USA).

[0516] Mean Fluorescence Intensity (MFI) was calculated at the 20 nM concentration and compared to wild type PD-L1 ECD-Fc protein with FlowJo Version 10 software (FlowJo LLC, USA). Results for the binding studies for exemplary tested PD-L1-ECD-Fc fusion molecules are shown in Table 21. As demonstrated, the selections resulted in the identification of variant PD-L1 proteins that bind either PD-1 alone, CD80 alone or both proteins with high affinity.

Table 21: Flow Binding to Cells Expressing PD-1 or CD80					
PD-L1 Mutation(s)	SEQ ID NO (ECD)	PD-1		CD80	
		MFI at 20nM	Fold Change Compared to WT PD-L1	MFI at 20nM	Fold Change Compared to WT PD-L1
K57R, S99G	1729	2953	0.9	16253	121.3
K57R, S99G, F189L	1730	1930	0.6	12906	96.3
M18V, M97L, F193S, R195G, E200K, H202Q	1731	69	0.0	241	1.8
I36S, M41K, M97L, K144Q, R195G, E200K, H202Q, L206F	1732	3498	1.1	68715	512.8
C22R, Q65L, L124S, K144Q, R195G, E200N, H202Q, T221L	1733	Little or no protein produced			
M18V, I98L, L124S, P198T, L206F	1734	2187	0.7	143	1.1
S99G, N117S, I148V, K171R, R180S	1735	Little or no protein produced			
I36T, M97L, A103V, Q155H	1736	120	0.0	128	1.0
K28I, S99G	1737	830	0.3	693	5.2
R195S	1738	3191	1.0	138	1.0
A79T, S99G, T185A, R195G, E200K, H202Q, L206F	1739	1963	0.6	643	4.8
K57R, S99G, L124S, K144Q	1740	2081	0.7	14106	105.3
K57R, S99G, R195G	1741	2479	0.8	10955	81.8
D55V, M97L, S99G	1742	11907	3.8	71242	531.7
E27G, I36T, D55N, M97L, K111E	1743	1904	0.6	88724	662.1
E54G, M97L, S99G	1744	8414	2.7	51905	387.4
G15A, I36T, M97L, K111E, H202Q	1745	112	0.0	13530	101.0
G15A, I36T, V129D	1746	114	0.0	136	1.0
G15A, I36T, V129D, R195G	1747	125	0.0	134	1.0
G15A, V129D	1748	2075	0.7	128	1.0
I36S, M97L	1749	3459	1.1	44551	332.5
I36T, D55N, M97L, K111E, A204T	1750	265	0.1	62697	467.9
I36T, D55N, M97L, K111E, V129A, F173L	1751	393	0.1	72641	542.1
I36T, D55S, M97L, K111E, I148V, R180S	1752	94	0.0	30704	229.1
I36T, G52R, M97L, V112A, K144E, V175A, P198T	1753	81	0.0	149	1.1
I36T, I46V, D55G, M97L, K106E, K144E, T185A, R195G	1754	69	0.0	190	1.4
I36T, I83T, M97L, K144E, P198T	1755	62	0.0	6216	46.4
I36T, M97L, K111E	1756	Little or no protein produced			

Table 21: Flow Binding to Cells Expressing PD-1 or CD80					
PD-L1 Mutation(s)	SEQ ID NO (ECD)	PD-1		CD80	
		MFI at 20nM	Fold Change Compared to WT PD-L1	MFI at 20nM	Fold Change Compared to WT PD-L1
I36T, M97L, K144E, P198T	1757	197	0.1	40989	305.9
I36T, M97L, Q155H, F193S, N201Y	1758	69	0.0	1251	9.3
I36T, M97L, V129D	1759	523	0.2	50905	379.9
L35P, I36S, M97L, K111E	1760	190	0.1	155	1.2
M18I, I36T, E53G, M97L, K144E, E199G, V207A	1761	104	0.0	47358	353.4
M18T, I36T, D55N, M97L, K111E	1762	138	0.0	71440	533.1
M18V, M97L, T176N, R195G	1763	1301	0.4	45300	338.1
M97L, S99G	1764	12906	4.1	81630	609.2
N17D, M97L, S99G	1765	10079	3.2	73249	546.6
S99G, T185A, R195G, P198T	1766	2606	0.8	22062	164.6
V129D, H202Q	1767	2001	0.6	219	1.6
V129D, P198T	1768	3245	1.0	152	1.1
V129D, T150A	1769	1941	0.6	142	1.1
V93E, V129D	1770	1221	0.4	150	1.1
Y10F, M18V, S99G, Q138R, T203A	1771	70	0.0	412	3.1
WT PD-L1 (IgV+IgC) Fc	1728	3121	1.0	134	1.0
CTLA4-Fc	-	59	N/A	199670	N/A
Anti-PD1 mAb	-	31482	N/A	134	N/A
Fc Control	1155	59	N/A	132	N/A

[0517] Additional variants identified in the screen as described in Example 3 are set forth in Table 22A.

TABLE 22A. Additional Affinity-Matured IgSF Domain-Containing Molecules			
PD-L1 Mutation(s)	SEQ ID NO (ECD)	PD-L1 Mutation(s)	SEQ ID NO (ECD)
N45D	1772	N45D, G102D, R194W, R195G	1796
K160M, R195G	1773	N45D, G52V, Q121L, P198S	1797
N45D, K144E	1774	N45D, I148V, R195G, N201D	1798
N45D, P198S	1775	N45D, K111T, T183A, I188V	1799
N45D, P198T	1776	N45D, Q89R, F189S, P198S	1800
N45D, R195G	1777	N45D, S99G, C137R, V207A	1801
N45D, R195S	1778	N45D, T163I, K167R, R195G	1802

N45D, S131F	1779	N45D, T183A, T192S, R194G	1803
N45D, V58D	1780	N45D, V50A, I119T, K144E	1804
V129D, R195S	1781	T19A, N45D, K144E, R195G	1805
I98T, F173Y, L196S	1782	V11E, N45D, T130A, P198T	1806
N45D, E134G, L213P	1783	V26A, N45D, T163I, T185A	1807
N45D, F173I, S177C	1784	K23N, N45D, L124S, K167T, R195G	1808
N45D, I148V, R195G	1785	K23N, N45D, Q73R, T163I	1809
N45D, K111T, R195G	1786	K28E, N45D, W149R, S158G, P198T	1810
N45D, N113Y, R195S	1787	K28R, N45D, K57E, I98V, R195S	1811
N45D, N165Y, E170G	1788	K28R, N45D, V129D, T163N, R195T	1812
N45D, Q89R, I98V	1789	M41K, D43G, N45D, R64S, R195G	1813
N45D, S131F, P198S	1790	M41K, D43G, N45D, R64S, S99G	1814
N45D, S75P, P198S	1791	N45D, R68L, F173L, D197G, P198S	1815
N45D, V50A, R195T	1792	N45D, V50A, I148V, R195G, N201D	1816
E27D, N45D, T183A, I188V	1793	M41K, D43G, K44E, N45D, R195G, N201D	1817
F173Y, T183I, L196S, T203A	1794	N45D, V50A, L124S, K144E, L179P, R195G	1818
K23N, N45D, S75P, N120S	1795		

[0518] Substantially as described above, flow cytometry binding studies were performed to assess specificity and affinity of PD-L1-extracellular domain (ECD) variant immunomodulatory proteins for cognate binding partner PD-1. To measure binding to PD-1, as described above Jurkat/IL-2 reporter cells transduced to stably express human PD-1 (Jurkat/PD-1 cells) were used. Mean Fluorescence Intensity (MFI) was calculated at the 20 nM concentration and compared to wild type PD-L1 ECD-Fc protein and an Fc only control. Results for the binding studies for exemplary tested PD-L1-ECD-Fc fusion molecules are shown in Table 22B. As demonstrated, the selections resulted in the identification of variant PD-L1 proteins that bind PD-1 alone with high affinity.

TABLE 22B. Flow binding to Jurkat cells expressing PD-1

PD-L1 Mutation(s)	SEQ ID NO (ECD)	MFI at 20nM conc.	Fold Increase over WT PD-L1 ECD-Fc
N45D	1772	95635	19.1
R195S	1827	5365	1.1
K160M, R195G	1773	3931	0.8
N45D, K144E	1774	99704	19.9
N45D, P198S	1775	117460	23.5
N45D, P198T	1776	122118	24.4
N45D, R195G	1777	121779	24.3
N45D, R195S	1778	128736	25.7

N45D, S131F	1779	122458	24.5
N45D, V58D	1780	152085	30.4
V129D, R195S	1781	7699	1.5
I98T, F173Y, L196S	1782	236	0.0
N45D, E134G, L213P	1783	2255	0.5
N45D, F173I, S177C	1784	2199	0.4
N45D, I148V, R195G	1785	109276	21.8
N45D, K111T, R195G	1786	65728	13.1
N45D, N113Y, R195S	1787	112042	22.4
N45D, N165Y, E170G	1788	88971	17.8
N45D, Q89R, I98V	1789	90467	18.1
N45D, S131F, P198S	1790	116162	23.2
N45D, S75P, P198S	1791	129814	25.9
N45D, V50A, R195T	1792	141881	28.3
E27D, N45D, T183A, I188V	1793	133100	26.6
K23N, N45D, S75P, N120S	1795	131995	26.4
N45D, G102D, R194W, R195G	1796	13381	2.7
N45D, G52V, Q121L, P198S	1797	296	0.1
N45D, I148V, R195G, N201D	1798	130537	26.1
N45D, K111T, T183A, I188V	1799	108670	21.7
N45D, S99G, C137R, V207A	1801	834	0.2
N45D, T163I, K167R, R195G	1802	133842	26.7
N45D, T183A, T192S, R194G	1803	1349	0.3
N45D, V50A, I119T, K144E	1804	34217	6.8
V11E, N45D, T130A, P198T	1806	137230	27.4
K23N, N45D, Q73R, T163I	1809	139149	27.8
K28E, N45D, W149R, S158G, P198T	1810	691	0.1
K28R, N45D, V129D, T163N, R195T	1812	137230	27.4
M41K, D43G, N45D, R64S, R195G	1813	137230	27.4
M41K, D43G, N45D, R64S, S99G	1814	134587	26.9
N45D, R68L, F173L, D197G, P198S	1815	59308	11.8
N45D, V50A, I148V, R195G, N201D	1816	131264	26.2
M41K, D43G, K44E, N45D, R195G, N201D	1817	144667	28.9
N45D, V50A, L124S, K144E, L179P, R195G	1818	18163	3.6
WT PD-L1 ECD-Fc N10653	1728	5005	1.0
Fc only control	1155	46	0.0

[0519] Bioactivity of the additional affinity-matured PD-L1 domain-containing molecules was further assessed using Jurkat effector cells expressing an IL-2-luciferase reporter and cell-surface PD-1substantially as described in Example 12B. As shown in Table 22C, increased luciferase activity of the Jurkat effector cells co-cultured with anti-CD3 and K562/CD80 cells

was observed for some Fc fusion molecules with the indicated PD-L1 variant. An average relative luminescence value (RLU) was determined for each test sample and a fold change in IL-2 reporter signal was calculated for each tested molecule compared to wild-type PD-L1 or the Fc only control protein. In the Table, Column 2 sets forth the SEQ ID NO identifier for each PD-L1 variant tested. The differences in luminescence signals demonstrate the differences in binding of the PD-L1variant Fc molecules to PD-1 and the resulting co-blockade of inhibitory activity.

TABLE 22C: Jurkat/IL2/PD-1 + K562/CD80 + soluble anti-CD3 Reporter Assay

PD-L1 Mutation(s)	SEQ ID NO (ECD)	Relative Luciferase Units (RLU) PD-L1 vECD-Fc Conc 50.0nM	Fold Increase over WT PD-L1 ECD-Fc
N45D	1772	460	2.3
R195S	1827	215	1.1
K160M, R195G	1773	215	1.1
N45D, K144E	1774	385	1.9
N45D, P198S	1775	457	2.3
N45D, P198T	1776	476	2.3
N45D, R195G	1777	405	2.0
N45D, R195S	1778	417	2.1
N45D, S131F	1779	429	2.1
N45D, V58D	1780	484	2.4
V129D, R195S	1781	223	1.1
I98T, F173Y, L196S	1782	209	1.0
N45D, E134G, L213P	1783	276	1.4
N45D, F173I, S177C	1784	265	1.3
N45D, I148V, R195G	1785	496	2.4
N45D, K111T, R195G	1786	338	1.7
N45D, N113Y, R195S	1787	492	2.4
N45D, N165Y, E170G	1788	446	2.2
N45D, Q89R, I98V	1789	550	2.7
N45D, S131F, P198S	1790	422	2.1
N45D, S75P, P198S	1791	549	2.7
N45D, V50A, R195T	1792	594	2.9
E27D, N45D, T183A, I188V	1793	554	2.7
K23N, N45D, S75P, N120S	1795	504	2.5
N45D, G102D, R194W, R195G	1796	211	1.0
N45D, G52V, Q121L, P198S	1797	225	1.1
N45D, I148V, R195G, N201D	1798	401	2.0
N45D, K111T, T183A, I188V	1799	354	1.7
N45D, S99G, C137R, V207A	1801	226	1.1
N45D, T163I, K167R, R195G	1802	440	2.2

N45D, T183A, T192S, R194G	1803	250	1.2
N45D, V50A, I119T, K144E	1804	292	1.4
V11E, N45D, T130A, P198T	1806	470	2.3
K23N, N45D, Q73R, T163I	1809	449	2.2
K28E, N45D, W149R, S158G, P198T	1810	197	1.0
K28R, N45D, V129D, T163N, R195T	1812	437	2.2
M41K, D43G, N45D, R64S, R195G	1813	590	2.9
M41K, D43G, N45D, R64S, S99G	1814	597	2.9
N45D, R68L, F173L, D197G, P198S	1815	327	1.6
N45D, V50A, I148V, R195G, N201D	1816	494	2.4
M41K, D43G, K44E, N45D, R195G, N201D	1817	464	2.3
N45D, V50A, L124S, K144E, L179P, R195G	1818	308	1.5
WT PD-L1 ECD-Fc	1728	203	1.0
Fc only control	1155	205	1.0

EXAMPLE 14

Generation of Secreted Immunomodulatory Protein and Assessment of Proliferation of Pan T cells transduced with PD-L1 SIP

[0520] To generate a PD-L1 secreted immunomodulatory protein (SIP), DNA encoding exemplary SIPs was obtained as gene blocks from Integrated DNA Technologies (Coralville, USA) and then cloned by Gibson assembly (New England Biolabs Gibson assembly kit) into a modified version of pRRL vector (Dull et al., (1998) J Virol, 72(11): 8463-8471) between restriction sites downstream of MND promoter to remove GFP. Exemplary SIP constructs were generated to encode a protein set forth in SEQ ID NO: 2012-2013, including the signal peptide. In this exemplary Example, the constructs were generated to additionally include a tag moiety. The gene blocks had the following structure in order: 39 base pair overlap with pRRL prior to first restriction site-first restriction site-GCCGCCACC (Kozak); complete ORF encoding PD-L1 IgV wildtype amino acid sequence set forth in SEQ ID NO: 309 or variant PD-L1 IgV set forth in SEQ ID NO: 303 (D43G/N45D/L56Q/V58A/G101G-ins (G101GG), also including in all cases the signal peptide MGSTAILALLLAVLQGVSA as set forth in SEQ ID NO: 2009; DNA encoding Flag-tag as set forth in SEQ ID NO:2010 (DYKDDDDK); DNA encoding His tag as set forth in SEQ ID NO: 2011 (HHHHHH); TAA stop codon; second restriction site- 41 base pair overlap with pRRL beyond second restriction site. For comparison, a SIP encoding wild-type PD-L1 also was assessed.

[0521] To prepare lentiviral vectors, $3x10^6$ HEK293 cells were plated per 100mm dish. On the next day, 4.5µg of P-Mix (3µg of PAX2 and 1.5µg of pMD2G) was added to 6µg of DNA encoding the SIPs constructs in a 5mL polypropylene tube. Diluent buffer (10mM HEPES/150mM NaCl pH7.05/1L TC grade H20) was added to the tube to bring up the total volume of 500µL. To the diluent DNA(PEI:total DNA 4:1), 42µL of PEI (1µg/µL) was added and mixed by vortexing. The mixture was incubated at room temperature for 10 minutes and cells were prepared by aspirating medium from the dish gently without disturbing the adherent cells, then replaced with 6mL of Opti-MEM(1X). DNA/PEI mixture was then added to the dish and incubated at 37°C for 24 hours. After 24 hours, media was aspirated from the dishes and replaced with 10mL of fresh DMEM media and then incubated at 37°C. Viral supernatant was collected after 48 hours using a syringe attached to a 0.45µm filter PES to remove cells and debris from the culture (Thermo Scientific Nalgene Syringe Filter). A separate lentiviral vector stock also was prepared encoding an anti-CD19 CAR (containing an anti-CD19 scFv, a hinge and transmembrane domain derived from CD8 and a CD3zeta signaling domain) substantially as described. The exemplary anti-CD19 CAR used is set forth in SEQ ID NO: 2016 (encoded by the sequence in set forth in SEQ ID NO: 2017) containing the scFv set forth in SEQ ID NO:1163, the CD8-derived hinge and transmembrane domain set forth in SEQ ID NO: 242, and the CD3zeta set forth in SEQ ID NO:243

[0522] T-cells were thawed and activated with anti-CD3/anti-CD28 beads (Dynal) at a 1:1 ratio. The T-cells (1×10^6 cells) were mixed with 1 mL total lentiviral vector supernatant containing equal volume (0.5 mL each) of the lentiviral vector supernatant encoding the indicated PD-L1 SIP (D43G/N45D/L56Q/V58A/G101GG or wildtype) and a lentiviral vector supernatant encoding the anti-CD19 CAR. As a control, cells were transduced only with the lentiviral vector encoding the anti-CD19 CAR or were transduced with mock vector control. Transduction was performed in the presence of 10 µg/mL polybrene and 50 IU/mL IL-2. Cells were spun down at 2500 rpm for 60 min at 30°C. After 24 hours, 3mL of Xvivo15 plus media and IL2 was added to each well. The cells were fed every two days with fresh media and cytokines.

[0523] At 14 days after activation, cells were re-stimulated with Nalm6 cells that had been transduced with a lenti-viral vector to provide expression of PD-L1 (Nalm6 PDL1+). Transduced T cells were labeled with Cell Trace Far Red and proliferation was measured at day 3 by determining the fraction of the cells that showed dilution of the dye. Results for the

proliferation studies for T cells transduced with exemplary tested variant PD-L1 SIP are shown in FIG. 10.

EXAMPLE 15

Assessment of PD-L1 Multi-Domain Stack Molecules on Activity of Primary Exhausted T cells

[0524] This Example describes studies to assess specificity and affinity of exemplary PD-L1/CD155 and PD-L1/CD112/CD155 variant IgV stack immunomodulatory proteins (stacked IgV-Fc), generated as described in Example 10, for modulating the activity of exhausted T cells via blocking interactions involving cognate binding partners PD-1, TIGIT and/or CD112R.

A. Generation of Exhausted T cells

[0525] To generate exhausted T cells, primary human T cells were stimulated for 7 days with mitomycin C-treated K562 cells that stably expressed anti-CD3 single-chain Fc (OKT3) at a ratio of 10 T cells to 1 K562/OKT3 cell. On day 3, 50 IU/mL of recombinant IL-2 was added to the culture media to promote T cell expansion and survival. On day 7, T cells were harvested, counted and then set up for two additional cycles of restimulation with K562/OKT3 plus IL-2. At the end of 21 days (3 rounds of stimulation), T cells were counted, characterized for expression of inhibitory receptors PD-L1, TIGIT and Lag-3 and then frozen for subsequent assays. Exhausted T cells were detected based on elevated expression of the inhibitory receptors PD-1, TIGIT and Lag-3.

B. Binding to Exhausted T cells

[0526] Exhausted T cells were generated as described above by three rounds of stimulation and expansion with K562/OKT3 + IL-2. Binding studies were performed essentially as described in Example 12 except with exhausted T cells. Exemplary stack molecules tested included PD-L1/CD155 Stack 4 (SEQ ID NO: 1719) and PD-L1/CD112/CD155 Stack 2 (SEQ ID NO: 1724) generated as described above in Example 10. As a control, binding activity of non-stack formats of each variant IgV fused to an Fc (set forth in SEQ ID NO: 1157, containing the mutations C220S, R292C, N297G and V302C by EU numbering (corresponding to C5S, R77C, N82G and V87C with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 187), were assessed, i.e., variant PD-L1 IgV-Fc (containing variant PD-L1 IgV set forth in SEQ

ID NO:303), CD155 IgV-Fc (containing variant CD155 IgV set forth in SEQ ID NO:1576), or CD112 IgV-Fc (containing variant CD112 IgV set forth in SEQ ID NO: 768).

[0527] Results for the binding studies for exemplary tested PD-L1/CD155 and PD-L1/CD112/CD155 stack Fc fusion molecules tested at various concentrations are shown in FIG. 11. As shown, the exemplary tested PD-L1/CD155 stack Fc fusion molecule demonstrated superior binding to exhausted T cells than either domain alone.

C. Stimulation and Assessment of Bioactivity

[0528] Previously derived exhausted T cells, generated as described above, were thawed and plated at 100,000 cells per well in a flat-bottom 96-well plate in assay buffer (X-vivo 15 media (Lonza, Corp., USA) supplemented with Glutamax (ThermoFisher, Inc. USA)). An exemplary stack Fc fusion molecule PD-L1/CD155 Stack 4 (SEQ ID NO: 1719), or control non-stack variant PD-L1 IgV-Fc or CD155 IgV-Fc were added to the T cells at final concentrations of 100nM, 10nM and 1nM. The control non-stack variant PD-L1 IgV-Fc or CD155 IgV-Fc fusion molecules contained the same variant PD-L1 IgV (SEQ ID NO:303) or variant CD155 IgV (SEQ ID NO:1576), used in the stacks. An anti-TIGIT antibody (eBioscience, Inc., USA) and anti-PD-1 antibody (Bristol-Myers Squibb, Inc., USA) or human IgG1 antibody (BioLegend, Inc., USA) were also used as controls and added to the T cells at the indicated concentrations.

[0529] K562 cells previously transduced to express anti-CD3 single-chain Fv (OKT3) and human PD-L1 were treated for 20 minutes with 50 μg/mL mitomycin C (Millipore Sigma, Corp., USA) to arrest proliferation, washed and then added to the assay plate at 10,000 cells per well. As a further control, T cells were incubated with K562-OKT3-PD-L1 cells in the absence of added molecule or T cells were incubated without stimulation with K562-OKT3-PD-L1 cells. The assay plate was then incubated for three days at 37°C in a humidified, 5% CO_2 incubator. After three days, IL-2, IFNγ and T cell proliferation were measured using standard ELISA and flow cytometry techniques.

[0530] Results for the bioactivity studies are shown in FIG. 12, which sets forth the levels of IFN-gamma in culture supernatants (pg/mL) at the indicated concentrations of the tested molecules. As shown, the exemplary tested PD-L1/CD155 stack Fc fusion molecule exhibited improved activities to increase IFNg production compared to non-stack controls, demonstrating blockade of both PD-1 and TIGIT pathways resulting in increased signal compared to only individual pathway blockade.

[0531] The present invention is not intended to be limited in scope to the particular disclosed embodiments, which are provided, for example, to illustrate various aspects of the invention. Various modifications to the compositions and methods described will become apparent from the description and teachings herein. Such variations may be practiced without departing from the true scope and spirit of the disclosure and are intended to fall within the scope of the present disclosure.

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WHAT IS CLAIMED:

1 A variant PD-L1 polypeptide, comprising an IgV domain or both an IgV domain and an IgC domain,

wherein the variant PD-L1 polypeptide comprises an amino acid substitution N45D in an unmodified human PD-L1 with reference to the numbering of SEQ ID NO:30;

wherein the variant PD-L1 polypeptide comprises a sequence of amino acids that exhibits at least 90% sequence identity to SEQ ID NO:30;

wherein the variant PD-L1 polypeptide specifically binds to the ectodomain of PD-1 with increased affinity compared to the binding of the unmodified human PD-L1 to the ectodomain of PD-1;

wherein the unmodified PD-L1 comprises the sequence of amino acids set forth in SEQ ID NO:30 or a portion thereof comprising the IgV domain or the IgV domain and the IgC domain.

2 The variant PD-L1 polypeptide of claim 1, wherein the variant PD-L1 comprises one or more amino acid substitutions selected from I20L/N45D, I36T/N45D, D43G/N45D, N45D/V58A, N45D/S75P, N45D/N78I, I20L/I36T/N45D, D43G/N45D/V58A, I20L/E27G/D43G/N45D/V58A/N78I, I20L/D43G/N45D/V58A/N78I, I20L/A33D/D43G/N45D/V58A/N78I, I20L/D43G/N45D/N78I, V11A/I20L/E27G/D43G/N45D/H5lY/S99G, I20L/K28E/D43G/N45D/V58A/Q89R, I20L/I36T/N45D, A33D/D43G/N45DN58A/S75P, K23R/D43G/N45D, D43G/N45D/L56Q/V58A/G101G-ins (G101GG), I20L/K23E/D43G/N45D/V58A/N78I, I20L/K23E/D43G/N45D/V50A/N78I, I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG), N45D, N45D/Kl44E, N45D/P198S, N45D/P198T, N45D/R195G, N45D/R195S, N45D/S131F, N45D/V58D, N45D/I148V/R195G, N45D/K111T/R195G, N45D/N113Y/R195S, N45D/N165Y/E170G, N45D/Q89R/198V, N45D/S131F/P198S, N45D/S75P/P198S, N45D/V50A/R195T, E27D/N45D/T183A/I188V, K23N/N45D/S75P/N120S, N45D/I148V/R195G/N201D, N45D/K111T/T183A/I188V, N45D/Q89R/F189S/P198S, N45D/T1631/K167R/R195G, N45D/V50A/1119T/K144E, T19A/N45D/K144E/R195G, V11E/N45D/T130A/P198T, V26A/N45D/T163I/T185A, K23N/N45D/Ll24S/K167T/R195G, K23N/N45D/Q73R/T163I, K28R/N45D/K57E/I98V/R195S, K28R/N45D/V129D/T163N/R195T, M41K/D43G/N45D/R64S/R195G, M41K/D43G/N45D/R64S/S99G,

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N45D/R68L/F173L/D197G/P198S, N45D/V50A/I148V/R195G/N201D, M41K/D43G/K44E/N45D/R195G/N201D, and N45D/V50A/L124S/K144E/L179P/R195G.

3 The variant PD-L1 polypeptide of claim 2, wherein the variant PD-L1 polypeptide comprises the amino acid modifications I20L/D43G/N45D/N78I.

4 The variant PD-L1 polypeptide of claim 2, wherein the variant PD-L1 polypeptide comprises the amino acid modifications D43G/N45D/L56Q/V58A/G101G-ins (G101GG).

5 The variant PD-L1 polypeptide of claim 2, wherein the variant PD-L1 polypeptide comprises the amino acid modifications I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG).

6 The variant PD-L1 polypeptide of any one of claims 1-5, wherein:
the variant PD-L1 polypeptide comprises the PD-L1 extracellular domain (ECD);
the variant PD-L1 polypeptide comprises the IgV domain and the IgC domain; or
the variant PD-L1 polypeptide comprises the IgV domain.

7 The variant PD-L1 polypeptide of claim 6, wherein the IgV domain is the only PD-L1 portion of the variant PD-L1 polypeptide.

8 The variant PD-L1 polypeptide of any one of claims 1-7, wherein the variant PD-L1 polypeptide comprises the sequence of amino acids set forth in any one of SEQ ID NOS: 66, 82, 101-104, 107, 109-110, 112-113, 115-117, 131, 147, 166-169, 172, 174-175, 177-178, 180-182, 254, 270, 289-292, 295, 297-298, 300-301, 303-305, 1725-1727, 1774-1780, 1785-1793, 1795, 1798-1800, 1802, 1804-1809, 1811-1818, 1863-1869, 1874-1882, 1884, 1887-1889, 1891, 1893-1898, 1900-1907, 1920-1922, 1935-1937, 1953, 1969, 1988-1991, 1994, 1996-1997, 1999-2000, 2002-2004, and 2008, or a sequence of amino acids that exhibits at least 95% sequence identity to any one of SEQ ID NOS: 66, 82, 101-104, 107, 109-110, 112-113, 115-117, 131, 147, 166-169, 172, 174-175, 177-178, 180-182, 254, 270, 289-292, 295, 297-298, 300-301, 303-305, 1725-1727, 1774-1780, 1785-1793, 1795, 1798-1800, 1802, 1804-1809, 1811-1818, 1863-1869, 1874-1882, 1884, 1887-1889, 1891, 1893-1898, 1900-1907, 1920-1922, 1935-1937, 1953, 1969, 1988-1991, 1994, 1996-1997, 1999-2000, 2002-2004, and 2008.

9 The variant PD-L1 polypeptide of claim 8, wherein the variant PD-L1 polypeptide comprises the amino acid sequence of SEQ ID NO: 292.

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10 The variant PD-L1 polypeptide of claim 8, wherein the variant PD-L1 polypeptide comprises the amino acid sequence of SEQ ID NO: 303.

11 The variant PD-L1 polypeptide of claim 8, wherein the variant PD-L1 polypeptide comprises the amino acid sequence of SEQ ID NO: 1727.

12 The variant PD-L1 polypeptide of any one of claims 1-11, wherein the variant PD-L1 polypeptide is a soluble protein.

13 The variant PD-L1 polypeptide of claim 12, wherein the variant PD-L1 polypeptide is linked to a multimerization domain.

14 An immunomodulatory protein, comprising the variant PD-L1 polypeptide of any one of claims 1-13 linked, directly or indirectly via a linker, to a second polypeptide comprising an immunoglobulin superfamily (IgSF) domain of an IgSF family member.

15 The immunomodulatory protein of claim 14, wherein the IgSF domain is an affinity modified IgSF domain, said affinity modified IgSF domain comprising one or more amino acid modifications compared to the unmodified or wild type IgSF domain of the IgSF family member and exhibits altered binding to one or more of its cognate binding partner(s) compared to the unmodified or wild- type IgSF domain.

16 The immunomodulatory protein of claim 15, wherein the IgSF domain is a CTLA-4 extracellular domain (ECD).

17 The immunomodulatory protein of claim 16, wherein the CTLA-4 ECD comprises one or more amino acid modifications with reference to SEQ ID NO: 36.

18 The immunomodulatory protein of any one of claims 14-17, wherein the immunomodulatory protein further comprises a multimerization domain linked to at least one of the variant PD-L1 polypeptide, or the second polypeptide.

19 The immunomodulatory protein of claim 18, wherein the multimerization domain is an Fc domain.

20 An immunomodulatory protein comprising the variant PD-L1 polypeptide of any one of claims 1-13 linked to an Fc domain or a variant thereof with reduced effector function.

21 A conjugate that is a fusion protein, comprising a variant PD-L1 polypeptide of any

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one of claims 1-13, or an immunomodulatory protein of any one of claims 14-20 linked to a targeting moiety that specifically binds to a molecule on the surface of a cell.

22 The conjugate of claim 21, wherein
the cell is an immune cell, and/or
the moiety is an antibody or antigen-binding fragment.

23 A nucleic acid molecule, encoding a variant PD-L1 polypeptide of any one of claims 1-13, an immunomodulatory protein of any one of claims 14-20, or the conjugate of claim 21 or 22.

24 A vector, comprising the nucleic acid molecule of claim 23.

25 The vector of claim 24, wherein the vector is an expression vector.

26 A cell comprising or engineered by the vector of claim 24 or 25, wherein the cell is isolated.

27 A method of producing a variant PD-L1 polypeptide or an immunomodulatory protein, comprising introducing the nucleic acid molecule of claim 23 or the vector of claim 24 or 25 into a host cell under conditions to express the protein in the cell, wherein the method is *ex vivo*.

28 A pharmaceutical composition, comprising the variant PD-L1 polypeptide of any one of claims 1-13, the immunomodulatory protein of any one of claims 14-20, the conjugate of claim 21 or 22, the nucleic acid of claim 23, the vector of claim 24 or 25, or the cell of claim 26.

29 The pharmaceutical composition of claim 28, wherein the pharmaceutical composition comprises a pharmaceutically acceptable excipient.

30 An article of manufacture comprising the pharmaceutical composition of claim 28 or 29 in a vial.

31 A kit comprising the pharmaceutical composition of claim 28 or 29 or the article of manufacture of claim 30, and instructions for use.

32 Use of a pharmaceutical composition in the manufacture of a medicament for modulating an immune response in a subject, wherein the pharmaceutical composition comprises the variant PD-L1 polypeptide of any one of claims 1-13, the immunomodulatory

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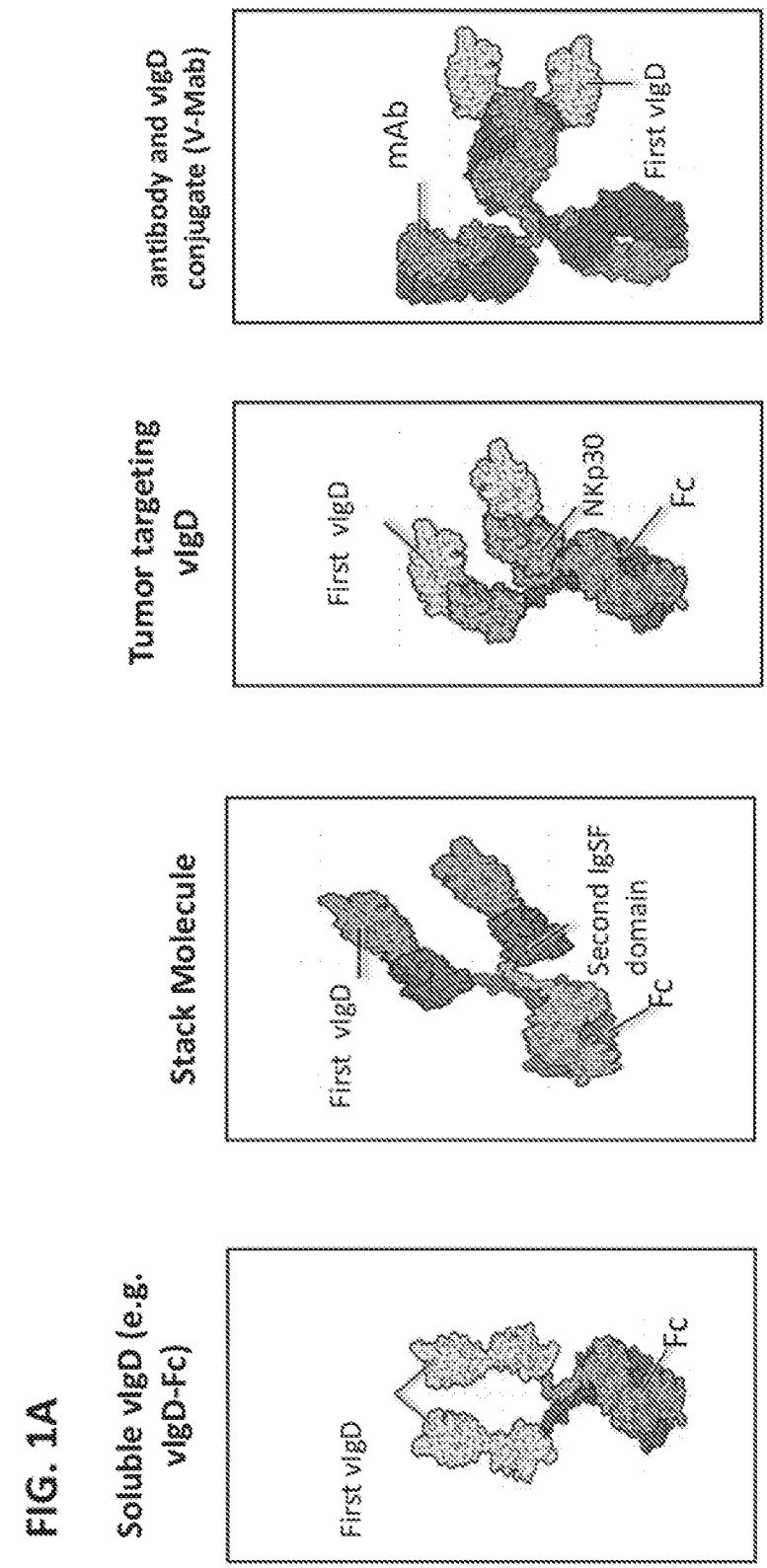
protein of any one of claims 14-20, the conjugate of claim 21 or 22, the nucleic acid of claim 23, the vector of claim 24 or 25, or the cell of claim 26.

33 The use of claim 32, wherein the pharmaceutical composition comprises a pharmaceutically acceptable excipient.

34 The use of claim 32 or 33, wherein modulating the immune response treats a disease or condition in the subject.

35 A method of modulating an immune response in a subject, comprising administering to the subject the variant PD-L1 polypeptide of any one of claims 1-13, the immunomodulatory protein of any one of claims 14-20, the conjugate of claim 21 or 22, the nucleic acid of claim 23, the vector of claim 24 or 25, or the cell of claim 26.

FIG. 1A


Soluble vIgD (e.g. vIgD-Fc)
First vIgD
Fc
Stack Molecule
First vIgD
Second IgSF domain
Fc
Tumor targeting vIgD
First vIgD
NKp30
Fc
antibody and vIgD conjugate (V-Mab)
mAb
First vIgD

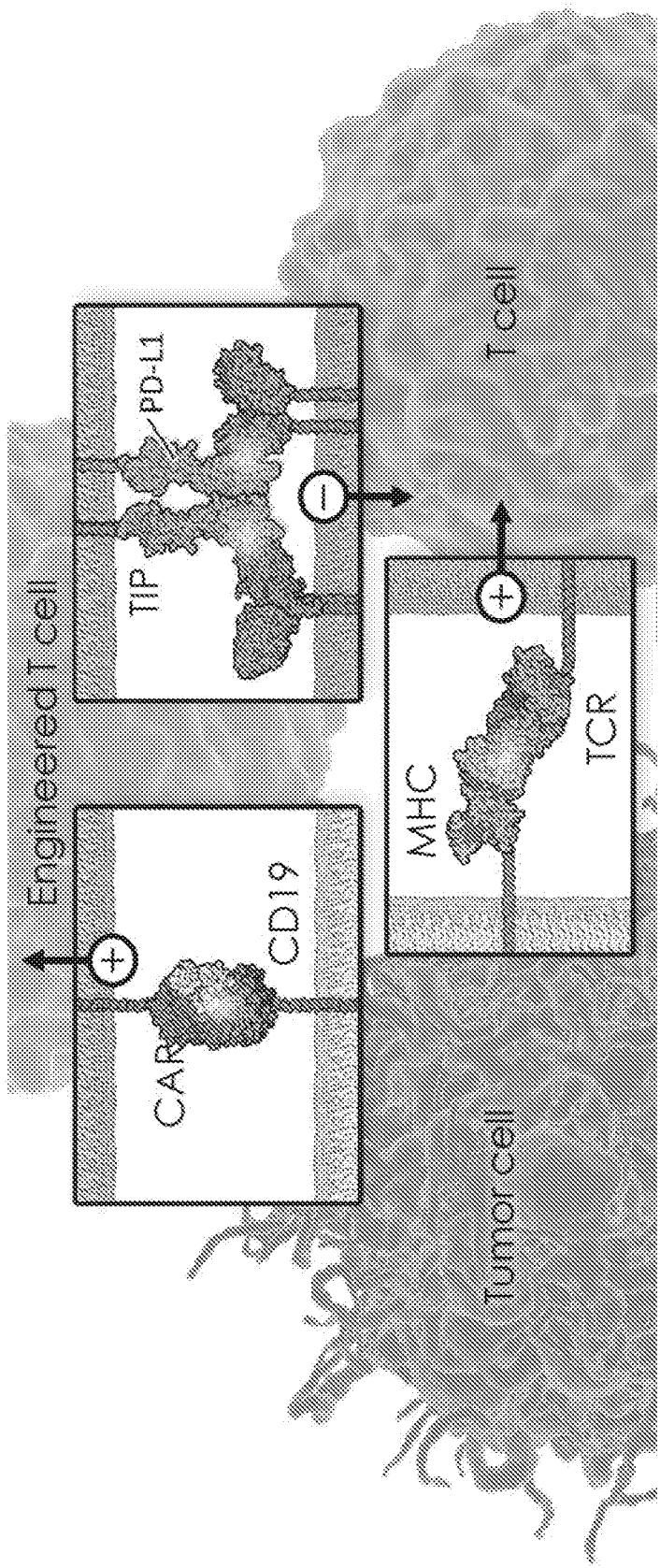


FIG. 1B

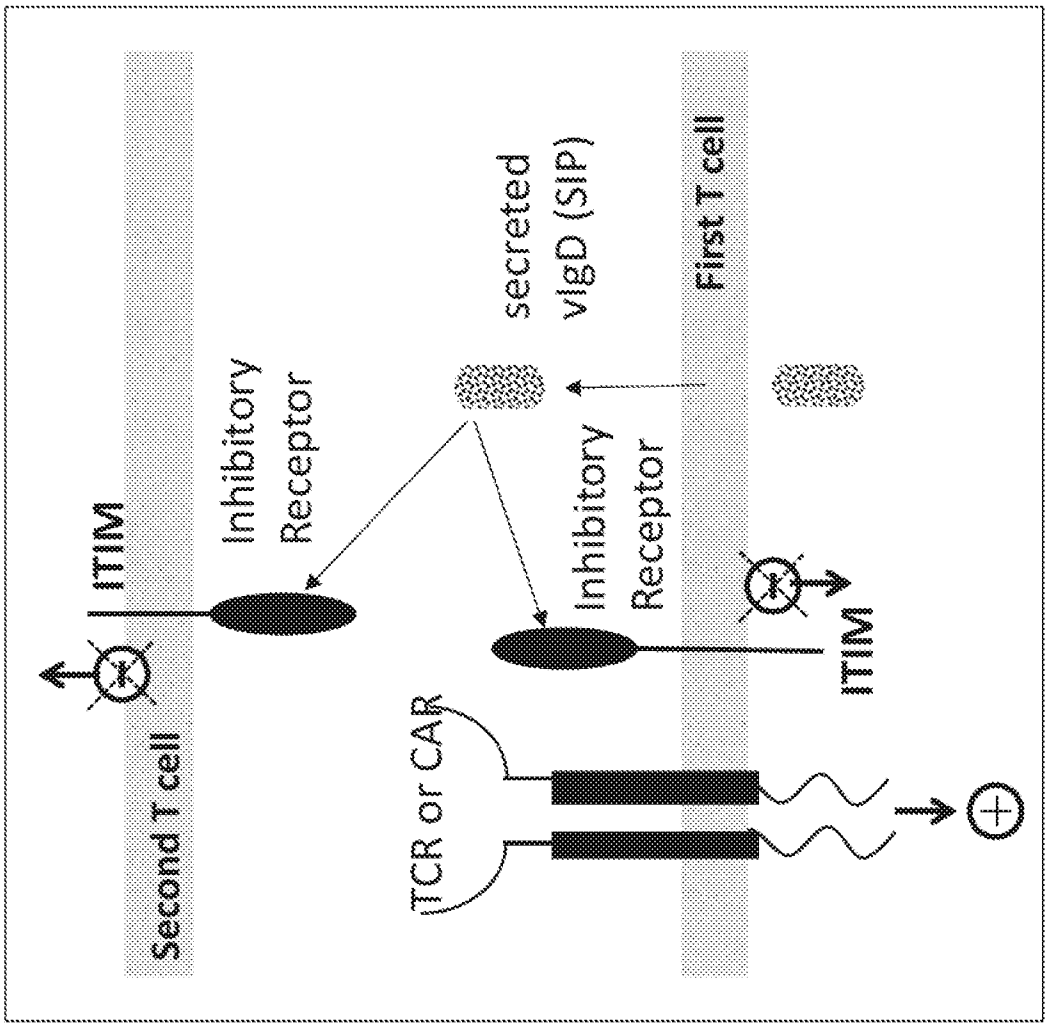

Second T cell
ITIM
Inhibitory Receptor
secreted vIgD (SIP)
First T cell
Inhibitory Receptor
ITIM
TCR or CAR

FIG. 1C

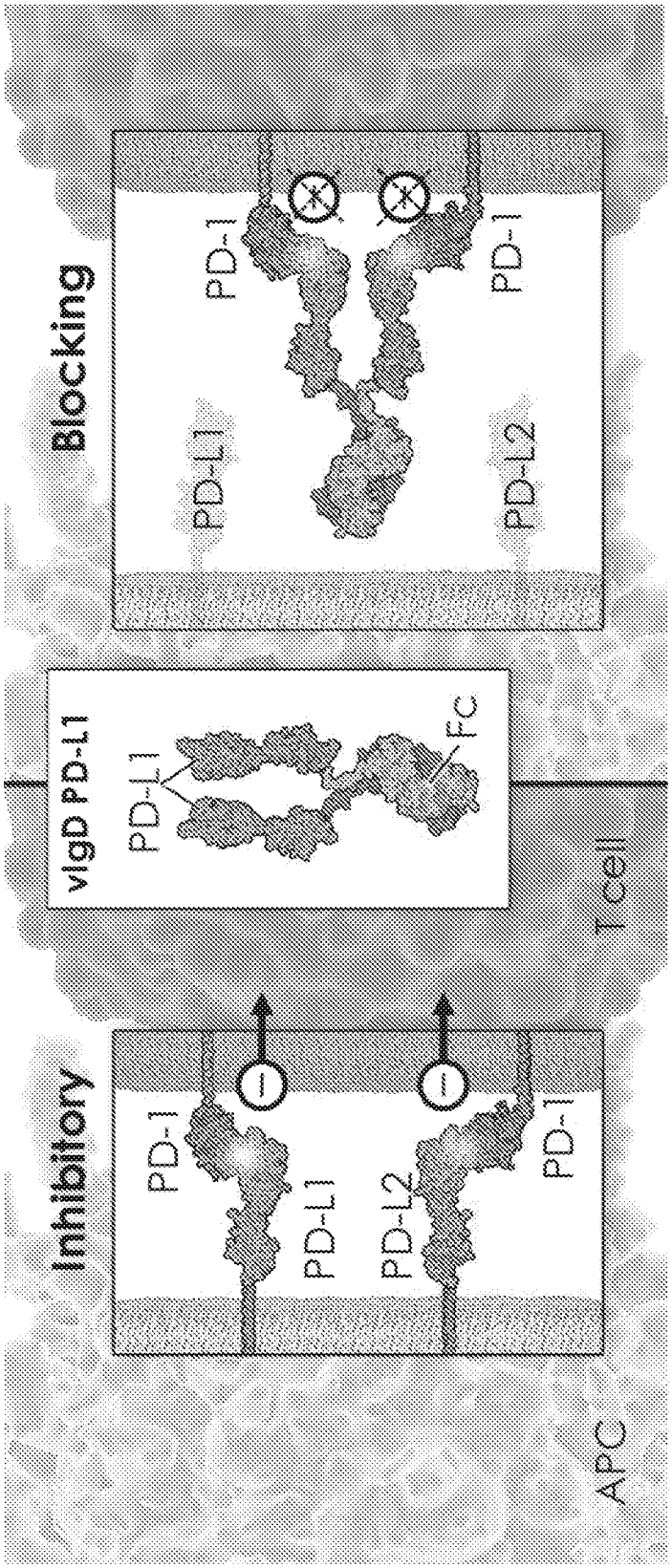
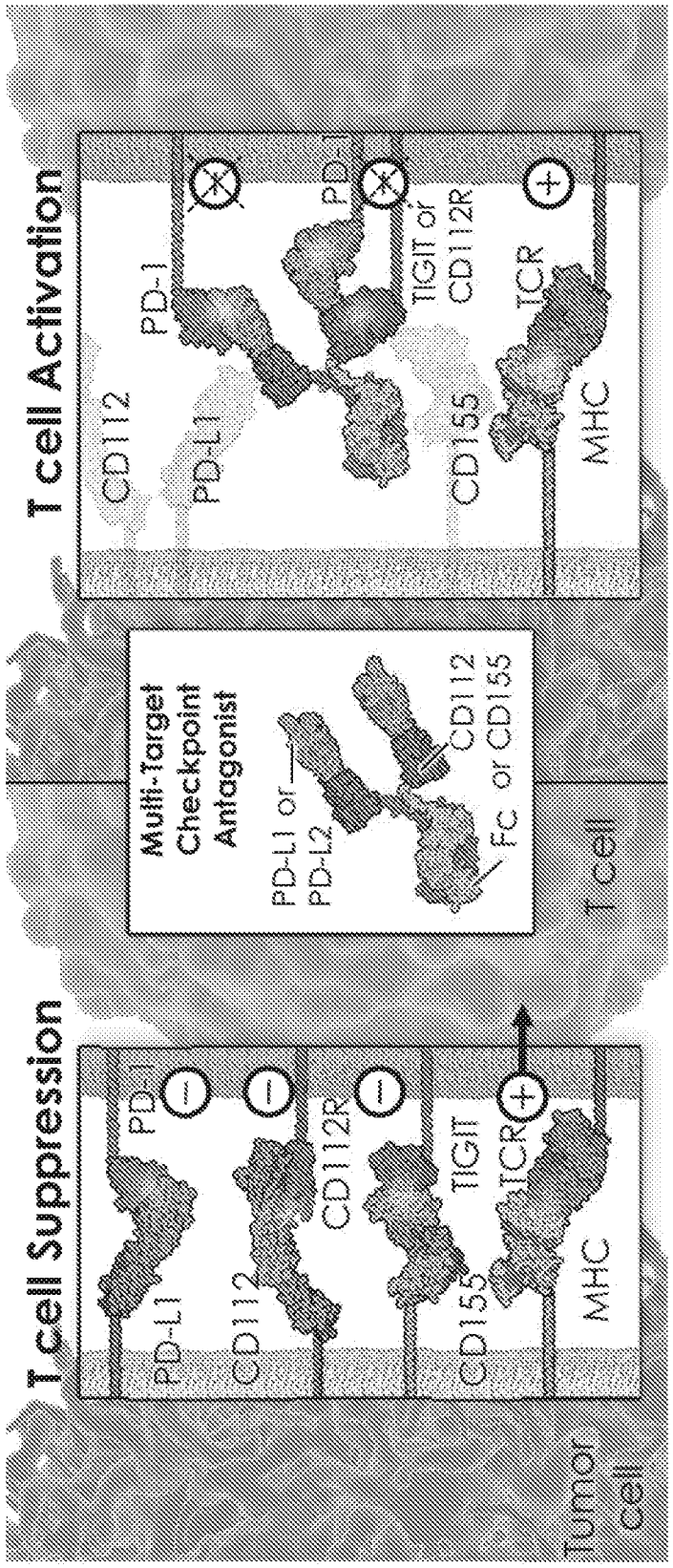

Blocking
PD-1
PD-1
PD-L1
PD-L2
VIgD PD-L1
PD-L1
Fc
T Cell
Inhibitory
PD-1
PD-L1
PD-L2
PD-1
APC

FIG. 2

FIG. 3


T cell Suppression
PD-1
PD-L1
CD112
CD112R
TIGIT
CD155
TCR
MHC
Tumor cell
Multi-Target Checkpoint Antagonist
PD-L1 or PD-L2
CD112 Fc or CD155
T cell
T cell Activation
CD112
PD-1
PD-L1
PD-1
TIGIT or CD112R
CD155
TCR
MHC

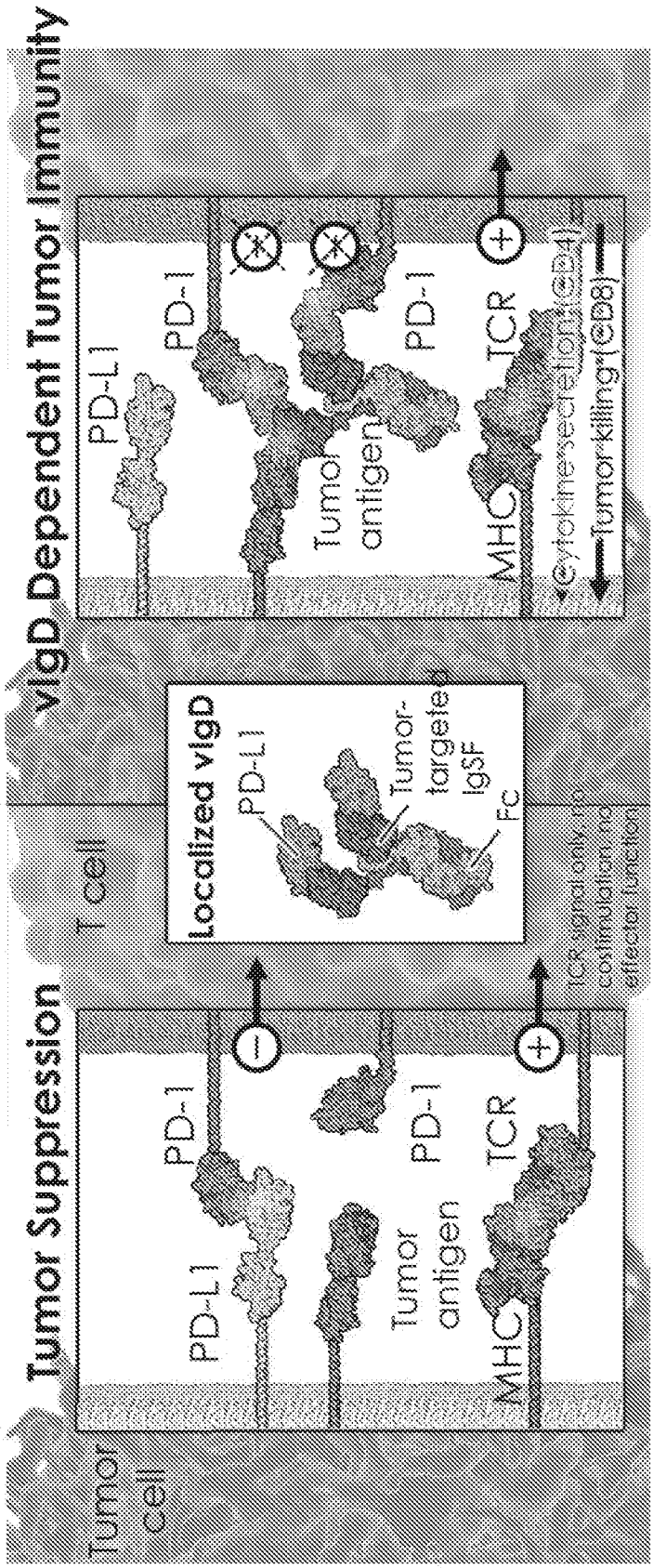
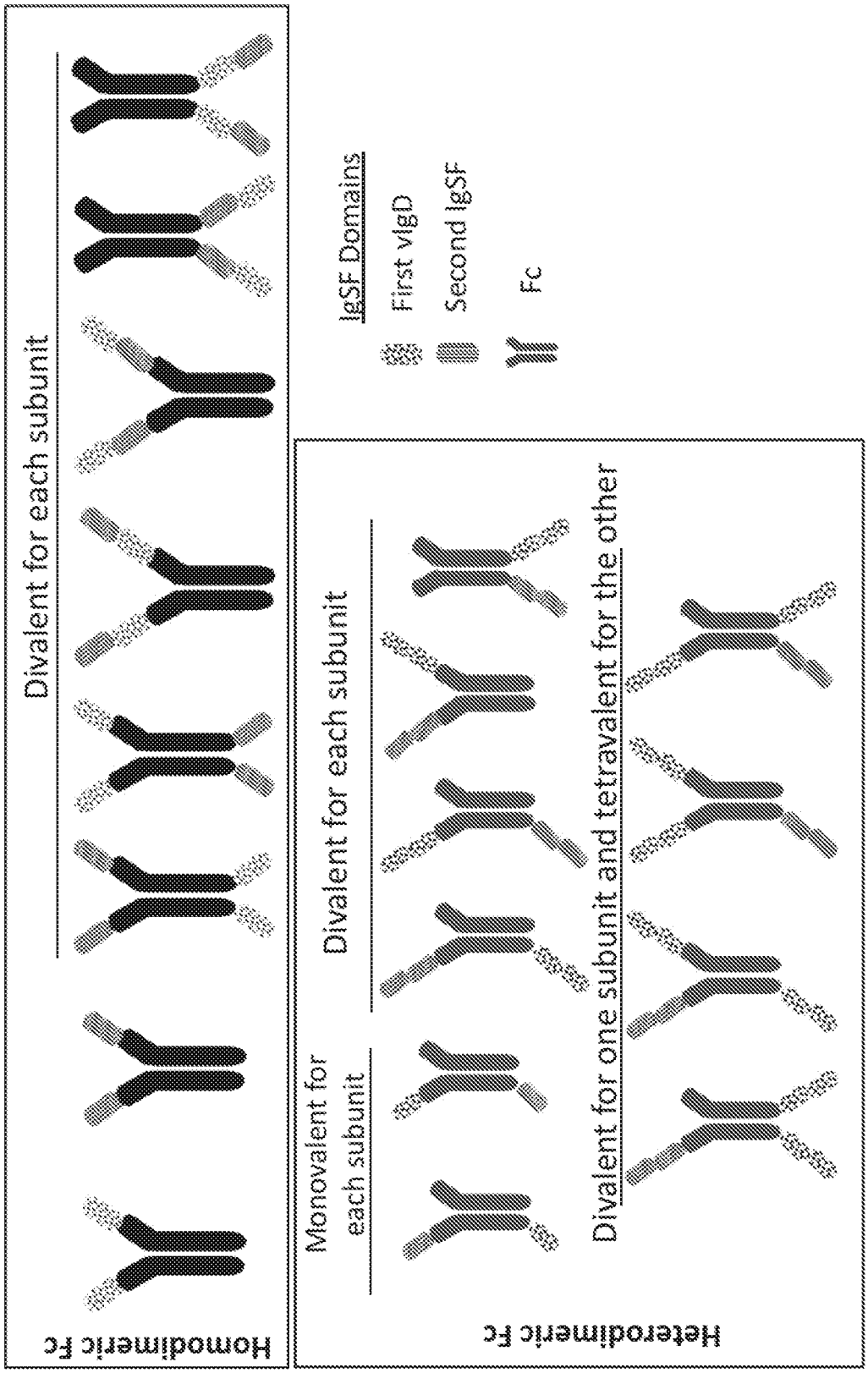

Tumor Suppression
vIgD Dependent Tumor Immunity
Tumor cell
T cell
PD-L1
PD-1
Tumor antigen
MHC
TCR
Localized vIgD
Tumor-targeted IgSF
Fc
TCR signal only, no costimulation and effector function
Cytokine secretion (CD4)
Tumor killing (CD8)

FIG. 4

FIG. 5A


Homodimeric Fc
Divalent for each subunit
Heterodimeric Fc
Monovalent for each subunit
Divalent for each subunit
Divalent for one subunit and tetravalent for the other
IgSF Domains
First vIgD
Second IgSF
Fc

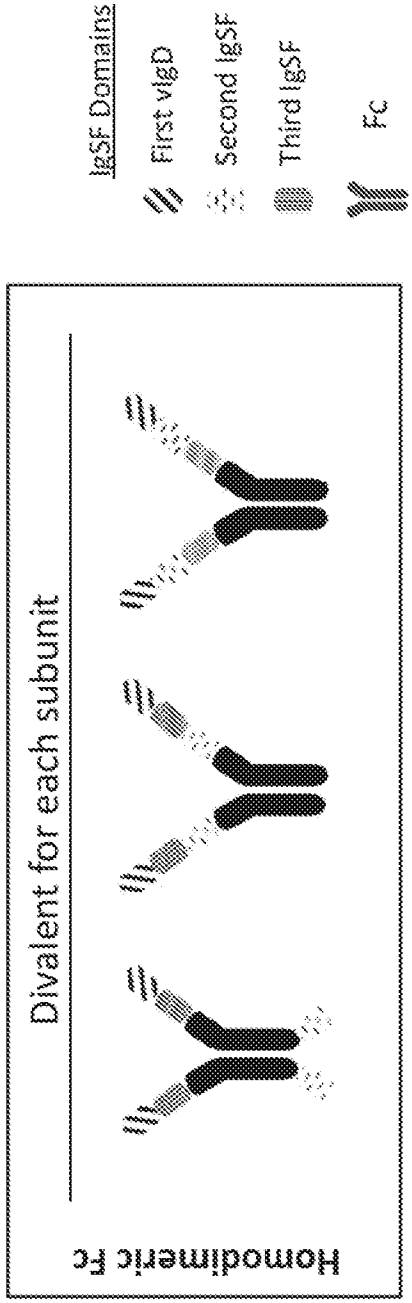
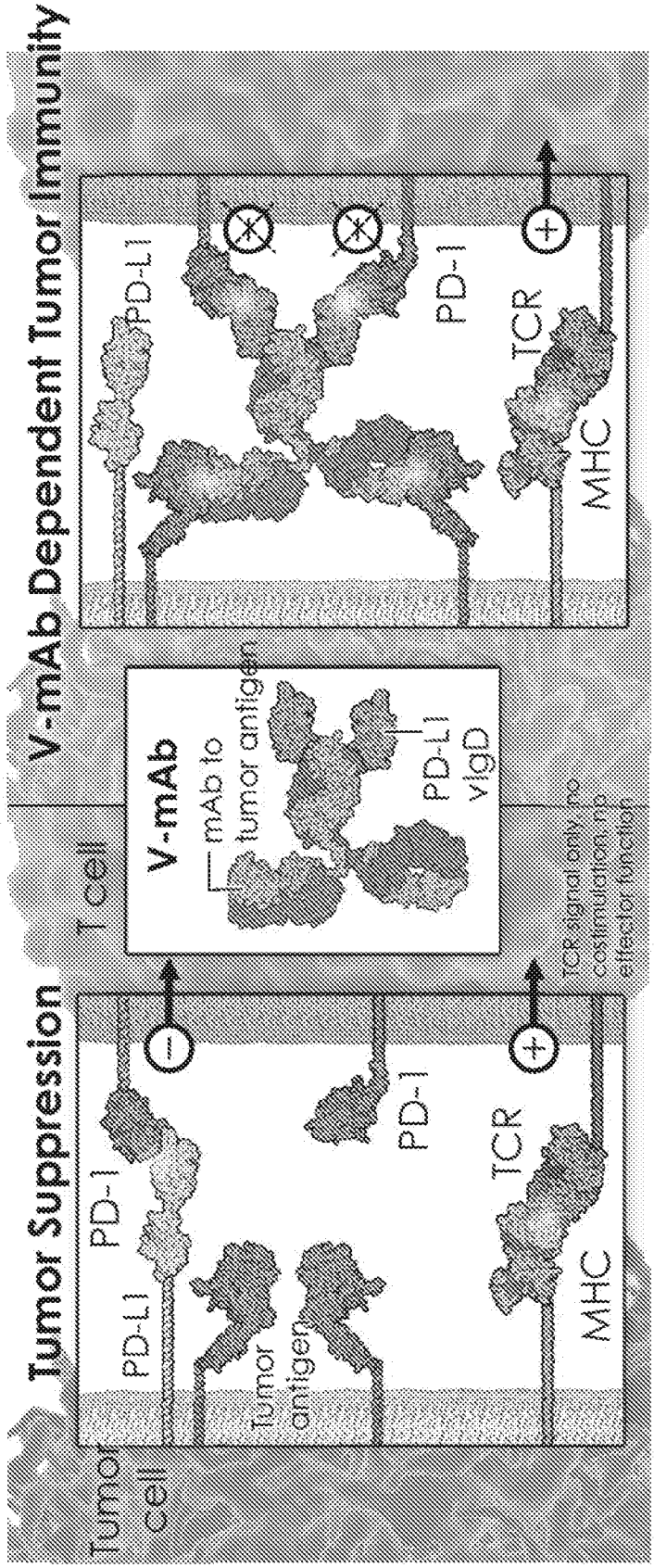

IgSF Domains
First vIgD
Second IgSF
Third IgSF
Fc
Homodimeric Fc
Divalent for each subunit

FIG. 5B

FIG. 6


Tumor Suppression
V-mAb Dependent Tumor Immunity
Tumor cell
T Cell
PD-L1
PD-1
Tumor antigen
MHC
TCR
V-mAb
mAb to tumor antigen
PD-L1 vIgD
TCR signal only, no costimulation, no effector function

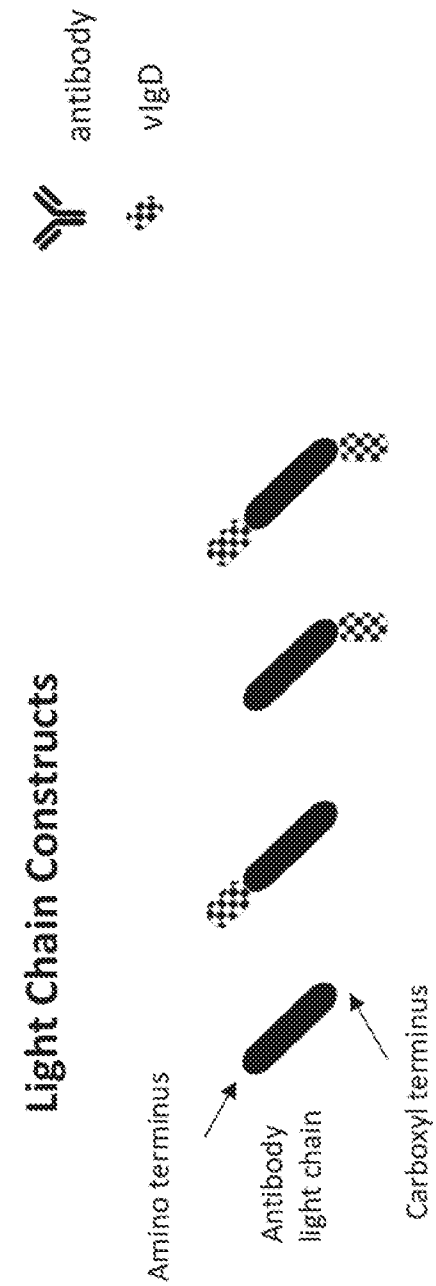

Light Chain Constructs
antibody
vIgD
Amino terminus
Antibody
light chain
Carboxyl terminus

FIG. 7A

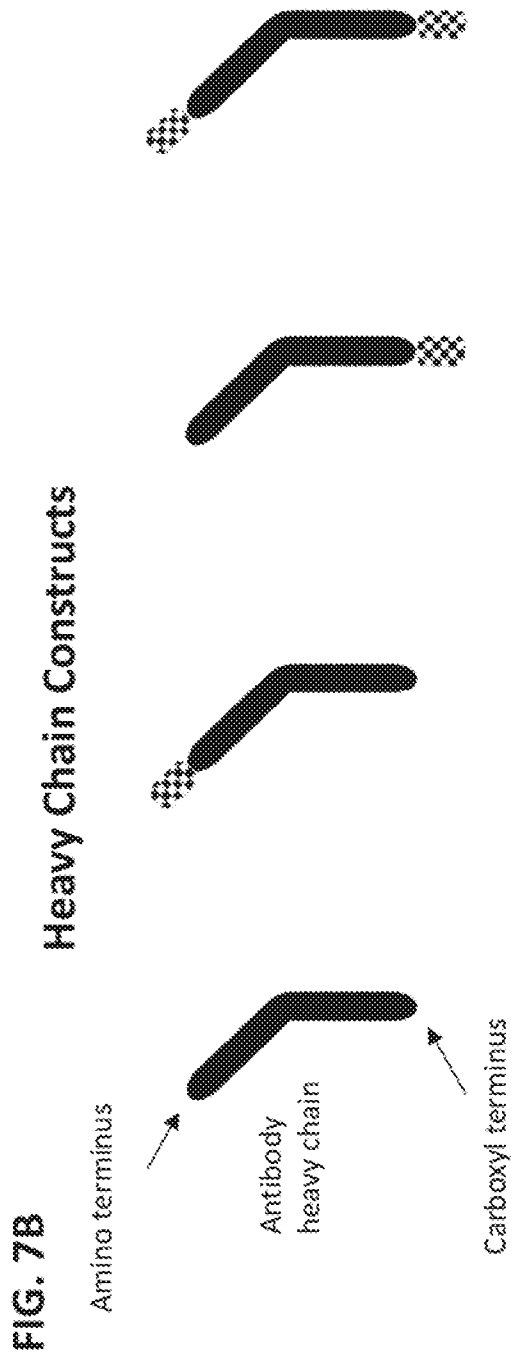

Heavy Chain Constructs
Amino terminus
Antibody
heavy chain
Carboxyl terminus

FIG. 7B

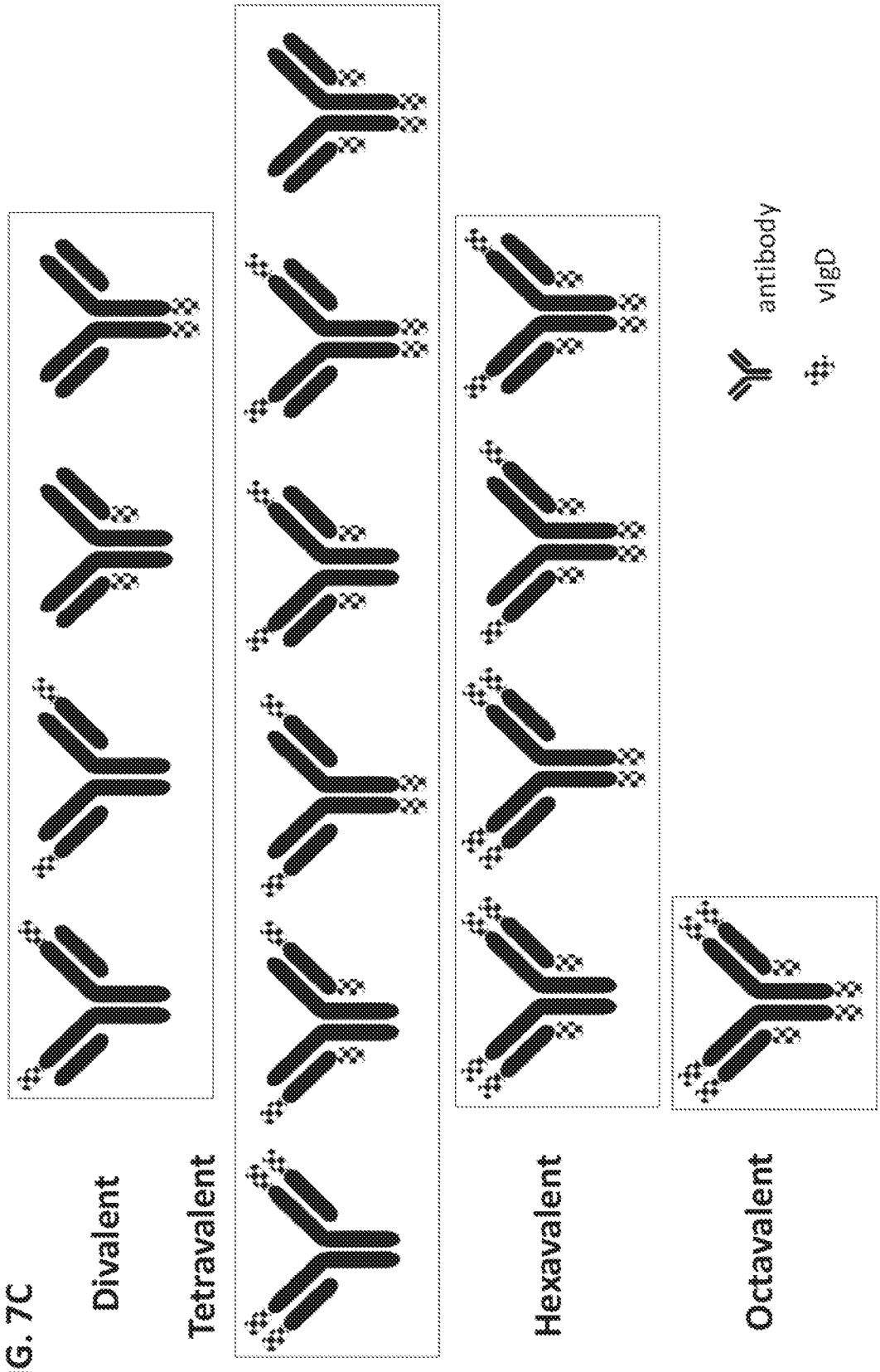

Divalent
Tetravalent
Hexavalent
Octavalent
antibody
vIgD

FIG. 7C

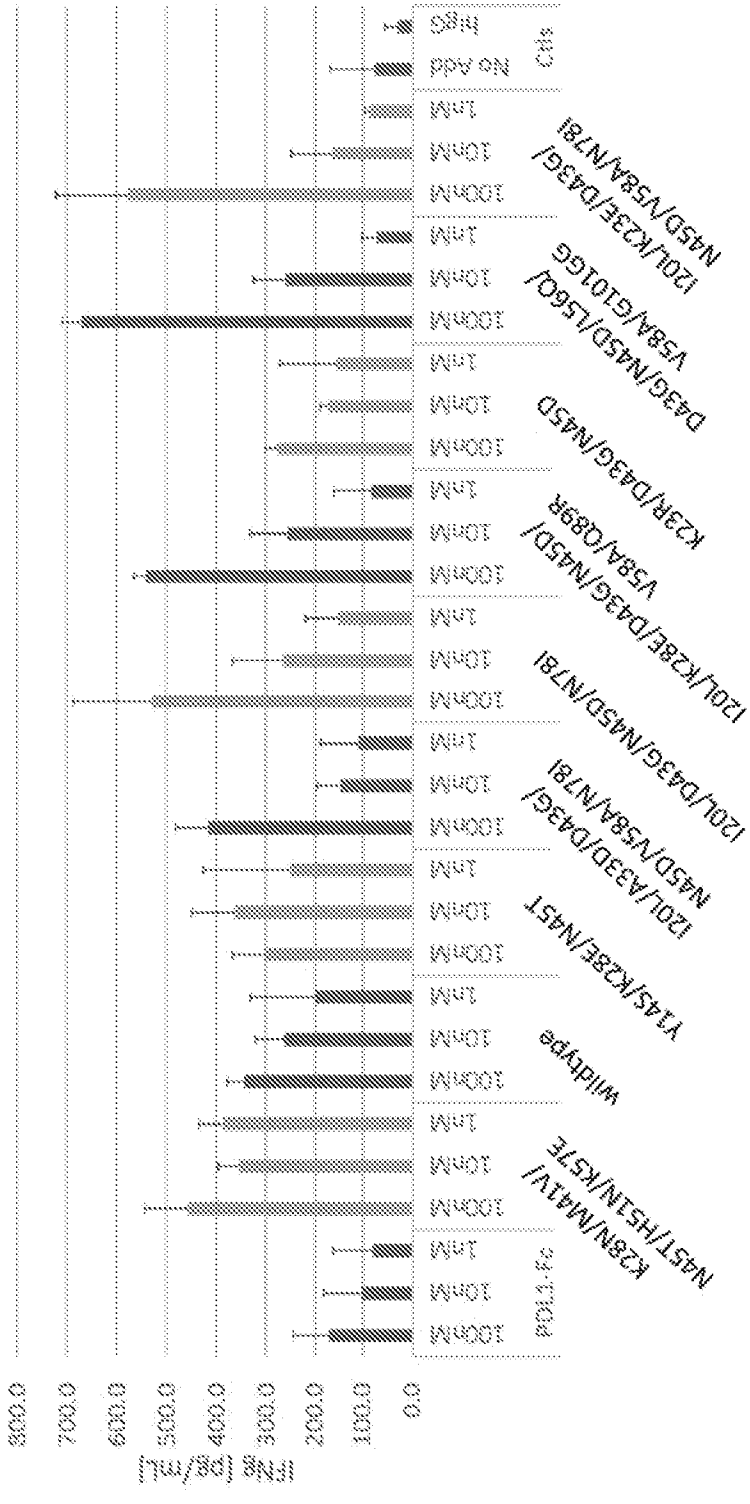

IFNg [pg/mL]
0.0
100.0
200.0
300.0
400.0
500.0
600.0
700.0
800.0
poly I:C
100nM
10nM
1nM
K28N/M41V/N45T/H51N/K57E
100nM
10nM
1nM
wildtype
100nM
10nM
1nM
Y34S/K28E/N45T
100nM
10nM
1nM
I20L/A33D/D43G/N45T
100nM
10nM
1nM
N45D/V58A/N78I
100nM
10nM
1nM
I20L/D43G/N45D/N78I
100nM
10nM
1nM
I20L/K28E/D43G/N45D/V58A/Q89R
100nM
10nM
1nM
K28R/D43G/N45D
100nM
10nM
1nM
D43G/N45D/L56Q/V58A/G101GG
100nM
10nM
1nM
I20L/K23E/D43G/N45D/V58A/N78I
100nM
10nM
1nM
Ctrl
No Add
hIgG

FIG. 8

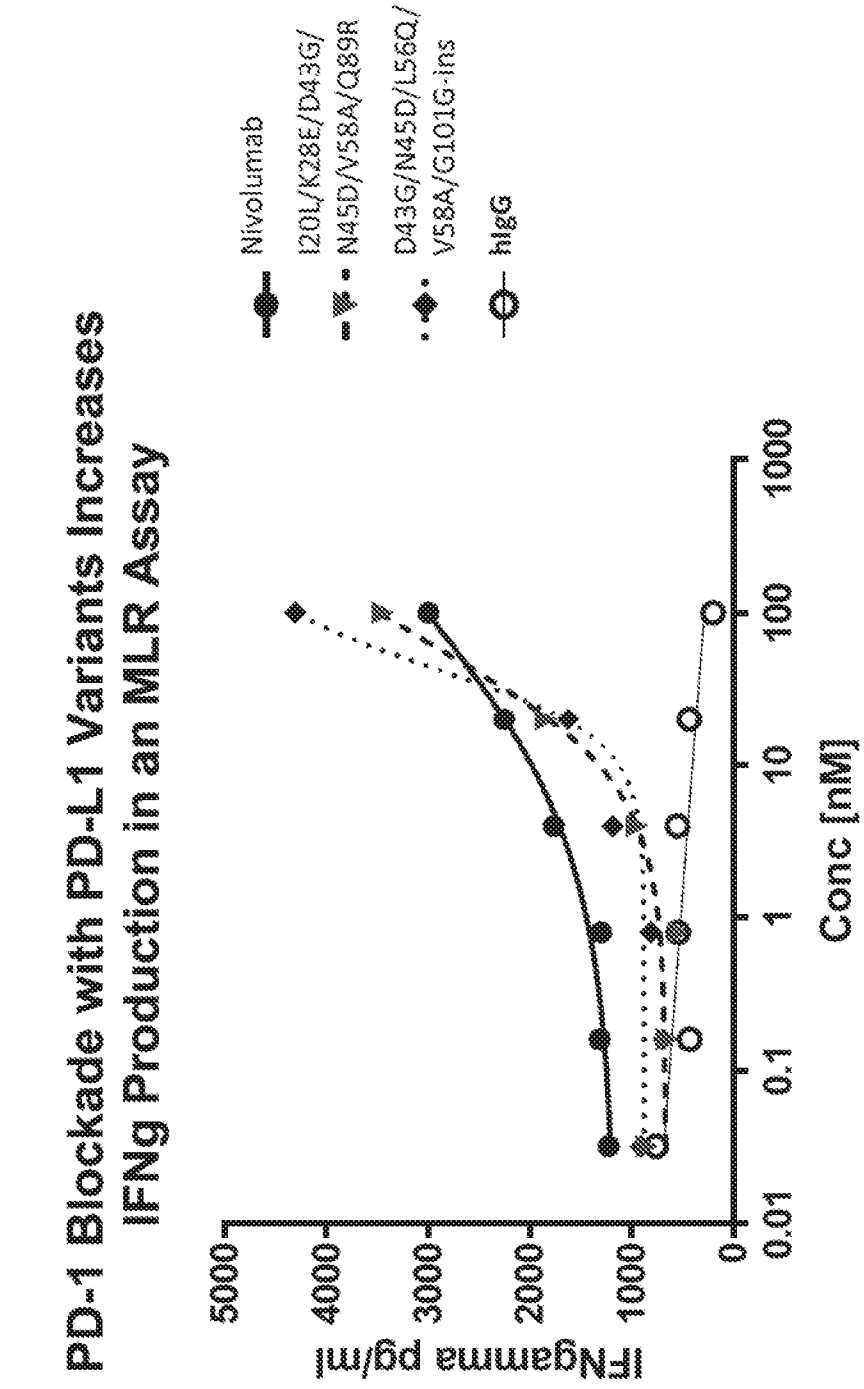

PD-1 Blockade with PD-L1 Variants Increases
IFNg Production in an MLR Assay
Nivolumab
I20L/K28E/D43G/
N45D/V58A/Q89R
D43G/N45D/L56Q/
V58A/G101G-ins
hIgG
IFNgamma pg/ml
5000
4000
3000
2000
1000
0
0.01
0.1
1
10
100
1000
Conc [nM]

FIG. 9

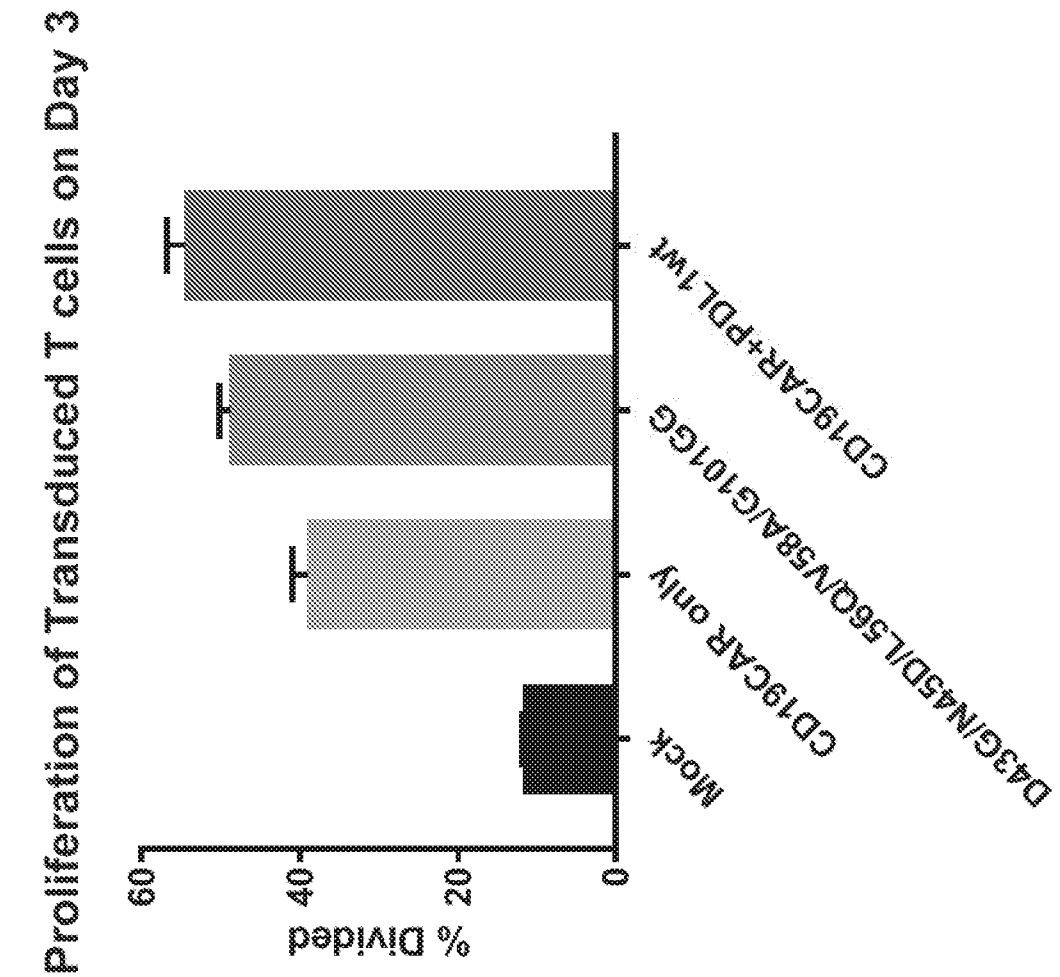
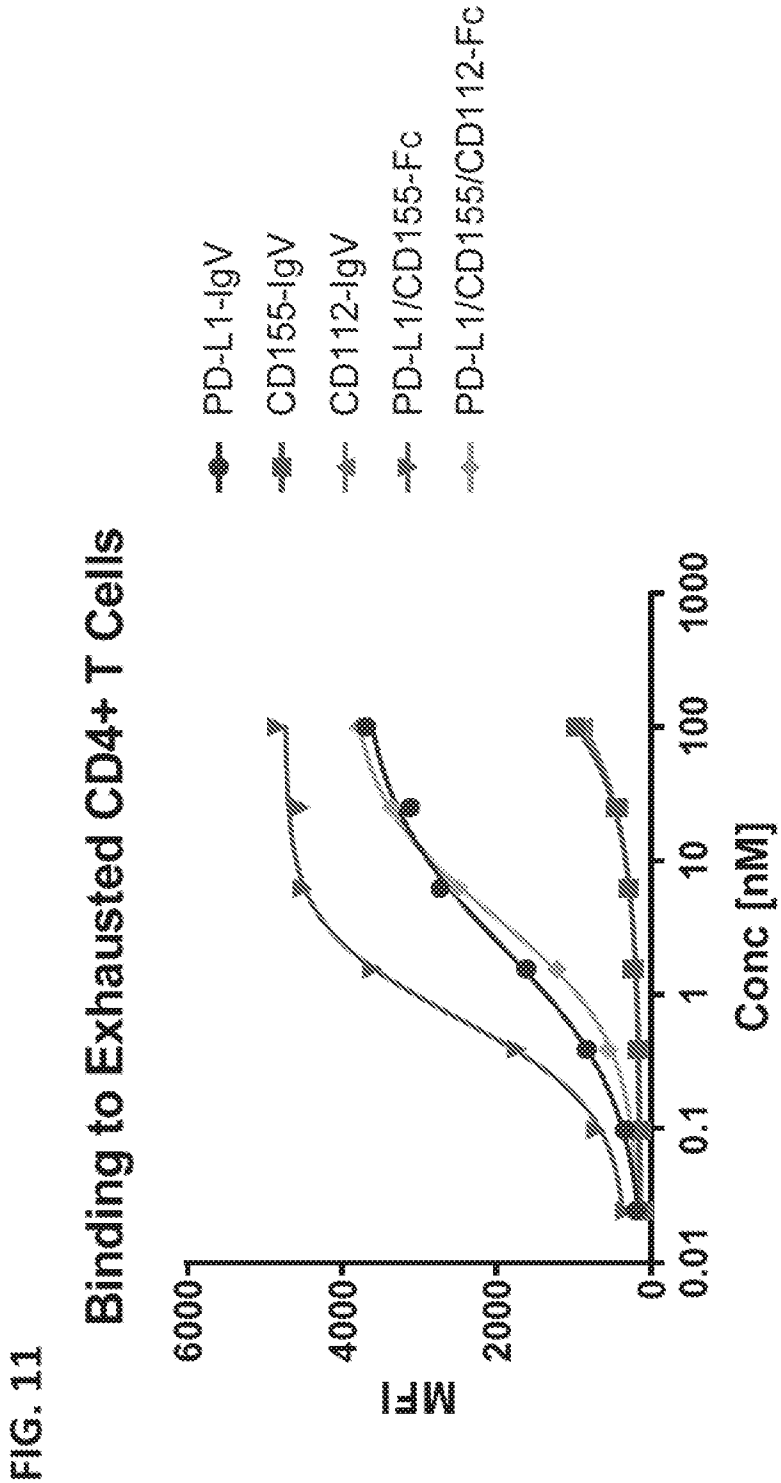

Proliferation of Transduced T cells on Day 3
% Divided
0
20
40
60
Mock
CD19CAR only
D43G/N45D/L56Q/V58A/G101GG
CD19CAR+PDL1wt

FIG. 10

FIG. 11


Binding to Exhausted CD4+ T Cells
PD-L1-IgV
CD155-IgV
CD112-IgV
PD-L1/CD155-Fc
PD-L1/CD155/CD112-Fc
MFI
6000
4000
2000
0
0.01
0.1
1
10
100
1000
Conc [nM]

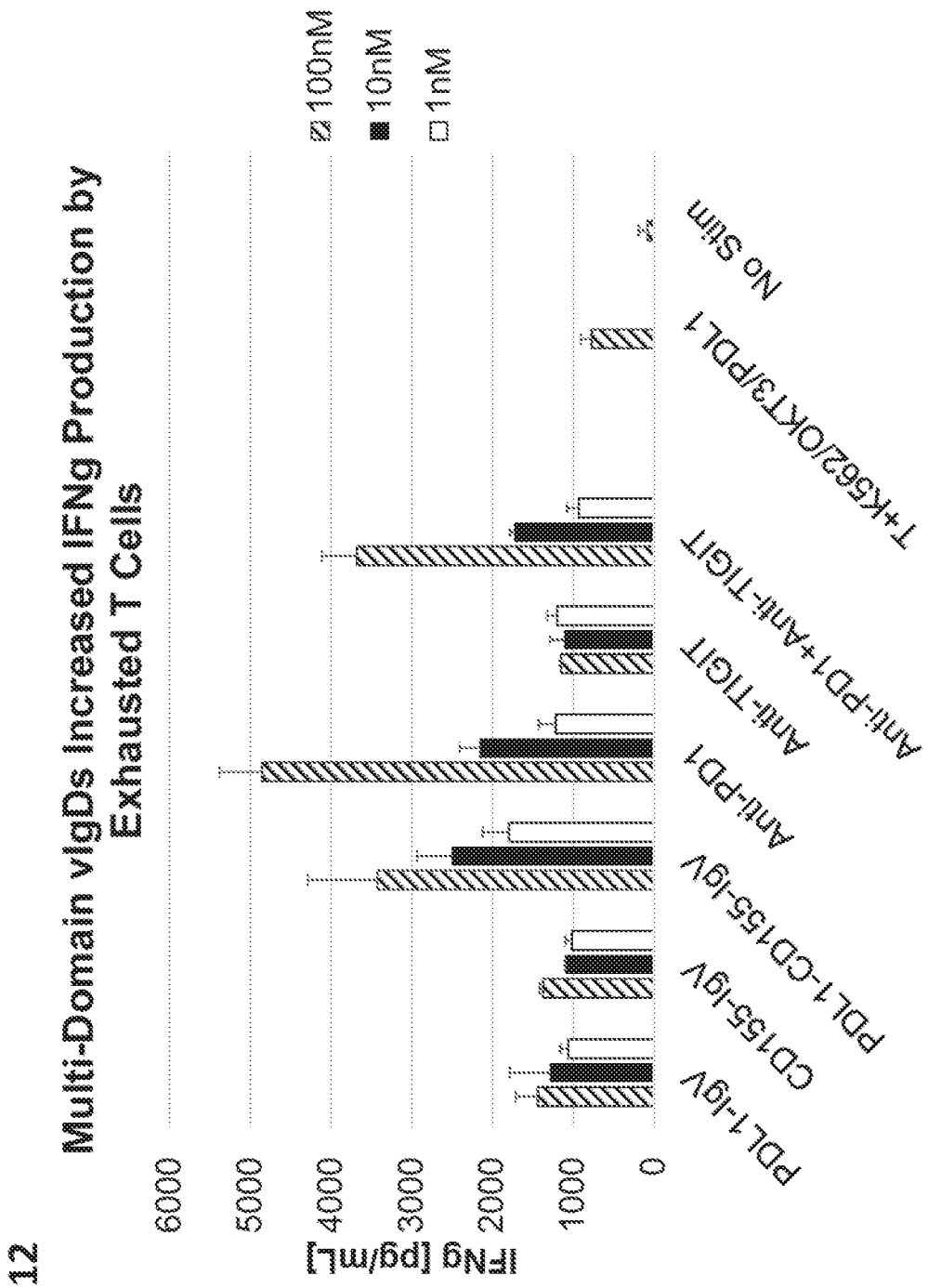

Multi-Domain vIgDs Increased IFNg Production by Exhausted T Cells
100nM
10nM
1nM
IFNg [pg/mL]
6000
5000
4000
3000
2000
1000
0
PDL1-IgV
CD155-IgV
PDL1-CD155-IgV
Anti-PD1
Anti-TIGIT
Anti-PD1+Anti-TIGIT
T+K562/OKT3/PDL1
No Stim

FIG. 12

SEQUENCE LISTING

<110> Alpine Immune Sciences, Inc.
SWANSON, Ryan
KORNACKER, Michael
MAURER, Mark F.
ARDOUREL, Dan
DEMONTE, Daniel William
KUIJPER, Joseph L.

<120> PD-L1 Variant Immunomodulatory Proteins and Uses Thereof

<130> 761612001040

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> 62/472,554
<151> 2017-03-16

<150> 62/475,076
<151> 2017-03-22

<150> 62/537,923
<151> 2017-07-27

<150> 62/582,249
<151> 2017-11-06

<160> 2032

<170> PatentIn version 3.5

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1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

```
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
        35                  40                  45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
    50                  55                  60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65                  70                  75                  80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
                85                  90                  95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
            100                 105                 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
        115                 120                 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
    130                 135                 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145                 150                 155                 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
                165                 170                 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
            180                 185                 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
        195                 200                 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
    210                 215                 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225                 230                 235                 240
```

```
Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
                245                 250                 255


Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
            260                 265                 270


Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
        275                 280                 285


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<213>  Homo sapiens


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1               5                   10                  15


Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
            20                  25                  30


Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
        35                  40                  45


Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
    50                  55                  60


Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65                  70                  75                  80


Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
                85                  90                  95


Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
            100                 105                 110
```

```
His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
        115                 120                 125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
    130                 135                 140

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145                 150                 155                 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
                165                 170                 175

Asn Ser Thr Ile Glu Tyr Asp Gly Val Met Gln Lys Ser Gln Asp Asn
            180                 185                 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
        195                 200                 205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
    210                 215                 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225                 230                 235                 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
                245                 250                 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
            260                 265                 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
        275                 280                 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
    290                 295                 300

Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305                 310                 315                 320
```

```
Ser Cys Asp Lys Ser Asp Thr Cys Phe
                325


<210>  3
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<213>  Homo sapiens


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Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1               5                   10                  15


Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
            20                  25                  30


Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
        35                  40                  45


Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
    50                  55                  60


Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65                  70                  75                  80


Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
                85                  90                  95


Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
            100                 105                 110


Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
        115                 120                 125


Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
    130                 135                 140
```

```
Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145                 150                 155                 160


Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
                165                 170                 175


Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
            180                 185                 190


Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
        195                 200                 205


Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
    210                 215                 220


Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225                 230                 235                 240


Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
                245                 250                 255


Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
            260                 265                 270


Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
        275                 280                 285


Glu Thr
    290


<210>  4
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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

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 Leu Leu His
    210                 215                 220


Ile Phe Ile Pro Phe Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val
225                 230                 235                 240


Ile Ala Leu Arg Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp
                245                 250                 255


Thr Thr Lys Arg Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala
            260                 265                 270


Ile
```

<210> 5
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Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1               5                   10                  15


Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
            20                  25                  30


Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
        35                  40                  45


Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
    50                  55                  60


Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65                  70                  75                  80
```

```
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
                85                  90                  95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
            100                 105                 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
        115                 120                 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
    130                 135                 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145                 150                 155                 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
                165                 170                 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
            180                 185                 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
        195                 200                 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
    210                 215                 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225                 230                 235                 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
                245                 250                 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
            260                 265                 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
        275                 280                 285
```

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

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Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala
1 5 10 15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

```
Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145                 150                 155                 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
                165                 170                 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
            180                 185                 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
        195                 200                 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
    210                 215                 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
225                 230                 235                 240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
                245                 250                 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
            260                 265                 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
        275                 280                 285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
    290                 295                 300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
305                 310                 315                 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
                325                 330                 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
            340                 345                 350
```

```
Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
        355                 360                 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
    370                 375                 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385                 390                 395                 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
                405                 410                 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
            420                 425                 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp
        435                 440                 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
    450                 455                 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu
465                 470                 475                 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
                485                 490                 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
            500                 505                 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
        515                 520                 525

Asp Gly Gln Glu Ile Ala
    530
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<210> 7
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<213> Homo sapiens

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Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1               5                  10                  15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
            20                  25                  30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
        35                  40                  45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
    50                  55                  60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
65                  70                  75                  80

His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
                85                  90                  95

Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
            100                 105                 110

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
        115                 120                 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
    130                 135                 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
145                 150                 155                 160

Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
                165                 170                 175
```

```
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
            180                 185                 190


Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
        195                 200                 205


Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
    210                 215                 220


Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225                 230                 235                 240


Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
                245                 250                 255


Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
            260                 265                 270


Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
        275                 280


<210>  8
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<213>  Homo sapiens


<220>
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Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1               5                   10                  15


Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
            20                  25                  30


Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35                  40                  45
```

```
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50                  55                  60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65                  70                  75                  80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
                85                  90                  95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130                 135                 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145                 150                 155                 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165                 170                 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            180                 185                 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        195                 200                 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    210                 215                 220
```

<210> 9
<211> 223
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> CTLA4

<400> 9

```
Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1               5                  10                  15


Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
            20                  25                  30


Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
        35                  40                  45


Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
    50                  55                  60


Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65                  70                  75                  80


Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
                85                  90                  95


Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
            100                 105                 110


Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
        115                 120                 125


Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
    130                 135                 140


Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145                 150                 155                 160


Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
                165                 170                 175


Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
            180                 185                 190
```

```
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
        195                 200                 205


Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
    210                 215                 220


<210>  10
<211>  288
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  PDCD1(PD-1)

<400>  10

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1               5                   10                  15


Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20                  25                  30


Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35                  40                  45


Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50                  55                  60


Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65                  70                  75                  80


Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85                  90                  95


Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100                 105                 110


Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115                 120                 125
```

```
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130                 135                 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145                 150                 155                 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
                165                 170                 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
            180                 185                 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
        195                 200                 205

Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
    210                 215                 220

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225                 230                 235                 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
                245                 250                 255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
            260                 265                 270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
        275                 280                 285


<210>  11
<211>  199
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  ICOS

<400>  11
```

```
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1               5                  10                  15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20                  25                  30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35                  40                  45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65                  70                  75                  80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100                 105                 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115                 120                 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130                 135                 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145                 150                 155                 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
                165                 170                 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180                 185                 190

Arg Leu Thr Asp Val Thr Leu
        195
```

<210> 12
<211> 289
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> BTLA(CD272)

<400> 12

```
Met Lys Thr Leu Pro Ala Met Leu Gly Thr Gly Lys Leu Phe Trp Val
1               5                  10                  15

Phe Phe Leu Ile Pro Tyr Leu Asp Ile Trp Asn Ile His Gly Lys Glu
            20                  25                  30

Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His Ser Ile
        35                  40                  45

Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala
    50                  55                  60

Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val
65                  70                  75                  80

Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn Ile Ser
                85                  90                  95

Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn Gly Ser
            100                 105                 110

Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser
        115                 120                 125

Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser
    130                 135                 140

Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Arg Leu Leu Pro
145                 150                 155                 160
```

```
Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys
                165                 170                 175


Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala
            180                 185                 190


Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr
        195                 200                 205


Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly
    210                 215                 220


Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser
225                 230                 235                 240


Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val
                245                 250                 255


Tyr Ala Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg Leu Ala
            260                 265                 270


Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg
        275                 280                 285


Ser
```

<210> 13
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD4

<400> 13

```
Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1               5                   10                  15
```

```
Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
            20                  25                  30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
        35                  40                  45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
    50                  55                  60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65                  70                  75                  80

Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
                85                  90                  95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
            100                 105                 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
        115                 120                 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
    130                 135                 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145                 150                 155                 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
                165                 170                 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
            180                 185                 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
        195                 200                 205

Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
    210                 215                 220
```

```
Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
225                 230                 235                 240


Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
                245                 250                 255


Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
            260                 265                 270


Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
        275                 280                 285


Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
    290                 295                 300


Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
305                 310                 315                 320


Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
                325                 330                 335


Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
            340                 345                 350


Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
        355                 360                 365


Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
    370                 375                 380


Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile
385                 390                 395                 400


Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile
                405                 410                 415


Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met
            420                 425                 430
```

```
Ser Gln Ile Lys Arg Leu Leu Ser Glu Lys Lys Thr Cys Gln Cys Pro
        435                 440                 445


His Arg Phe Gln Lys Thr Cys Ser Pro Ile
    450                 455


<210>  14
<211>  235
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD8A(CD8-alpha)

<400>  14

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
            20                  25                  30


Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
        35                  40                  45


Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
    50                  55                  60


Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65                  70                  75                  80


Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
                85                  90                  95


Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
            100                 105                 110


Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
        115                 120                 125
```

```
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
    130                 135                 140

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145                 150                 155                 160

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
                165                 170                 175

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
            180                 185                 190

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
        195                 200                 205

Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
    210                 215                 220

Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225                 230                 235
```

<210> 15
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD8B(CD8-beta)

<400> 15

```
Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
1               5                   10                  15

His Gly Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln
            20                  25                  30

Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
        35                  40                  45
```

```
Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
    50                  55                  60

Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
65                  70                  75                  80

His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala
                85                  90                  95

Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
            100                 105                 110

Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
        115                 120                 125

Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
    130                 135                 140

Thr Lys Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro
145                 150                 155                 160

Glu Thr Gln Lys Gly Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu
                165                 170                 175

Val Ala Gly Val Leu Val Leu Leu Val Ser Leu Gly Val Ala Ile His
            180                 185                 190

Leu Cys Cys Arg Arg Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Phe
        195                 200                 205

Tyr Lys
    210
```

<210> 16
<211> 525
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> LAG3

<400> 16

```
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
1               5                  10                  15

Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20                  25                  30

Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
        35                  40                  45

Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50                  55                  60

His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65                  70                  75                  80

Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85                  90                  95

Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100                 105                 110

Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115                 120                 125

Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130                 135                 140

Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145                 150                 155                 160

Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165                 170                 175

Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180                 185                 190
```

```
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195                 200                 205

Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210                 215                 220

Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225                 230                 235                 240

Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245                 250                 255

Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260                 265                 270

Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275                 280                 285

Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290                 295                 300

Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305                 310                 315                 320

Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325                 330                 335

Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340                 345                 350

Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355                 360                 365

Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370                 375                 380

Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385                 390                 395                 400
```

```
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405                 410                 415


Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420                 425                 430


Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435                 440                 445


His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser Leu Leu Leu Leu
    450                 455                 460


Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg Gln Trp Arg Pro
465                 470                 475                 480


Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro Pro Gln Ala Gln
                485                 490                 495


Ser Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Pro Glu Pro Glu Pro
            500                 505                 510


Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln Leu
        515                 520                 525


<210>  17
<211>  301
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  HAVCR2(TIM-3)

<400>  17

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
1               5                   10                  15


Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
            20                  25                  30
```

```
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
        35                  40                  45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
    50                  55                  60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65                  70                  75                  80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
                85                  90                  95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
            100                 105                 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
        115                 120                 125

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
    130                 135                 140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145                 150                 155                 160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
                165                 170                 175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
            180                 185                 190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
        195                 200                 205

Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
    210                 215                 220

Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225                 230                 235                 240
```

```
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
                245                 250                 255


Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
            260                 265                 270


Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
        275                 280                 285


Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
    290                 295                 300


<210>  18
<211>  526
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CEACAM1

<400>  18

Met Gly His Leu Ser Ala Pro Leu His Arg Val Arg Val Pro Trp Gln
1               5                   10                  15


Gly Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30


Thr Ala Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly
        35                  40                  45


Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly
    50                  55                  60


Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val
65                  70                  75                  80


Gly Tyr Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser
                85                  90                  95
```

```
Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
            100                 105                 110

Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
        115                 120                 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
    130                 135                 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
                165                 170                 175

Leu Trp Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
        195                 200                 205

Asp Thr Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn
    210                 215                 220

Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro
225                 230                 235                 240

Thr Ile Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser
                245                 250                 255

Leu Ser Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu
            260                 265                 270

Ile Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser
    290                 295                 300
```

```
Val Thr Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu
305                 310                 315                 320

Leu Ser Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr
                325                 330                 335

Val Thr Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp
            340                 345                 350

Thr Gly Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser
        355                 360                 365

Ser Glu Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn
    370                 375                 380

Pro Val Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn
385                 390                 395                 400

Pro Ile Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr
                405                 410                 415

Asn Ala Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly Ala Ile Ala Gly
            420                 425                 430

Ile Val Ile Gly Val Val Ala Leu Val Ala Leu Ile Ala Val Ala Leu
        435                 440                 445

Ala Cys Phe Leu His Phe Gly Lys Thr Gly Arg Ala Ser Asp Gln Arg
    450                 455                 460

Asp Leu Thr Glu His Lys Pro Ser Val Ser Asn His Thr Gln Asp His
465                 470                 475                 480

Ser Asn Asp Pro Pro Asn Lys Met Asn Glu Val Thr Tyr Ser Thr Leu
                485                 490                 495

Asn Phe Glu Ala Gln Gln Pro Thr Gln Pro Thr Ser Ala Ser Pro Ser
            500                 505                 510
```

Leu Thr Ala Thr Glu Ile Ile Tyr Ser Glu Val Lys Lys Gln
515 520 525

<210> 19
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> TIGIT

<400> 19

Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu Arg Gln Ala
1 5 10 15

Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn
20 25 30

Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser
35 40 45

Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln
50 55 60

Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser
65 70 75 80

Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln
85 90 95

Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr
100 105 110

Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu
115 120 125

Ser Ser Val Ala Glu His Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly
130 135 140

```
Ala Met Ala Ala Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val
145                 150                 155                 160


Val Ala Leu Thr Arg Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu
                165                 170                 175


Gly Asp Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser
            180                 185                 190


Ala Pro Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala
        195                 200                 205


Gly Leu Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp
    210                 215                 220


Tyr Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe
225                 230                 235                 240


Thr Glu Thr Gly



<210>  20
<211>  417
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  PVR(CD155)

<400>  20

Met Ala Arg Ala Met Ala Ala Ala Trp Pro Leu Leu Leu Val Ala Leu
1               5                   10                  15


Leu Val Leu Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln
            20                  25                  30


Ala Pro Thr Gln Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro
        35                  40                  45
```

```
Cys Tyr Leu Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu
    50                  55                  60

Thr Trp Ala Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln
65                  70                  75                  80

Thr Gln Gly Pro Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala
                85                  90                  95

Ala Arg Leu Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly
            100                 105                 110

Leu Arg Val Glu Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe
        115                 120                 125

Pro Gln Gly Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys
    130                 135                 140

Pro Gln Asn Thr Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro
145                 150                 155                 160

Val Pro Met Ala Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln
                165                 170                 175

Ile Thr Trp His Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val
            180                 185                 190

Pro Gly Phe Leu Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu
        195                 200                 205

Val Pro Ser Ser Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu
    210                 215                 220

His Glu Ser Phe Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val
225                 230                 235                 240

Tyr Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr
                245                 250                 255
```

```
Leu Gly Gln Asn Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro
            260                 265                 270

Glu Pro Thr Gly Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro
        275                 280                 285

Phe Ala Val Ala Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys
    290                 295                 300

Pro Ile Asn Thr Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala
305                 310                 315                 320

Arg Gln Ala Glu Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu
                325                 330                 335

His Ser Gly Ile Ser Arg Asn Ala Ile Ile Phe Leu Val Leu Gly Ile
            340                 345                 350

Leu Val Phe Leu Ile Leu Leu Gly Ile Gly Ile Tyr Phe Tyr Trp Ser
        355                 360                 365

Lys Cys Ser Arg Glu Val Leu Trp His Cys His Leu Cys Pro Ser Ser
    370                 375                 380

Thr Glu His Ala Ser Ala Ser Ala Asn Gly His Val Ser Tyr Ser Ala
385                 390                 395                 400

Val Ser Arg Glu Asn Ser Ser Ser Gln Asp Pro Gln Thr Glu Gly Thr
                405                 410                 415

Arg
```

<210> 21
<211> 538
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> PVRL2(CD112)

<400> 21

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Met Ala Arg Ala Ala Ala Leu Leu Pro Ser Arg Ser Pro Pro Thr Pro
1               5                  10                  15

Leu Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Glu Thr Gly Ala Gln
            20                  25                  30

Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly
        35                  40                  45

Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr
    50                  55                  60

Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln
65                  70                  75                  80

Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro
                85                  90                  95

Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr
            100                 105                 110

Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His
        115                 120                 125

Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr
    130                 135                 140

Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala
145                 150                 155                 160

Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp
                165                 170                 175

Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala
            180                 185                 190
```

```
Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln
        195                 200                 205

Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr
    210                 215                 220

Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val
225                 230                 235                 240

Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu Ser
                245                 250                 255

Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn Trp
            260                 265                 270

Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser Asn
        275                 280                 285

Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe Pro
    290                 295                 300

Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val Asp
305                 310                 315                 320

Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val Gly
                325                 330                 335

Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn Thr
            340                 345                 350

Ala Gly Ala Gly Ala Thr Gly Gly Ile Ile Gly Gly Ile Ile Ala Ala
        355                 360                 365

Ile Ile Ala Thr Ala Val Ala Ala Thr Gly Ile Leu Ile Cys Arg Gln
    370                 375                 380

Gln Arg Lys Glu Gln Thr Leu Gln Gly Ala Glu Glu Asp Glu Asp Leu
385                 390                 395                 400
```

```
Glu Gly Pro Pro Ser Tyr Lys Pro Pro Thr Pro Lys Ala Lys Leu Glu
                405                 410                 415


Ala Gln Glu Met Pro Ser Gln Leu Phe Thr Leu Gly Ala Ser Glu His
            420                 425                 430


Ser Pro Leu Lys Thr Pro Tyr Phe Asp Ala Gly Ala Ser Cys Thr Glu
        435                 440                 445


Gln Glu Met Pro Arg Tyr His Glu Leu Pro Thr Leu Glu Glu Arg Ser
    450                 455                 460


Gly Pro Leu His Pro Gly Ala Thr Ser Leu Gly Ser Pro Ile Pro Val
465                 470                 475                 480


Pro Pro Gly Pro Pro Ala Val Glu Asp Val Ser Leu Asp Leu Glu Asp
                485                 490                 495


Glu Glu Gly Glu Glu Glu Glu Glu Tyr Leu Asp Lys Ile Asn Pro Ile
            500                 505                 510


Tyr Asp Ala Leu Ser Tyr Ser Ser Pro Ser Asp Ser Tyr Gln Gly Lys
        515                 520                 525


Gly Phe Val Met Ser Arg Ala Met Tyr Val
    530                 535


<210>  22
<211>  336
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD226

<400>  22

Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
1               5                   10                  15
```

```
Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
            20                  25                  30

Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
        35                  40                  45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
    50                  55                  60

Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
65                  70                  75                  80

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
                85                  90                  95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
            100                 105                 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
        115                 120                 125

Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
    130                 135                 140

Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
145                 150                 155                 160

Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
                165                 170                 175

Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
            180                 185                 190

Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
        195                 200                 205

Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
    210                 215                 220
```

```
Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
225                 230                 235                 240


Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
                245                 250                 255


Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
            260                 265                 270


Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
        275                 280                 285


Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
    290                 295                 300


Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
305                 310                 315                 320


Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
                325                 330                 335


<210>  23
<211>  351
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD2

<400>  23

Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
1               5                   10                  15


Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
            20                  25                  30


Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
        35                  40                  45
```

```
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
    50                  55                  60

Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65                  70                  75                  80

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
                85                  90                  95

Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
            100                 105                 110

Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
        115                 120                 125

Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
    130                 135                 140

Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
145                 150                 155                 160

Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
                165                 170                 175

Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
            180                 185                 190

Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
        195                 200                 205

Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
    210                 215                 220

Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
225                 230                 235                 240

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
                245                 250                 255
```

```
Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
            260                 265                 270


Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
        275                 280                 285


Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
    290                 295                 300


Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
305                 310                 315                 320


His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
                325                 330                 335


Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
            340                 345                 350


<210>  24
<211>  180
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD160

<400>  24

Met Leu Leu Glu Pro Gly Arg Gly Cys Cys Ala Leu Ala Ile Leu Leu
1               5                   10                  15


Ala Ile Val Asp Ile Gln Ser Gly Gly Cys Ile Asn Ile Thr Ser Ser
            20                  25                  30


Ala Ser Gln Glu Gly Thr Arg Leu Asn Leu Ile Cys Thr Val Trp His
        35                  40                  45


Lys Lys Glu Glu Ala Glu Gly Phe Val Val Phe Leu Cys Lys Asp Arg
    50                  55                  60
```

```
Ser Gly Asp Cys Ser Pro Glu Thr Ser Leu Lys Gln Leu Arg Leu Lys
65                  70                  75                  80


Arg Asp Pro Gly Ile Asp Gly Val Gly Glu Ile Ser Ser Gln Leu Met
                85                  90                  95


Phe Thr Ile Ser Gln Val Thr Pro Leu His Ser Gly Thr Tyr Gln Cys
            100                 105                 110


Cys Ala Arg Ser Gln Lys Ser Gly Ile Arg Leu Gln Gly His Phe Phe
        115                 120                 125


Ser Ile Leu Phe Thr Glu Thr Gly Asn Tyr Thr Val Thr Gly Leu Lys
    130                 135                 140


Gln Arg Gln His Leu Glu Phe Ser His Asn Glu Gly Thr Leu Ser Ser
145                 150                 155                 160


Gly Phe Leu Gln Glu Lys Val Trp Val Met Leu Val Thr Ser Leu Val
                165                 170                 175


Ala Leu Gln Ala
            180


<210>  25
<211>  278
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD200

<400>  25

Met Glu Arg Leu Val Ile Arg Met Pro Phe Ser His Leu Ser Thr Tyr
1               5                   10                  15


Ser Leu Val Trp Val Met Ala Ala Val Val Leu Cys Thr Ala Gln Val
            20                  25                  30
```

```
Gln Val Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Pro Ala Ser
        35                  40                  45

Leu Lys Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val Thr Trp
    50                  55                  60

Gln Lys Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe Ser Glu
65                  70                  75                  80

Asn His Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile Asn Ile
                85                  90                  95

Thr Gln Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn Ile Thr
            100                 105                 110

Leu Glu Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe Gly Phe
        115                 120                 125

Gly Lys Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln Pro Ile
    130                 135                 140

Val Ser Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile Thr Cys
145                 150                 155                 160

Ser Ala Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val Pro Arg
                165                 170                 175

Ser Gly Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn Gly Thr
            180                 185                 190

Thr Ser Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val
        195                 200                 205

Gly Lys Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp
    210                 215                 220

Phe Lys Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro Leu Leu
225                 230                 235                 240
```

```
Leu Ser Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser Ile Leu
                245                 250                 255


Leu Tyr Trp Lys Arg His Arg Asn Gln Asp Arg Gly Glu Leu Ser Gln
            260                 265                 270


Gly Val Gln Lys Met Thr
        275


<210>  26
<211>  325
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD200R1(CD200R)

<400>  26

Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1               5                   10                  15


Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20                  25                  30


Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35                  40                  45


Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50                  55                  60


Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65                  70                  75                  80


Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85                  90                  95


Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100                 105                 110
```

```
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115                 120                 125

Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130                 135                 140

Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145                 150                 155                 160

Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165                 170                 175

Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180                 185                 190

Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195                 200                 205

His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210                 215                 220

Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys Ser
225                 230                 235                 240

Ala Lys Leu Tyr Ile Pro Tyr Ile Ile Leu Thr Ile Ile Ile Leu Thr
                245                 250                 255

Ile Val Gly Phe Ile Trp Leu Leu Lys Val Asn Gly Cys Arg Lys Tyr
            260                 265                 270

Lys Leu Asn Lys Thr Glu Ser Thr Pro Val Val Glu Glu Asp Glu Met
        275                 280                 285

Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Asn Asn Pro Leu Tyr Asp Thr
    290                 295                 300

Thr Asn Lys Val Lys Ala Ser Glu Ala Leu Gln Ser Glu Val Asp Thr
305                 310                 315                 320
```

Asp Leu His Thr Leu
325

<210> 27
<211> 201
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> NC R3 (NKp30)

<400> 27

Met Ala Trp Met Leu Leu Leu Ile Leu Ile Met Val His Pro Gly Ser
1 5 10 15

Cys Ala Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly
20 25 30

Ser Ser Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu
35 40 45

Ala Ile Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys
50 55 60

Glu Val Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu
65 70 75 80

Ala Ser Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg
85 90 95

Asp Val Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val
100 105 110

Leu Gly Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu
115 120 125

Lys Glu His Pro Gln Leu Gly Ala Gly Thr Val Leu Leu Leu Arg Ala
130 135 140

```
Gly Phe Tyr Ala Val Ser Phe Leu Ser Val Ala Val Gly Ser Thr Val
145                 150                 155                 160


Tyr Tyr Gln Gly Lys Cys Leu Thr Trp Lys Gly Pro Arg Arg Gln Leu
                165                 170                 175


Pro Ala Val Val Pro Ala Pro Leu Pro Pro Pro Cys Gly Ser Ser Ala
            180                 185                 190


His Leu Leu Pro Pro Val Pro Gly Gly
        195                 200


<210>  28
<211>  208
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD80(B7-1) ECD

<400>  28

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95
```

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 29
<211> 224
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD86(B7-2) ECD

<400> 29

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

```
Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
                85                  90                  95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn
            100                 105                 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
        115                 120                 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
    130                 135                 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145                 150                 155                 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
                165                 170                 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
            180                 185                 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
        195                 200                 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
    210                 215                 220


<210>  30
<211>  220
<212>  PRT
<213>  Homo sapiens


<220>
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<221> MISC_FEATURE
<223> CD274 (PD-L1, B7-H1) ECD

<400> 30

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 31
<211> 201
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> PDCD1LG2(PD-L2, CD273) ECD

<400> 31

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
        195                 200


<210>  32
<211>  238
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  ICOSLG(B7RP1, CD275, ICOSL, B7-H2) ECD

<400>  32

Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu
1               5                   10                  15


Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val
            20                  25                  30


Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His
        35                  40                  45


Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn
    50                  55                  60


Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu
65                  70                  75                  80
```

```
Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu
                85                  90                  95


Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val
            100                 105                 110


Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro
        115                 120                 125


His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn
    130                 135                 140


Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser
145                 150                 155                 160


Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg
                165                 170                 175


Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser
            180                 185                 190


Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu
        195                 200                 205


Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile
    210                 215                 220


Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
225                 230                 235


<210>  33
<211>  438
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD276(B7-H3) ECD

<400>  33
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```
Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr
1               5                  10                  15

Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
            20                  25                  30

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val
        35                  40                  45

His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg
    50                  55                  60

Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg
65                  70                  75                  80

Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val
                85                  90                  95

Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala
            100                 105                 110

Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg
        115                 120                 125

Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro
    130                 135                 140

Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly
145                 150                 155                 160

Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val
                165                 170                 175

His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys
            180                 185                 190

Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr
        195                 200                 205
```

```
Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro
    210                 215                 220

Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys
225                 230                 235                 240

Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile
                245                 250                 255

Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly
            260                 265                 270

Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp
        275                 280                 285

Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val
    290                 295                 300

Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly
305                 310                 315                 320

Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser
                325                 330                 335

Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr
            340                 345                 350

Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp
        355                 360                 365

Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln
    370                 375                 380

Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
385                 390                 395                 400

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val
                405                 410                 415
```

Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met
420 425 430

Thr Phe Pro Pro Glu Ala
435

<210> 34
<211> 235
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> VTCN1(B7-H4) ECD

<400> 34

Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile Thr Val Thr
1 5 10 15

Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys
20 25 30

Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu
35 40 45

Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp
50 55 60

Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe
65 70 75 80

Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val
85 90 95

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser Lys
100 105 110

Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser Met
115 120 125

```
Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu Arg Cys
    130                 135                 140


Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser Gln
145                 150                 155                 160


Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr Ser Phe Glu
                165                 170                 175


Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val Leu Tyr Asn
            180                 185                 190


Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn Asp Ile Ala
        195                 200                 205


Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile Lys Arg Arg
    210                 215                 220


Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser
225                 230                 235


<210>  35
<211>  134
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD28 ECD

<400>  35

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1               5                   10                  15


Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
            20                  25                  30


Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
        35                  40                  45
```

```
Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr
    50                  55                  60


Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr
65                  70                  75                  80


Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
                85                  90                  95


Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
            100                 105                 110


Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
        115                 120                 125


Pro Gly Pro Ser Lys Pro
    130


<210>  36
<211>  126
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CTLA4 ECD

<400>  36

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60
```

```
Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110


Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120                 125


<210>  37
<211>  150
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  PDCD1(PD-1) ECD

<400>  37

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1               5                   10                  15


Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
            20                  25                  30


Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
        35                  40                  45


Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
    50                  55                  60


Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65                  70                  75                  80


Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
                85                  90                  95
```

```
Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
            100                 105                 110


Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
        115                 120                 125


Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
    130                 135                 140


Gln Phe Gln Thr Leu Val
145                 150


<210>  38
<211>  120
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  ICOS ECD

<400>  38

Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
1               5                   10                  15


Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
            20                  25                  30


Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
        35                  40                  45


Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
    50                  55                  60


Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65                  70                  75                  80


His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                85                  90                  95
```

```
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
            100                 105                 110


Ser Gln Leu Cys Cys Gln Leu Lys
        115                 120


<210>  39
<211>  127
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  BTLA(CD272) ECD

<400>  39

Lys Glu Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His
1               5                   10                  15


Ser Ile Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr
            20                  25                  30


Cys Ala Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr
        35                  40                  45


Cys Val Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn
    50                  55                  60


Ile Ser Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn
65                  70                  75                  80


Gly Ser Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser
                85                  90                  95


His Ser Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg
            100                 105                 110


Pro Ser Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Arg
        115                 120                 125
```

<210> 40
<211> 371
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD4 ECD

<400> 40

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
1 5 10 15

Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
20 25 30

Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
35 40 45

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
50 55 60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp
65 70 75 80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
85 90 95

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
100 105 110

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
115 120 125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
130 135 140

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
145 150 155 160

```
Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
                165                 170                 175

Leu Ala Phe Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu
            180                 185                 190

Gln Val Glu Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr
        195                 200                 205

Gly Ser Gly Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys
    210                 215                 220

Ser Trp Ile Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg
225                 230                 235                 240

Val Thr Gln Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His
                245                 250                 255

Leu Thr Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu
            260                 265                 270

Thr Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn
        275                 280                 285

Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu
    290                 295                 300

Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu
305                 310                 315                 320

Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu
                325                 330                 335

Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln
            340                 345                 350

Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp Ser Thr Pro
        355                 360                 365
```

Val Gln Pro
    370

<210> 41
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD8A(CD8-alpha) ECD

<400> 41

Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly Glu
1   5   10   15

Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
            20   25   30

Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
        35   40   45

Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
    50   55   60

Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
65   70   75   80

Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
                85   90   95

Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu
            100   105   110

Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
        115   120   125

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
    130   135   140

```
Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
145                 150                 155                 160


Asp



<210>  42
<211>  149
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD8B(CD8-beta) ECD

<400>  42

Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
1               5                   10                  15


Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20                  25                  30


Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35                  40                  45


Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50                  55                  60


Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65                  70                  75                  80


Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85                  90                  95


Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100                 105                 110


Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125
```

```
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140


Pro Leu Cys Ser Pro
145


<210>  43
<211>  422
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  LAG3 ECD

<400>  43

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys
1               5                   10                  15


Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
            20                  25                  30


Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
        35                  40                  45


Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
    50                  55                  60


Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
65                  70                  75                  80


Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
                85                  90                  95


Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
            100                 105                 110


Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
        115                 120                 125
```

```
Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
    130                 135                 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
145                 150                 155                 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
                165                 170                 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
            180                 185                 190

Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser
        195                 200                 205

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
    210                 215                 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
225                 230                 235                 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
                245                 250                 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
            260                 265                 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
        275                 280                 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
    290                 295                 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
305                 310                 315                 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
                325                 330                 335
```

```
Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
            340                 345                 350


Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
        355                 360                 365


Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
    370                 375                 380


Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
385                 390                 395                 400


Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
                405                 410                 415


Leu Pro Ala Gly His Leu
            420


<210>  44
<211>  181
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  HAVCR2(TIM-3) ECD

<400>  44

Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
1               5                   10                  15


Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp
            20                  25                  30


Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg
        35                  40                  45


Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn
    50                  55                  60
```

```
Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn Val Thr
65                  70                  75                  80


Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile
                85                  90                  95


Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys
            100                 105                 110


Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe Thr Ala Ala Phe Pro
        115                 120                 125


Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu
    130                 135                 140


Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn
145                 150                 155                 160


Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala
                165                 170                 175


Thr Ile Arg Ile Gly
            180


<210>  45
<211>  394
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CEACAM1 ECD

<400>  45

Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15


Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
            20                  25                  30
```

```
Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
        35                  40                  45

Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
    50                  55                  60

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85                  90                  95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn Asp Thr
                165                 170                 175

Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro Thr Ile
        195                 200                 205

Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser Leu Ser
    210                 215                 220

Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asn
225                 230                 235                 240
```

```
Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser Val Thr
            260                 265                 270

Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu Leu Ser
        275                 280                 285

Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val Thr
    290                 295                 300

Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr Gly
305                 310                 315                 320

Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser Glu
                325                 330                 335

Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn Pro Val
            340                 345                 350

Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro Ile
        355                 360                 365

Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn Ala
    370                 375                 380

Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly
385                 390
```

<210> 46
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> TIGIT ECD

<400> 46

```
Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1               5                   10                  15


Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
            20                  25                  30


Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
        35                  40                  45


Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
    50                  55                  60


Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn
65                  70                  75                  80


Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
                85                  90                  95


Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
            100                 105                 110


His Gly Ala Arg Phe Gln Ile Pro
        115                 120


<210>  47
<211>  323
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  PVR(CD155) ECD

<400>  47

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30
```

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

```
Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  48
<211>  329
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  PVRL2(CD112) ECD

<400>  48

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60
```

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270
```

```
Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  49
<211>  236
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD226 ECD

<400>  49

Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser
1               5                   10                  15


Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp
            20                  25                  30


Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr
        35                  40                  45


His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu
    50                  55                  60


Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala
65                  70                  75                  80


Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro
                85                  90                  95
```

```
Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe
            100                 105                 110


Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys
        115                 120                 125


Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala
    130                 135                 140


Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr
145                 150                 155                 160


Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln
                165                 170                 175


Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro
            180                 185                 190


Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala
        195                 200                 205


Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu
    210                 215                 220


Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala
225                 230                 235


<210>  50
<211>  185
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD2 ECD

<400>  50

Lys Glu Ile Thr Asn Ala Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp
1               5                   10                  15
```

```
Ile Asn Leu Asp Ile Pro Ser Phe Gln Met Ser Asp Asp Ile Asp Asp
            20                  25                  30

Ile Lys Trp Glu Lys Thr Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg
        35                  40                  45

Lys Glu Lys Glu Thr Phe Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys
    50                  55                  60

Asn Gly Thr Leu Lys Ile Lys His Leu Lys Thr Asp Asp Gln Asp Ile
65                  70                  75                  80

Tyr Lys Val Ser Ile Tyr Asp Thr Lys Gly Lys Asn Val Leu Glu Lys
                85                  90                  95

Ile Phe Asp Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser
            100                 105                 110

Trp Thr Cys Ile Asn Thr Thr Leu Thr Cys Glu Val Met Asn Gly Thr
        115                 120                 125

Asp Pro Glu Leu Asn Leu Tyr Gln Asp Gly Lys His Leu Lys Leu Ser
    130                 135                 140

Gln Arg Val Ile Thr His Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe
145                 150                 155                 160

Lys Cys Thr Ala Gly Asn Lys Val Ser Lys Glu Ser Ser Val Glu Pro
                165                 170                 175

Val Ser Cys Pro Glu Lys Gly Leu Asp
            180                 185
```

<210> 51
<211> 133
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> CD160 ECD

<400> 51

```
Ile Asn Ile Thr Ser Ser Ala Ser Gln Glu Gly Thr Arg Leu Asn Leu
1               5                  10                  15


Ile Cys Thr Val Trp His Lys Lys Glu Glu Ala Glu Gly Phe Val Val
            20                  25                  30


Phe Leu Cys Lys Asp Arg Ser Gly Asp Cys Ser Pro Glu Thr Ser Leu
        35                  40                  45


Lys Gln Leu Arg Leu Lys Arg Asp Pro Gly Ile Asp Gly Val Gly Glu
    50                  55                  60


Ile Ser Ser Gln Leu Met Phe Thr Ile Ser Gln Val Thr Pro Leu His
65                  70                  75                  80


Ser Gly Thr Tyr Gln Cys Cys Ala Arg Ser Gln Lys Ser Gly Ile Arg
                85                  90                  95


Leu Gln Gly His Phe Phe Ser Ile Leu Phe Thr Glu Thr Gly Asn Tyr
            100                 105                 110


Thr Val Thr Gly Leu Lys Gln Arg Gln His Leu Glu Phe Ser His Asn
        115                 120                 125


Glu Gly Thr Leu Ser
    130
```

<210> 52
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD200 ECD

<400> 52

```
Gln Val Gln Val Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Pro
1               5                  10                  15

Ala Ser Leu Lys Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val
            20                  25                  30

Thr Trp Gln Lys Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe
        35                  40                  45

Ser Glu Asn His Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile
    50                  55                  60

Asn Ile Thr Gln Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn
65                  70                  75                  80

Ile Thr Leu Glu Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe
                85                  90                  95

Gly Phe Gly Lys Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln
            100                 105                 110

Pro Ile Val Ser Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile
        115                 120                 125

Thr Cys Ser Ala Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val
    130                 135                 140

Pro Arg Ser Gly Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn
145                 150                 155                 160

Gly Thr Thr Ser Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn
                165                 170                 175

Gln Val Gly Lys Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val
            180                 185                 190

Thr Asp Phe Lys Gln Thr Val Asn Lys Gly
        195                 200
```

<210> 53
<211> 215
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD200R1(CD200R) ECD

<400> 53

Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu
1 5 10 15

Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys
20 25 30

Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile
35 40 45

Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr
50 55 60

Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val
65 70 75 80

Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile
85 90 95

Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn
100 105 110

Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr
115 120 125

Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly
130 135 140

Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr
145 150 155 160

```
Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys
                165                 170                 175


His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His Val Ser His
            180                 185                 190


Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly
        195                 200                 205


Ala Lys Lys Ser Ala Lys Leu
    210                 215


<210>  54
<211>  117
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  NC R3 (NKp30) ECD

<400>  54

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1               5                   10                  15


Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
            20                  25                  30


Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
        35                  40                  45


Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
    50                  55                  60


Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65                  70                  75                  80


Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
                85                  90                  95
```

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
115

<210> 55
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV

<400> 55

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 56
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v1

<400> 56

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Asn Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val Asn Gly Glu Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 57
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v2

<400> 57

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Thr Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 58
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v3

<400> 58

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Glu Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  59
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v4

<400>  59

Phe Thr Val Thr Val Ser Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Thr Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 60

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v5

<400> 60

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

```
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  61
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v6

<400>  61

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
```

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 62
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v7

<400> 62

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  63
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v8

<400>  63

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
```

210 215 220

<210> 64
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v9

<400> 64

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  65
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v10

<400>  65

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 66
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v11

<400> 66

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  67
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v12
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<400> 67

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Gly Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
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195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 68
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v13

<400> 68

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Ser Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  69
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v14

<400>  69

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 70
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v15

<400> 70

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

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Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
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<210> 71
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v16

<400> 71

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 72
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v17

<400> 72

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  73
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v18

<400>  73

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 74
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v19

<400> 74

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Glu Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
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<210> 75
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v20

<400> 75

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Ile Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asn Ile Ile Gln
35 40 45

Phe Val Arg Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 76
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v21

<400> 76

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln Arg Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  77
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v22

<400>  77

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
```

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 78
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v23

<400> 78

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Gly
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Glu Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
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Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 79
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v24

<400> 79

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 80
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v25

<400> 80

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  81
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v26

<400>  81

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
```

35 40 45

Phe Val His Gly Val Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 82
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v27

<400> 82

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 83
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v28

<400> 83

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Gly Met Glu Val Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 84
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v29

<400> 84

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Ser Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  85
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v30

<400>  85

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 86

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v31

<400> 86

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

```
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  87
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v32

<400>  87

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
```

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 88
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v33

<400> 88

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  89
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v34

<400>  89

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
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210 215 220

<210> 90
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v35

<400> 90

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  91
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v36

<400>  91

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Met Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 92
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v37

<400> 92

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

```
Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 93
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v38

<400> 93

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Pro Pro Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 94
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v39

<400> 94

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  95
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v40

<400>  95

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Arg Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 96
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v41

<400> 96

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 97
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v42

<400> 97

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Val Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 98
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v43

<400> 98

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Gly Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  99
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v44

<400>  99

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 100
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v45

<400> 100

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 101
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v46

<400> 101

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 102
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v47

<400> 102

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 103
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v48

<400> 103

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 104
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v49

<400> 104

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 105
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v50

<400> 105

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 106
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v51

<400> 106

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  107
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v52

<400>  107

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Ala Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
```

35 40 45

Phe Val Tyr Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 108
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v53

<400> 108

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Thr Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

```
Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  109
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v54

<400>  109

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
```

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 110
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v55

<400> 110

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  111
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v56

<400>  111

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
```

```
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Gly Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 112

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v57

<400> 112

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 113
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v58

<400> 113

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 114
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v59

<400> 114

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Gly Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Asp Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  115
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v60

<400>  115

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110

Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp
        115                 120                 125

Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro
    130                 135                 140

Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly
145                 150                 155                 160

Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val
                165                 170                 175

Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys
            180                 185                 190

Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val
        195                 200                 205

Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
```

210 215 220

<210> 116
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v61

<400> 116

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  117
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v62

<400>  117

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 118
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v63

<400> 118

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Ile Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Ile Ile Ile Gln
35 40 45

```
Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Lys Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  119
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v64
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<400> 119

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 120
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v65

<400> 120

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

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Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  121
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v1

<400>  121

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Asn Gln Leu Asp Leu Ala Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln Phe Val Asn Gly Glu
        35                  40                  45


Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
```

85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v2

<400> 122

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Thr Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 123
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v3

<400> 123

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Asp Glu Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 124
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v4

<400> 124

Ser Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

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Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Thr Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  125
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v5

<400>  125

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
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100 105

<210> 126
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v6

<400> 126

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v7

<400> 127

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu

1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 128
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v8

<400> 128

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

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Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  129
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v9

<400>  129

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  130
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<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v10

<400> 130

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 131
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v11

<400> 131

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val

20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 132
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v12

<400> 132

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asp Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Gly Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 133
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v13

<400> 133

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Ser Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 134
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v14

<400> 134

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85   90   95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105

<210> 135
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v15

<400> 135

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu

35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v16

<400> 136

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 137
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v17

<400> 137

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v18

<400> 138

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20 25 30

Tyr Trp Glu Lys Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
        35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100 105

<210> 139
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v19

<400> 139

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu

50 55 60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Glu
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 140
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v20

<400> 140

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Ile Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Gly Lys Asn Ile Ile Gln Phe Val Arg Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 141
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v21

<400> 141

Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln Arg Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 142
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v22

<400> 142

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Ala His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85   90   95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105

<210> 143
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v23

<400> 143

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Gly Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Glu Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp

65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 144
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v24

<400> 144

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Ile Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 145
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v25

<400> 145

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 146
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v26

<400> 146

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Val
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 147
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v27

<400> 147

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly

85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 148
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v28

<400> 148

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Gly Met Glu Val Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 149
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v29

<400> 149

Pro Lys Asp Leu Tyr Val Val Glu Ser Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 150
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v30

<400> 150

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

```
Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  151
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v31

<400>  151

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
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100 105

<210> 152
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v32

<400> 152

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 153
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v33

<400> 153

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu

1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 154
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v34

<400> 154

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 155
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v35

<400> 155

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 156

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v36

<400> 156

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85   90   95

Gly Ala Asp Tyr Lys Arg Ile Thr Met Lys Val
            100   105

<210> 157
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v37

<400> 157

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val

20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 158
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v38

<400> 158

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Pro Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 159
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v39

<400> 159

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 160
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v40

<400> 160

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85   90   95

Gly Ala Asp Tyr Arg Arg Ile Thr Val Lys Val
            100   105

<210> 161
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v41

<400> 161

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu

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        35                  40                  45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105
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<210> 162
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v42

<400> 162

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Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20                  25                  30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Val Ile Ser Tyr Gly
                85                  90                  95
```

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 163
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v43

<400> 163

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Gly Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 164
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v44

<400> 164

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50 55 60

Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100 105

<210> 165
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v45

<400> 165

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
        35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu

50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 166
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v46

<400> 166

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 167
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v47

<400> 167

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 168
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v48

<400> 168

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

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Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  169
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v49

<400>  169

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
```

65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 170
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v50

<400> 170

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 171
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v51

<400> 171

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 172
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v52

<400> 172

Pro Lys Asp Leu Tyr Ala Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val Tyr Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Gly Tyr Gly
                85   90   95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105

<210> 173
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v53

<400> 173

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1   5   10   15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Gly Lys Thr Ile Ile Gln Phe Ala His Gly Glu
        35   40   45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly

85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 174
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v54

<400> 174

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 175
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v55

<400> 175

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 176
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v56

<400> 176

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Gly
35 40 45

```
Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  177
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v57

<400>  177

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Asp Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
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100 105

<210> 178
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v58

<400> 178

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 179
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v59

<400> 179

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu

1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Gly Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Asp
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 180
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v60

<400> 180

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

```
Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  181
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v61

<400>  181

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1               5                   10                  15


Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20                  25                  30


Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  182
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<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v62

<400> 182

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 183
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v63

<400> 183

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Ile Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Ile Val

20 25 30

Tyr Trp Glu Met Glu Asp Lys Ile Ile Ile Gln Phe Ala His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Lys Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 184
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v64

<400> 184

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 185
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v65

<400> 185

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 186
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> VH signal peptide

<400> 186

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
1   5   10   15

Val Ser Ala

<210> 187
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 Fc

<400> 187

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 188
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG2 Fc

<400> 188

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
1 5 10 15

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
20 25 30

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45

```
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
    50                  55                  60

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65                  70                  75                  80

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
                85                  90                  95

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            100                 105                 110

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
        115                 120                 125

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
    130                 135                 140

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145                 150                 155                 160

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                165                 170                 175

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
            180                 185                 190

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        195                 200                 205

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    210                 215                 220

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230                 235


<210>  189
<211>  254
<212>  PRT
```

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD80(B7-1)

<400> 189

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175
```

```
Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe
    210                 215                 220


Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg
225                 230                 235                 240


Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
                245                 250


<210>  190
<211>  306
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD86(B7-2)

<400>  190

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1               5                   10                  15


Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
            20                  25                  30


Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
        35                  40                  45


Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60


Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80
```

```
Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
                85                  90                  95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn
            100                 105                 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
        115                 120                 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
    130                 135                 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145                 150                 155                 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
                165                 170                 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
            180                 185                 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
        195                 200                 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
    210                 215                 220

Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val Phe
225                 230                 235                 240

Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser
                245                 250                 255

Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr
            260                 265                 270

Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln
        275                 280                 285
```

```
Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr
    290                 295                 300


Cys Phe
305


<210>  191
<211>  272
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD274 (PD-L1, B7-H1)

<400>  191

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125
```

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His Leu Val
    210                 215                 220


Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr Phe Ile
225                 230                 235                 240


Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys Gly Ile
                245                 250                 255


Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu Glu Thr
            260                 265                 270


<210>  192
<211>  254
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature PDCD1LG2(PD-L2, CD273)

<400>  192

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>  193
<211>  284
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature ICOSLG(B7RP1, CD275, ICOSL, B7-H2)

<400>  193

Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu
1               5                   10                  15


Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val
            20                  25                  30


Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His
        35                  40                  45


Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn
    50                  55                  60


Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu
65                  70                  75                  80


Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu
                85                  90                  95


Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val
            100                 105                 110


Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro
        115                 120                 125
```

```
His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn
    130                 135                 140

Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser
145                 150                 155                 160

Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg
                165                 170                 175

Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser
            180                 185                 190

Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu
        195                 200                 205

Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile
    210                 215                 220

Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr Trp Ser
225                 230                 235                 240

Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala Ile Gly
                245                 250                 255

Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly Ala Trp
            260                 265                 270

Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
        275                 280
```

<210> 194
<211> 506
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD276(B7-H3)

<400> 194

```
Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr
1               5                  10                  15

Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
            20                  25                  30

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val
        35                  40                  45

His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg
    50                  55                  60

Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg
65                  70                  75                  80

Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val
                85                  90                  95

Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala
            100                 105                 110

Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg
        115                 120                 125

Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro
    130                 135                 140

Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly
145                 150                 155                 160

Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val
                165                 170                 175

His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys
            180                 185                 190

Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr
        195                 200                 205
```

```
Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro
    210                 215                 220

Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys
225                 230                 235                 240

Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile
                245                 250                 255

Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly
            260                 265                 270

Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp
        275                 280                 285

Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val
    290                 295                 300

Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly
305                 310                 315                 320

Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser
                325                 330                 335

Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr
            340                 345                 350

Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp
        355                 360                 365

Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln
    370                 375                 380

Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
385                 390                 395                 400

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val
                405                 410                 415
```

```
Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met
            420                 425                 430


Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys
        435                 440                 445


Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile
    450                 455                 460


Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly
465                 470                 475                 480


Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp
                485                 490                 495


Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
            500                 505


<210>  195
<211>  258
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature VTCN1(B7-H4)

<400>  195

Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile Thr Val Thr
1               5                   10                  15


Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys
            20                  25                  30


Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu
        35                  40                  45


Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp
    50                  55                  60
```

```
Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe
65                  70                  75                  80

Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val
                85                  90                  95

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser Lys
            100                 105                 110

Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser Met
        115                 120                 125

Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu Arg Cys
    130                 135                 140

Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser Gln
145                 150                 155                 160

Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr Ser Phe Glu
                165                 170                 175

Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val Leu Tyr Asn
            180                 185                 190

Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn Asp Ile Ala
        195                 200                 205

Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile Lys Arg Arg
    210                 215                 220

Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys Val Ser Ser
225                 230                 235                 240

Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met
                245                 250                 255

Leu Lys
```

<210> 196
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD28

<400> 196

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr
50 55 60

Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr
65 70 75 80

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
145 150 155 160

```
Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
                165                 170                 175


Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
            180                 185                 190


Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        195                 200


<210>  197
<211>  188
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CTLA4

<400>  197

Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg
1               5                   10                  15


Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr
            20                  25                  30


Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu
        35                  40                  45


Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp
    50                  55                  60


Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr
65                  70                  75                  80


Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val
                85                  90                  95


Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr
            100                 105                 110
```

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu
115 120 125

Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe
130 135 140

Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro
145 150 155 160

Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys
165 170 175

Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
180 185

<210> 198
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature PDCD1(PD-1)

<400> 198

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

```
Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
                85                  90                  95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
            100                 105                 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
        115                 120                 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
    130                 135                 140

Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly Leu Leu Gly Ser
145                 150                 155                 160

Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys Ser Arg Ala Ala
                165                 170                 175

Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro Leu Lys Glu Asp
            180                 185                 190

Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly Glu Leu Asp Phe
        195                 200                 205

Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro Cys Val Pro Glu
    210                 215                 220

Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly Met Gly Thr Ser
225                 230                 235                 240

Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg Ser Ala Gln Pro
                245                 250                 255

Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
            260                 265
```

<210> 199
<211> 179
<212> PRT

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature ICOS

<400> 199

```
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
1               5                   10                  15

Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
            20                  25                  30

Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
        35                  40                  45

Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
    50                  55                  60

Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65                  70                  75                  80

His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                85                  90                  95

Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
            100                 105                 110

Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
        115                 120                 125

Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
    130                 135                 140

Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
145                 150                 155                 160

Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
                165                 170                 175
```

Val Thr Leu

<210> 200
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature BTLA(CD272)

<400> 200

Lys Glu Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His
1 5 10 15

Ser Ile Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr
20 25 30

Cys Ala Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr
35 40 45

Cys Val Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn
50 55 60

Ile Ser Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn
65 70 75 80

Gly Ser Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser
85 90 95

His Ser Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg
100 105 110

Pro Ser Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Arg Leu
115 120 125

Leu Pro Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu
130 135 140

```
Phe Cys Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp
145                 150                 155                 160


Thr Ala Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu
                165                 170                 175


Gln Thr Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu
            180                 185                 190


Thr Gly Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu
        195                 200                 205


Gly Ser Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly
    210                 215                 220


Ile Val Tyr Ala Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg
225                 230                 235                 240


Leu Ala Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys
                245                 250                 255


Val Arg Ser



<210>  201
<211>  433
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD4

<400>  201

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
1               5                   10                  15


Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
            20                  25                  30
```

```
Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
        35                  40                  45

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
    50                  55                  60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp
65                  70                  75                  80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
                85                  90                  95

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
            100                 105                 110

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
        115                 120                 125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
    130                 135                 140

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
145                 150                 155                 160

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
                165                 170                 175

Leu Ala Phe Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu
            180                 185                 190

Gln Val Glu Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr
        195                 200                 205

Gly Ser Gly Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys
    210                 215                 220

Ser Trp Ile Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg
225                 230                 235                 240
```

```
Val Thr Gln Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His
                245                 250                 255

Leu Thr Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu
            260                 265                 270

Thr Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn
        275                 280                 285

Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu
    290                 295                 300

Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu
305                 310                 315                 320

Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu
                325                 330                 335

Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln
            340                 345                 350

Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp Ser Thr Pro
        355                 360                 365

Val Gln Pro Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu
    370                 375                 380

Leu Phe Ile Gly Leu Gly Ile Phe Phe Cys Val Arg Cys Arg His Arg
385                 390                 395                 400

Arg Arg Gln Ala Glu Arg Met Ser Gln Ile Lys Arg Leu Leu Ser Glu
                405                 410                 415

Lys Lys Thr Cys Gln Cys Pro His Arg Phe Gln Lys Thr Cys Ser Pro
            420                 425                 430

Ile
```

<210> 202
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD8A(CD8-alpha)

<400> 202

```
Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly Glu
1               5                   10                  15


Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
            20                  25                  30


Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
        35                  40                  45


Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
    50                  55                  60


Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
65                  70                  75                  80


Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
                85                  90                  95


Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu
            100                 105                 110


Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
        115                 120                 125


Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
    130                 135                 140


Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
145                 150                 155                 160
```

```
Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
                165                 170                 175


Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
            180                 185                 190


Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser
        195                 200                 205


Leu Ser Ala Arg Tyr Val
    210


<210>  203
<211>  189
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD8B(CD8-beta)

<400>  203

Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
1               5                   10                  15


Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20                  25                  30


Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35                  40                  45


Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50                  55                  60


Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65                  70                  75                  80


Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85                  90                  95
```

```
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100                 105                 110


Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125


Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140


Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145                 150                 155                 160


Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165                 170                 175


Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Phe Tyr Lys
            180                 185


<210>  204
<211>  497
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature LAG3

<400>  204

Val Pro Val Val Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys
1               5                   10                  15


Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
            20                  25                  30


Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
        35                  40                  45


Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
    50                  55                  60
```

```
Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
65                  70                  75                  80

Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
                85                  90                  95

Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
            100                 105                 110

Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
        115                 120                 125

Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
    130                 135                 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
145                 150                 155                 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
                165                 170                 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
            180                 185                 190

Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser
        195                 200                 205

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
    210                 215                 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
225                 230                 235                 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
                245                 250                 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
            260                 265                 270
```

```
Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
        275                 280                 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
    290                 295                 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
305                 310                 315                 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
                325                 330                 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
            340                 345                 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
        355                 360                 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
    370                 375                 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
385                 390                 395                 400

Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
                405                 410                 415

Leu Pro Ala Gly His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser
            420                 425                 430

Leu Leu Leu Leu Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg
        435                 440                 445

Gln Trp Arg Pro Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro
    450                 455                 460

Pro Gln Ala Gln Ser Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Pro
465                 470                 475                 480
```

```
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln
                485                 490                 495


Leu



<210>  205
<211>  280
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature HAVCR2(TIM-3)

<400>  205

Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
1               5                   10                  15


Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp
            20                  25                  30


Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg
        35                  40                  45


Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn
    50                  55                  60


Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn Val Thr
65                  70                  75                  80


Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile
                85                  90                  95


Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys
            100                 105                 110


Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe Thr Ala Ala Phe Pro
        115                 120                 125
```

```
Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu
    130                 135                 140

Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn
145                 150                 155                 160

Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala
                165                 170                 175

Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu
            180                 185                 190

Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe Lys Trp Tyr Ser His
        195                 200                 205

Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile Ser Leu Ala Asn Leu
    210                 215                 220

Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu Gly Ile Arg Ser Glu
225                 230                 235                 240

Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Glu Pro
                245                 250                 255

Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln Gln Pro Ser Gln Pro
            260                 265                 270

Leu Gly Cys Arg Phe Ala Met Pro
        275                 280
```

<210> 206
<211> 492
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CEACAM1

<400> 206

```
Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                  10                  15

Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
        35                  40                  45

Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
    50                  55                  60

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85                  90                  95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn Asp Thr
                165                 170                 175

Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro Thr Ile
        195                 200                 205
```

```
Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser Leu Ser
    210                 215                 220

Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser Val Thr
            260                 265                 270

Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu Leu Ser
        275                 280                 285

Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val Thr
    290                 295                 300

Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr Gly
305                 310                 315                 320

Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser Glu
                325                 330                 335

Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn Pro Val
            340                 345                 350

Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro Ile
        355                 360                 365

Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn Ala
    370                 375                 380

Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly Ala Ile Ala Gly Ile Val
385                 390                 395                 400

Ile Gly Val Val Ala Leu Val Ala Leu Ile Ala Val Ala Leu Ala Cys
                405                 410                 415
```

```
Phe Leu His Phe Gly Lys Thr Gly Arg Ala Ser Asp Gln Arg Asp Leu
            420                 425                 430


Thr Glu His Lys Pro Ser Val Ser Asn His Thr Gln Asp His Ser Asn
        435                 440                 445


Asp Pro Pro Asn Lys Met Asn Glu Val Thr Tyr Ser Thr Leu Asn Phe
    450                 455                 460


Glu Ala Gln Gln Pro Thr Gln Pro Thr Ser Ala Ser Pro Ser Leu Thr
465                 470                 475                 480


Ala Thr Glu Ile Ile Tyr Ser Glu Val Lys Lys Gln
                485                 490


<210>  207
<211>  222
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature TIGIT

<400>  207

Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys Gly
1               5                   10                  15


Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln Val
            20                  25                  30


Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys Asn
        35                  40                  45


Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala
    50                  55                  60


Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn Asp
65                  70                  75                  80
```

```
Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
                85                  90                  95


Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
            100                 105                 110


Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly Ala Met Ala Ala Thr Leu
        115                 120                 125


Val Val Ile Cys Thr Ala Val Ile Val Val Val Ala Leu Thr Arg Lys
    130                 135                 140


Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp Leu Arg Arg Lys
145                 150                 155                 160


Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro Ser Pro Pro Gly
                165                 170                 175


Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu Cys Gly Glu Gln
            180                 185                 190


Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe Asn Val Leu Ser
        195                 200                 205


Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu Thr Gly
    210                 215                 220


<210>  208
<211>  397
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature PVR(CD155)

<400>  208

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15
```

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

```
Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn Ala Ile Ile Phe Leu Val Leu Gly Ile Leu Val Phe Leu
                325                 330                 335

Ile Leu Leu Gly Ile Gly Ile Tyr Phe Tyr Trp Ser Lys Cys Ser Arg
            340                 345                 350

Glu Val Leu Trp His Cys His Leu Cys Pro Ser Ser Thr Glu His Ala
        355                 360                 365

Ser Ala Ser Ala Asn Gly His Val Ser Tyr Ser Ala Val Ser Arg Glu
    370                 375                 380

Asn Ser Ser Ser Gln Asp Pro Gln Thr Glu Gly Thr Arg
385                 390                 395
```

<210> 209
<211> 507
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> Mature PVRL2(CD112)

<400> 209

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                  10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190
```

```
Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly Ile Ile Gly Gly Ile Ile Ala
                325                 330                 335

Ala Ile Ile Ala Thr Ala Val Ala Ala Thr Gly Ile Leu Ile Cys Arg
            340                 345                 350

Gln Gln Arg Lys Glu Gln Thr Leu Gln Gly Ala Glu Glu Asp Glu Asp
        355                 360                 365

Leu Glu Gly Pro Pro Ser Tyr Lys Pro Pro Thr Pro Lys Ala Lys Leu
    370                 375                 380

Glu Ala Gln Glu Met Pro Ser Gln Leu Phe Thr Leu Gly Ala Ser Glu
385                 390                 395                 400
```

```
His Ser Pro Leu Lys Thr Pro Tyr Phe Asp Ala Gly Ala Ser Cys Thr
                405                 410                 415


Glu Gln Glu Met Pro Arg Tyr His Glu Leu Pro Thr Leu Glu Glu Arg
            420                 425                 430


Ser Gly Pro Leu His Pro Gly Ala Thr Ser Leu Gly Ser Pro Ile Pro
        435                 440                 445


Val Pro Pro Gly Pro Pro Ala Val Glu Asp Val Ser Leu Asp Leu Glu
    450                 455                 460


Asp Glu Glu Gly Glu Glu Glu Glu Glu Tyr Leu Asp Lys Ile Asn Pro
465                 470                 475                 480


Ile Tyr Asp Ala Leu Ser Tyr Ser Ser Pro Ser Asp Ser Tyr Gln Gly
                485                 490                 495


Lys Gly Phe Val Met Ser Arg Ala Met Tyr Val
            500                 505


<210>  210
<211>  318
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD226

<400>  210

Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser
1               5                   10                  15


Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp
            20                  25                  30


Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr
        35                  40                  45
```

```
His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu
    50                  55                  60

Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala
65                  70                  75                  80

Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro
                85                  90                  95

Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe
            100                 105                 110

Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys
        115                 120                 125

Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala
    130                 135                 140

Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr
145                 150                 155                 160

Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln
                165                 170                 175

Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro
            180                 185                 190

Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala
        195                 200                 205

Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu
    210                 215                 220

Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val
225                 230                 235                 240

Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe
                245                 250                 255
```

```
Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser
            260                 265                 270


Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr
        275                 280                 285


Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr
    290                 295                 300


Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
305                 310                 315


<210>  211
<211>  327
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD2

<400>  211

Lys Glu Ile Thr Asn Ala Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp
1               5                   10                  15


Ile Asn Leu Asp Ile Pro Ser Phe Gln Met Ser Asp Asp Ile Asp Asp
            20                  25                  30


Ile Lys Trp Glu Lys Thr Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg
        35                  40                  45


Lys Glu Lys Glu Thr Phe Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys
    50                  55                  60


Asn Gly Thr Leu Lys Ile Lys His Leu Lys Thr Asp Asp Gln Asp Ile
65                  70                  75                  80


Tyr Lys Val Ser Ile Tyr Asp Thr Lys Gly Lys Asn Val Leu Glu Lys
                85                  90                  95
```

```
Ile Phe Asp Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser
            100                 105                 110

Trp Thr Cys Ile Asn Thr Thr Leu Thr Cys Glu Val Met Asn Gly Thr
        115                 120                 125

Asp Pro Glu Leu Asn Leu Tyr Gln Asp Gly Lys His Leu Lys Leu Ser
    130                 135                 140

Gln Arg Val Ile Thr His Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe
145                 150                 155                 160

Lys Cys Thr Ala Gly Asn Lys Val Ser Lys Glu Ser Ser Val Glu Pro
                165                 170                 175

Val Ser Cys Pro Glu Lys Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile
            180                 185                 190

Cys Gly Gly Gly Ser Leu Leu Met Val Phe Val Ala Leu Leu Val Phe
        195                 200                 205

Tyr Ile Thr Lys Arg Lys Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu
    210                 215                 220

Leu Glu Thr Arg Ala His Arg Val Ala Thr Glu Glu Arg Gly Arg Lys
225                 230                 235                 240

Pro His Gln Ile Pro Ala Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln
                245                 250                 255

His Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg
            260                 265                 270

Pro Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro
        275                 280                 285

Pro Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu
    290                 295                 300
```

```
Pro Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn
305                 310                 315                 320


Ser Leu Ser Pro Ser Ser Asn
                325


<210>  212
<211>  154
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD160

<400>  212

Ile Asn Ile Thr Ser Ser Ala Ser Gln Glu Gly Thr Arg Leu Asn Leu
1               5                   10                  15


Ile Cys Thr Val Trp His Lys Lys Glu Glu Ala Glu Gly Phe Val Val
            20                  25                  30


Phe Leu Cys Lys Asp Arg Ser Gly Asp Cys Ser Pro Glu Thr Ser Leu
        35                  40                  45


Lys Gln Leu Arg Leu Lys Arg Asp Pro Gly Ile Asp Gly Val Gly Glu
    50                  55                  60


Ile Ser Ser Gln Leu Met Phe Thr Ile Ser Gln Val Thr Pro Leu His
65                  70                  75                  80


Ser Gly Thr Tyr Gln Cys Cys Ala Arg Ser Gln Lys Ser Gly Ile Arg
                85                  90                  95


Leu Gln Gly His Phe Phe Ser Ile Leu Phe Thr Glu Thr Gly Asn Tyr
            100                 105                 110


Thr Val Thr Gly Leu Lys Gln Arg Gln His Leu Glu Phe Ser His Asn
        115                 120                 125
```

```
Glu Gly Thr Leu Ser Ser Gly Phe Leu Gln Glu Lys Val Trp Val Met
    130                 135                 140


Leu Val Thr Ser Leu Val Ala Leu Gln Ala
145                 150


<210>  213
<211>  248
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD200

<400>  213

Gln Val Gln Val Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Pro
1               5                   10                  15


Ala Ser Leu Lys Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val
            20                  25                  30


Thr Trp Gln Lys Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe
        35                  40                  45


Ser Glu Asn His Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile
    50                  55                  60


Asn Ile Thr Gln Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn
65                  70                  75                  80


Ile Thr Leu Glu Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe
                85                  90                  95


Gly Phe Gly Lys Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln
            100                 105                 110


Pro Ile Val Ser Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile
        115                 120                 125
```

```
Thr Cys Ser Ala Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val
    130                 135                 140


Pro Arg Ser Gly Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn
145                 150                 155                 160


Gly Thr Thr Ser Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn
                165                 170                 175


Gln Val Gly Lys Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val
            180                 185                 190


Thr Asp Phe Lys Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro
        195                 200                 205


Leu Leu Leu Ser Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser
    210                 215                 220


Ile Leu Leu Tyr Trp Lys Arg His Arg Asn Gln Asp Arg Gly Glu Leu
225                 230                 235                 240


Ser Gln Gly Val Gln Lys Met Thr
                245


<210>  214
<211>  297
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD200R1(CD200R)

<400>  214

Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu
1               5                   10                  15


Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys
            20                  25                  30
```

```
Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile
        35                  40                  45

Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr
    50                  55                  60

Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val
65                  70                  75                  80

Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile
                85                  90                  95

Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn
            100                 105                 110

Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr
        115                 120                 125

Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly
    130                 135                 140

Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr
145                 150                 155                 160

Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys
                165                 170                 175

His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His Val Ser His
            180                 185                 190

Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly
        195                 200                 205

Ala Lys Lys Ser Ala Lys Leu Tyr Ile Pro Tyr Ile Ile Leu Thr Ile
    210                 215                 220

Ile Ile Leu Thr Ile Val Gly Phe Ile Trp Leu Leu Lys Val Asn Gly
225                 230                 235                 240
```

Cys Arg Lys Tyr Lys Leu Asn Lys Thr Glu Ser Thr Pro Val Val Glu
245 250 255

Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Asn Asn Pro
260 265 270

Leu Tyr Asp Thr Thr Asn Lys Val Lys Ala Ser Glu Ala Leu Gln Ser
275 280 285

Glu Val Asp Thr Asp Leu His Thr Leu
290 295

<210> 215
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature NC R3 (NKp30)

<400> 215

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

```
Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
            100                 105                 110


His Pro Gln Leu Gly Ala Gly Thr Val Leu Leu Leu Arg Ala Gly Phe
        115                 120                 125


Tyr Ala Val Ser Phe Leu Ser Val Ala Val Gly Ser Thr Val Tyr Tyr
    130                 135                 140


Gln Gly Lys Cys Leu Thr Trp Lys Gly Pro Arg Arg Gln Leu Pro Ala
145                 150                 155                 160


Val Val Pro Ala Pro Leu Pro Pro Pro Cys Gly Ser Ser Ala His Leu
                165                 170                 175


Leu Pro Pro Val Pro Gly Gly
            180


<210>  216
<211>  414
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  VSIG8

<400>  216

Met Arg Val Gly Gly Ala Phe His Leu Leu Leu Val Cys Leu Ser Pro
1               5                   10                  15


Ala Leu Leu Ser Ala Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu
            20                  25                  30


Tyr Leu Ala Glu Gly Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu
        35                  40                  45


Asp Pro Glu Asp Tyr Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln
    50                  55                  60
```

```
Val Asn Ser Asp Pro Ala His His Arg Glu Asn Val Phe Leu Ser Tyr
65                  70                  75                  80

Gln Asp Lys Arg Ile Asn His Gly Ser Leu Pro His Leu Gln Gln Arg
                85                  90                  95

Val Arg Phe Ala Ala Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn
            100                 105                 110

Leu Met Asn Leu Gln Val Ser Asp Thr Ala Thr Tyr Glu Cys Arg Val
        115                 120                 125

Lys Lys Thr Thr Met Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala
    130                 135                 140

Arg Pro Ala Val Pro Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly
145                 150                 155                 160

Asn Asp Val Val Leu Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu
                165                 170                 175

Ser Tyr Lys Trp Ala Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala
            180                 185                 190

Gly Ser Tyr Thr Ser Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln
        195                 200                 205

Glu Ser Phe His Ser Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu
    210                 215                 220

Val Leu Lys Asp Ile Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr
225                 230                 235                 240

Val Ala Asn Asn Val Gly Tyr Ser Val Cys Val Val Glu Val Lys Val
                245                 250                 255

Ser Asp Ser Arg Arg Ile Gly Val Ile Ile Gly Ile Val Leu Gly Ser
            260                 265                 270
```

```
Leu Leu Ala Leu Gly Cys Leu Ala Val Gly Ile Trp Gly Leu Val Cys
        275                 280                 285


Cys Cys Cys Gly Gly Ser Gly Ala Gly Gly Ala Arg Gly Ala Phe Gly
    290                 295                 300


Tyr Gly Asn Gly Gly Gly Val Gly Gly Gly Ala Cys Gly Asp Leu Ala
305                 310                 315                 320


Ser Glu Ile Arg Glu Asp Ala Val Ala Pro Gly Cys Lys Ala Ser Gly
                325                 330                 335


Arg Gly Ser Arg Val Thr His Leu Leu Gly Tyr Pro Thr Gln Asn Val
            340                 345                 350


Ser Arg Ser Leu Arg Arg Lys Tyr Ala Pro Pro Pro Cys Gly Gly Pro
        355                 360                 365


Glu Asp Val Ala Leu Ala Pro Cys Thr Ala Ala Ala Ala Cys Glu Ala
    370                 375                 380


Gly Pro Ser Pro Val Tyr Val Lys Val Lys Ser Ala Glu Pro Ala Asp
385                 390                 395                 400


Cys Ala Glu Gly Pro Val Gln Cys Lys Asn Gly Leu Leu Val
                405                 410


<210>  217
<211>  393
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature VSIG8

<400>  217

Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1               5                   10                  15
```

```
Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
            20                  25                  30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
        35                  40                  45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
    50                  55                  60

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65                  70                  75                  80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
                85                  90                  95

Val Ser Asp Thr Ala Thr Tyr Glu Cys Arg Val Lys Lys Thr Thr Met
            100                 105                 110

Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala Arg Pro Ala Val Pro
        115                 120                 125

Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn Asp Val Val Leu
    130                 135                 140

Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu Ser Tyr Lys Trp Ala
145                 150                 155                 160

Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala Gly Ser Tyr Thr Ser
                165                 170                 175

Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu Ser Phe His Ser
            180                 185                 190

Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu Val Leu Lys Asp Ile
        195                 200                 205

Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr Val Ala Asn Asn Val
    210                 215                 220
```

```
Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser Asp Ser Arg Arg
225                 230                 235                 240


Ile Gly Val Ile Ile Gly Ile Val Leu Gly Ser Leu Leu Ala Leu Gly
                245                 250                 255


Cys Leu Ala Val Gly Ile Trp Gly Leu Val Cys Cys Cys Cys Gly Gly
            260                 265                 270


Ser Gly Ala Gly Gly Ala Arg Gly Ala Phe Gly Tyr Gly Asn Gly Gly
        275                 280                 285


Gly Val Gly Gly Gly Ala Cys Gly Asp Leu Ala Ser Glu Ile Arg Glu
    290                 295                 300


Asp Ala Val Ala Pro Gly Cys Lys Ala Ser Gly Arg Gly Ser Arg Val
305                 310                 315                 320


Thr His Leu Leu Gly Tyr Pro Thr Gln Asn Val Ser Arg Ser Leu Arg
                325                 330                 335


Arg Lys Tyr Ala Pro Pro Pro Cys Gly Gly Pro Glu Asp Val Ala Leu
            340                 345                 350


Ala Pro Cys Thr Ala Ala Ala Ala Cys Glu Ala Gly Pro Ser Pro Val
        355                 360                 365


Tyr Val Lys Val Lys Ser Ala Glu Pro Ala Asp Cys Ala Glu Gly Pro
    370                 375                 380


Val Gln Cys Lys Asn Gly Leu Leu Val
385                 390


<210>  218
<211>  242
<212>  PRT
<213>  Homo sapiens


<220>
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<221> MISC_FEATURE
<223> VSIG8 ECD

<400> 218

```
Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1               5                  10                  15

Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
            20                  25                  30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
        35                  40                  45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
    50                  55                  60

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65                  70                  75                  80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
                85                  90                  95

Val Ser Asp Thr Ala Thr Tyr Glu Cys Arg Val Lys Lys Thr Thr Met
            100                 105                 110

Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala Arg Pro Ala Val Pro
        115                 120                 125

Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn Asp Val Val Leu
    130                 135                 140

Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu Ser Tyr Lys Trp Ala
145                 150                 155                 160

Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala Gly Ser Tyr Thr Ser
                165                 170                 175

Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu Ser Phe His Ser
            180                 185                 190
```

Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu Val Leu Lys Asp Ile
195 200 205

Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr Val Ala Asn Asn Val
210 215 220

Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser Asp Ser Arg Arg
225 230 235 240

Ile Gly

<210> 219
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 Signal Peptide

<400> 219

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

<210> 220
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> IgGkappa light chain

<400> 220

Met Asp Met Arg Val Leu Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys
1 5 10 15

Phe Pro Gly Ala Arg Cys
20

<210> 221
<211> 18
<212> PRT

<213> Artificial Sequence

<220>
<223> HSA signal peptide

<400> 221

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 222
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig kappa light chain

<400> 222

Met Asp Met Arg Ala Pro Ala Gly Ile Phe Gly Phe Leu Leu Val Leu
1 5 10 15

Phe Pro Gly Tyr Arg Ser
20

<210> 223
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Human azurocidin preprotein signal sequence

<400> 223

Met Thr Arg Leu Thr Val Leu Ala Leu Leu Ala Gly Leu Leu Ala Ser
1 5 10 15

Ser Arg Ala

<210> 224

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 224

Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 225
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 225

Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1 5 10 15

Val Gln Cys

<210> 226
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 226

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser

<210> 227
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 227

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 228
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 228

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
1 5 10 15

Val Gln Ser

<210> 229
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 229

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 230
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 230

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1   5   10   15

Val Gln Cys

<210> 231
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 231

Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
1   5   10   15

Leu Val Ala Ala Pro Arg Trp Val Leu Ser
            20   25

<210> 232
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG Kappa light chain signal seqeunce

<400> 232

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1   5   10   15

Leu Ser Gly Ala Arg Cys
            20

<210> 233
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG Kappa light chain signal seqeunce

<400> 233

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1   5   10   15

Ala Gln Pro Ala Met Ala
            20

<210> 234
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Gaussia luciferase

<400> 234

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1   5   10   15

Ala

<210> 235
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Human albumin

<400> 235

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala

1 5 10 15

Tyr Ser

<210> 236
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Human chymotrypsinogen

<400> 236

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly

<210> 237
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Human interleukin-2

<400> 237

Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val
1 5 10

<210> 238
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human trysinogen-2

<400> 238

Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala
1 5 10 15

<210> 239
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> IgV-IgV linker

<400> 239

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 240
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> IgV-Fc linker 1

<400> 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 241
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IgV-Fc linker 2

<400> 241

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala
1 5 10

<210> 242
<211> 71
<212> PRT
<213> Artificial Seqeunce

<220>
<223> CD8-derived hinge and transmembrane domain

<400> 242

```
Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
1               5                   10                  15


Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Ser Arg Pro Ala
            20                  25                  30


Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Ser Asp Ile
        35                  40                  45


Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
    50                  55                  60


Leu Val Ile Thr Leu Tyr Cys
65                  70


<210>  243
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD3zeta intracellular signaling domain

<400>  243

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1               5                   10                  15


Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20                  25                  30


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35                  40                  45


Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50                  55                  60


Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65                  70                  75                  80


Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
```

85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 244
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v1

<400> 244

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Asn Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val Asn Gly Glu Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 245
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v2

<400> 245

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Thr Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 246
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v3

<400> 246

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Glu Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 247
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v4

<400> 247

Phe Thr Val Thr Val Ser Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Thr Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 248
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v5

<400> 248

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 249
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v6

<400> 249

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 250

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v7

<400> 250

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 251
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v8

<400> 251

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser

1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 252
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v9

<400> 252

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 253
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v10

<400> 253

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 254
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v11

<400> 254

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 255
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v12

<400> 255

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35   40   45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Gly Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 256
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v13

<400> 256

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Ser Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 257
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v14

<400> 257

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln

35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 258
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v15

<400> 258

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 259
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v16

<400> 259

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 260
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v17

<400> 260

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 261
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v18

<400> 261

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 262
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v19

<400> 262

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Glu Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 263
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v20

<400> 263

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Ile Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asn Ile Ile Gln
        35   40   45

Phe Val Arg Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 264
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v21

<400> 264

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln Arg Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 265
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v22

<400> 265

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 266
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v23

<400> 266

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Gly
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Glu Asp Gln Leu Pro Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 267
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v24

<400> 267

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 268
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v25

<400> 268

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 269
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v26

<400> 269

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Val Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val

100 105 110

Asn Ala

<210> 270
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v27

<400> 270

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 271
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v28

<400> 271

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Gly Met Glu Val Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 272
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v29

<400> 272

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Ser Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 273
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v30

<400> 273

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 274
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v31

<400> 274

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 275
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v32

<400> 275

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 276

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v33

<400> 276

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 277
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v34

<400> 277

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser

1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 278
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v35

<400> 278

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 279
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v36

<400> 279

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Met Lys Val
100 105 110

Asn Ala

<210> 280
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v37

<400> 280

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 281
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v38

<400> 281

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Pro Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 282
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v39

<400> 282

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 283
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v40

<400> 283

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Arg Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 284
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v41

<400> 284

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 285
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v42

<400> 285

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Val Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 286
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v43

<400> 286

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Gly Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 287
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v44

<400> 287

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 288
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v45

<400> 288

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 289
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v46

<400> 289

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 290
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v47

<400> 290

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 291
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v48

<400> 291

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 292
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v49

<400> 292

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala
```

<210> 293
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v50

<400> 293

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 294
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v51

<400> 294

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 295
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v52

<400> 295

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Ala Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val Tyr Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val

100 105 110

Asn Ala

<210> 296
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v53

<400> 296

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 297
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v54

<400> 297

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 298
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v55

<400> 298

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 299
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v56

<400> 299

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35   40   45

Phe Val His Gly Gly Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 300
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v57

<400> 300

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 301
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v58

<400> 301

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 302

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v59

<400> 302

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Gly Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Asp Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 303
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v60

<400> 303

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser

1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
100 105 110

Val Asn Ala
115

<210> 304
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v61

<400> 304

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 305
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v62

<400> 305

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 306
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v63

<400> 306

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Ile Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Ile Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Lys Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 307
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v64

<400> 307

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 308
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v65

<400> 308

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 309
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> PD-L1 IgV wildtype

<400> 309

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala
```

<210> 310
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD155 IgV

<400> 310

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60
```

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 311
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 ECD

<400> 311

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Ser
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 312
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 ECD

<400> 312

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 313
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v3 ECD

<400> 313

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Pro Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 314
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v4 ECD

<400> 314

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 315
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v5 ECD

<400> 315

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Val Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 316
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v6 ECD

<400> 316

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 317
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v7 ECD

<400> 317

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 318

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v8 ECD

<400> 318

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Pro Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 319
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 ECD

<400> 319

```
Trp Pro Pro Pro Gly Thr Glu Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 320
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v10 ECD

<400> 320

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Asp Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 321
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v11 ECD

<400> 321

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Pro Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 322
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 ECD

<400> 322

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Leu Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 323
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v14 ECD

<400> 323

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 324
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v15 ECD

<400> 324

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu His Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 325
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v16 ECD

<400> 325

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg

35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 326
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v17 ECD

<400> 326

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

```
Val Glu Pro Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 327
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v18 ECD

<400> 327

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Pro Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 328
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v19 ECD

<400> 328

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu His Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 329
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v20 ECD

<400> 329

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 330
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v21 ECD

<400> 330

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Ala Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 331
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 ECD

<400> 331

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Lys Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 332
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 IgV

<400> 332

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Ser Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 333
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 IgV

<400> 333

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 334
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v3 IgV

<400> 334

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Pro Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115
```

<210> 335
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v4 IgV

<400> 335

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
```

20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 336
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v5 IgV

<400> 336

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Val Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 337
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v6 IgV

<400> 337

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val

100 105 110

Asp Ile Trp Leu
115

<210> 338
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v7 IgV

<400> 338

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 339
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v8 IgV

<400> 339

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Pro Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 340
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 IgV

<400> 340

Pro Gly Thr Glu Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1   5   10   15

```
Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  341
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v10 IgV

<400>  341

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
```

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Asp Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 342
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v11 IgV

<400> 342

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Pro Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 343
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 IgV

<400> 343

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Leu Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 344

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v14 IgV

<400> 344

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 345
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v15 IgV

<400> 345

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu His Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 346
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v16 IgV

<400> 346

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

```
Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  347
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v17 IgV

<400>  347

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Val Glu Pro
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
```

85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 348
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v18 IgV

<400> 348

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Pro Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 349
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v19 IgV

<400> 349

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu His Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 350
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v20 IgV

<400> 350

```
Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  351
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v21 IgV

<400>  351

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
```

35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Ala
100 105 110

Asp Ile Trp Leu
115

<210> 352
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 IgV

<400> 352

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Lys Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

```
Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  353
<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD155 IgV wildtype

<400>  353

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110
```

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 354
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 IgV

<400> 354

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Ser
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 355
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 IgV

<400> 355

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 356
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v3 IgV

<400> 356

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln

20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Pro Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 357
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v4 IgV

<400> 357

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  358
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v5 IgV

<400>  358

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Val Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 359
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v6 IgV

<400> 359

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 360
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v7 IgV

<400> 360

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 361
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v8 IgV

<400> 361

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Pro Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 362
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 IgV

<400> 362

Trp Pro Pro Pro Gly Thr Glu Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 363
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v10 IgV

<400> 363

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Asp Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  364
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v11 IgV

<400>  364

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Pro Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  365
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<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 IgV

<400> 365

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Leu Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 366
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v14 IgV

<400> 366

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 367
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v15 IgV

<400> 367

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu His Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  368
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v16 IgV

<400>  368

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Cys Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
```

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 369
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v17 IgV

<400> 369

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Val Glu Pro Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 370
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v18 IgV

<400> 370

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Pro Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 371
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v19 IgV

<400> 371

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu His Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  372
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v20 IgV

<400>  372

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Ser Gly Ser Met Val Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 373
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v21 IgV

<400> 373

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Ala Asp Ile Trp Leu Arg Val Leu
115 120

<210> 374
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 IgV

<400> 374

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Lys Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 375
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 ECD

<400> 375

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 376
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 ECD

<400> 376

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 377
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 ECD

<400> 377

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 378
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v26 ECD

<400> 378

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 379
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v27 ECD

<400> 379

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 380
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 ECD

<400> 380

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 381
<211> 323
<212> PRT
<213> Artificial Seqeunce

<220>
<223> CD155 v39 ECD

<400> 381

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  382
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v30 ECD

<400>  382

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

```
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
```

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 383
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 ECD

<400> 383

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 384
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 ECD

<400> 384

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 385
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v33 ECD

<400> 385

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 386
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v34 ECD

<400> 386

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 387
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 ECD

<400> 387

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

```
Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  388
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v36 ECD

<400>  388

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Gln Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
```

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 389
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 ECD

<400> 389

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 390
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v38 ECD

<400> 390

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 391

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v39 ECD

<400> 391

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 392
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v40 ECD

<400> 392

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 393
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v41 ECD

<400> 393

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 394
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 ECD

<400> 394

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 395
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 ECD

<400> 395

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 396
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 ECD

<400> 396

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 397
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v45 ECD

<400> 397

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Met Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

```
Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  398
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v46 ECD

<400>  398

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
```

```
        35                  40                  45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
```

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 399
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v47 ECD

<400> 399

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 400
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v48 ECD

<400> 400

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Leu Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 401
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v49 ECD

<400> 401

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 402
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 ECD

<400> 402

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 403
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 ECD

<400> 403

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 404
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v52 ECD

<400> 404

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 405
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v53 ECD

<400> 405

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 406
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v54 ECD

<400> 406

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 407
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 ECD

<400> 407

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Leu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  408
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v56 ECD

<400>  408

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

```
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
```

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 409
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 ECD

<400> 409

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 410
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v58 ECD

<400> 410

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 411
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v59 ECD

<400> 411

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 412
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v60 ECD

<400> 412

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Val Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
```

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 413
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 ECD

<400> 413

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 414
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 ECD

<400> 414

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 415
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 ECD

<400> 415

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 416
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 ECD

<400> 416

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 417

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v65 ECD

<400> 417

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  418
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v66 ECD

<400>  418

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 419
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v67 ECD

<400> 419

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 420
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 ECD

<400> 420

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 421
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v69 ECD

<400> 421

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 422
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v70 ECD

<400> 422

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Ala His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
    50                  55                  60


Asn Tyr Leu Glu Ser Lys Arg Leu Gly Phe Val Ala Ala Gly Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 423
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v71 ECD

<400> 423

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
    50                  55                  60

Asn Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

```
Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  424
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v72 ECD

<400>  424

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
```

```
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
```

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 425
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v73 ECD

<400> 425

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

Asn Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 426
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v74 ECD

<400> 426

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 427
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v75 ECD

<400> 427

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 428
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 ECD

<400> 428

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 429
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 ECD

<400> 429

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 430
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v78 ECD

<400> 430

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

His Tyr His Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 431
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v79 ECD

<400> 431

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 432
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 ECD

<400> 432

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gly Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 433
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v81 ECD

<400> 433

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Pro Val Thr His Val Pro Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  434
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v82 ECD

<400>  434

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

```
            20                  25                  30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
```

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 435
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 ECD

<400> 435

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Val Arg Leu Ser
65                  70                  75                  80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 436
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 ECD

<400> 436

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Ser Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 437
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v85 ECD

<400> 437

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 438
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v86 ECD

<400> 438

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr His Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
```

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 439
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 ECD

<400> 439

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45

His Gly Glu Lys Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 440
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 ECD

<400> 440

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 441
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 ECD

<400> 441

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 442
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 ECD

<400> 442

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Asp
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 443

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v91 ECD

<400> 443

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Thr Phe His Gln Ser Gln Gly Pro
    50                  55                  60


Tyr Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  444
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v92 ECD

<400>  444

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 445
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 445

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro
    50                  55                  60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 446
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 446

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Met Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 447
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 447

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Ala Gly Gln Leu Gly Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 448
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 ECD

<400> 448

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val His Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Ile Trp Ala Arg
        35                  40                  45


His Gly Glu Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro
    50                  55                  60


Asp Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 449
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v97 ECD

<400> 449

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Val Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Leu His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Trp Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

```
Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 450
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v98 ECD

<400> 450

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ile Trp Ala Arg
```

```
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
```

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 451
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v99 ECD

<400> 451

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Gly Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Ala Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 452
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v100 ECD

<400> 452

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val His Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr Arg Val Gly Gln Leu Ile Trp Ala Arg
35 40 45

His Gly Glu Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro
50 55 60

Asp Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Tyr Phe Leu Thr His Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 453
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v101 ECD

<400> 453

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Val Val Thr His Val Gly Gln Leu Gly Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 454
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 ECD

<400> 454

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 455
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 ECD

<400> 455

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 456
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v104 ECD

<400> 456

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gly Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 457
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v105 ECD

<400> 457

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asn Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 458
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 ECD

<400> 458

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65                  70                  75                  80


Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 459
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v107 ECD

<400> 459

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Thr Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  460
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v108 ECD

<400>  460

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

```
            20                  25                  30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Gly Gly Ser Met Ala Ala Phe His Gln Thr Met Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
```

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 461
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 ECD

<400> 461

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 462
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 ECD

<400> 462

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
50 55 60

Thr Tyr Ser Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Gly Ser Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser

100 105 110

Arg Ser Val Asn Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 463
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v111 ECD

<400> 463

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Pro Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Gly Gln Gly Pro
50 55 60

His Tyr Glu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asn Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 464
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v112 ECD

<400> 464

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
        35                  40                  45


His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
    50                  55                  60


Thr Tyr Ser Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Ala Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
```

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 465
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 ECD

<400> 465

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
        35                  40                  45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
    50                  55                  60

Thr Tyr Ser Gly Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Gly Ser Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 466
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v114 ECD

<400> 466

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 467
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 ECD

<400> 467

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 468
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 ECD

<400> 468

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 469

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v117 ECD

<400> 469

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ser Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Lys Gln Gly Pro
    50                  55                  60


Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 470
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v118 ECD

<400> 470

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 471
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v119 ECD

<400> 471

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Val Phe Gly Leu Arg Ala Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 472
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 IgV

<400> 472

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly

85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 473
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 IgV

<400> 473

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 474
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 IgV

<400> 474

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 475
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v26 IgV

<400> 475

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  476
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v27 IgV

<400>  476

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
```

35 40 45

Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu Arg Val Leu
115

<210> 477
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 IgV

<400> 477

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

```
Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  478
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v29 IgV

<400>  478

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
```

115

<210> 479
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v30 IgV

<400> 479

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 480
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 IgV

<400> 480

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 481
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 IgV

<400> 481

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 482
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v33 IgV

<400> 482

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 483
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v34 IgV

<400> 483

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 484
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 IgV

<400> 484

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 485
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v36 IgV

<400> 485

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Gln Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 486
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 IgV

<400> 486

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn

20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 487
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v38 IgV

<400> 487

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

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Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  488
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v39 IgV

<400>  488

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
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100 105 110

Asp Ile Trp Leu
115

<210> 489
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v40 IgV

<400> 489

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 490
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v41 IgV

<400> 490

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 491
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 IgV

<400> 491

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 492
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 IgV

<400> 492

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35   40   45

Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 493
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 IgV

<400> 493

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 494
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v45 IgV

<400> 494

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Met Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 495

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v46 IgV

<400> 495

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Gln Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 496
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v47 IgV

<400> 496

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 497
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v48 IgV

<400> 497

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Gln Gly Ser Met Ala Leu Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 498
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v49 IgV

<400> 498

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly

85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 499
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 IgV

<400> 499

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 500
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 IgV

<400> 500

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 501
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v52 IgV

<400> 501

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Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Arg Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  502
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v53 IgV

<400>  502

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
```

35 40 45

Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 503
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v54 IgV

<400> 503

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Arg Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 504
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 IgV

<400> 504

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Leu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu

115

<210> 505
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v56 IgV

<400> 505

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Met Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 506
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 IgV

<400> 506

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 507
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v58 IgV

<400> 507

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35   40   45

Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 508
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v59 IgV

<400> 508

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 509
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v60 IgV

<400> 509

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Val Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 510
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 IgV

<400> 510

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35   40   45

Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 511
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 IgV

<400> 511

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 512
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 IgV

<400> 512

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn

20 25 30

Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Glu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 513
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 IgV

<400> 513

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Met Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

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Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  514
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v65 IgV

<400>  514

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
```

100 105 110

Asp Ile Trp Leu
115

<210> 515
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v66 IgV

<400> 515

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 516
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v67 IgV

<400> 516

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 517
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 IgV

<400> 517

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

```
Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  518
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v69 IgV

<400>  518

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
```

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 519
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v70 IgV

<400> 519

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Ala His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro Asn Tyr Leu
50 55 60

Glu Ser Lys Arg Leu Gly Phe Val Ala Ala Gly Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 520
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v71 IgV

<400> 520

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro Asn Tyr Leu
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 521

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v72 IgV

<400> 521

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 522
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v73 IgV

<400> 522

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro Asn Tyr Leu
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 523
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v74 IgV

<400> 523

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 524
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v75 IgV

<400> 524

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly

85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 525
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 IgV

<400> 525

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 526
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 IgV

<400> 526

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 527
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v78 IgV

<400> 527

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Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro His Tyr His
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  528
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v79 IgV

<400>  528

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
```

35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Glu Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 529
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 IgV

<400> 529

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Gly Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser Pro Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Tyr
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 530
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v81 IgV

<400> 530

Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Pro Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Glu Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu

115

<210> 531
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v82 IgV

<400> 531

Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Tyr
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 532
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 IgV

<400> 532

Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Val Arg Leu Ser Pro Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Tyr
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 533
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 IgV

<400> 533

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Ser Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser Pro Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Tyr
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 534
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v85 IgV

<400> 534

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 535
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v86 IgV

<400> 535

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr His Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 536
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 IgV

<400> 536

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35   40   45

Lys Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 537
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 IgV

<400> 537

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35   40   45

Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 538
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 IgV

<400> 538

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn

20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 539
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 IgV

<400> 539

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro Trp Tyr Ala
50 55 60

```
Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Asp Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  540
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v91 IgV

<400>  540

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Thr Phe His Gln Ser Gln Gly Pro Tyr Tyr Ala
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
```

100 105 110

Asp Ile Trp Leu
115

<210> 541
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v92 IgV

<400> 541

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 542
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v93 IgV

<400> 542

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro Trp Tyr Ala
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 543
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 IgV

<400> 543

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

```
Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Met Gln Gly Pro Trp Tyr Ala
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  544
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v95 IgV

<400>  544

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Ala Gly Gln Leu Gly Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
```

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 545
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 IgV

<400> 545

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val His Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Gly Gln Leu Ile Trp Ala Arg His Gly Glu
35 40 45

Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro Asp Tyr Ser
50 55 60

Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 546
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v97 IgV

<400> 546

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Gly Gln Leu Val Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Leu His Gln Thr Gln Gly Pro Ser Tyr Trp
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 547

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v98 IgV

<400> 547

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Ile Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 548
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v99 IgV

<400> 548

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Gly Gln Leu Gly Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Asn Phe Ala Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 549
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v100 IgV

<400> 549

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val His Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr Arg Val Gly Gln Leu Ile Trp Ala Arg His Gly Glu
35 40 45

```
Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro Asp Tyr Ser
    50                  55                  60


Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Tyr Phe Leu Thr His Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  550
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v101 IgV

<400>  550

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Val Val Thr His Val Gly Gln Leu Gly Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
```

85 90 95

Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 551
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 IgV

<400> 551

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 552
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 IgV

<400> 552

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 553
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v104 IgV

<400> 553

```
Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Pro Val Thr His Val Leu Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Gly Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Glu Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  554
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v105 IgV

<400>  554

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Arg Gly Glu
```

35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asn Ile Trp Leu
115

<210> 555
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 IgV

<400> 555

Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser Pro Glu Leu
65 70 75 80

```
Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  556
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v107 IgV

<400>  556

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Thr Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
```

115

<210> 557
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v108 IgV

<400> 557

Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Gly Gly Ser Met Ala Ala Phe His Gln Thr Met Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 558
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 IgV

<400> 558

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 559
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 IgV

<400> 559

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

```
Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg His Gly Glu
        35                  40                  45


Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro Thr Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Gly Ser Gly
                85                  90                  95


Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asn Ile Trp Leu
        115


<210>  560
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v111 IgV

<400>  560

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Pro Gln Leu Gln Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Gly Gln Gly Pro His Tyr Glu
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
```

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asn Ile Trp Leu
115

<210> 561
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v112 IgV

<400> 561

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg His Gly Glu
35 40 45

Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro Thr Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Ala Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 562
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 IgV

<400> 562

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg His Gly Glu
        35   40   45

Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro Thr Tyr Ser
    50   55   60

Gly Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Gly Ser Gly
                85   90   95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 563
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v114 IgV

<400> 563

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
        35                  40                  45


Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115
```

<210> 564
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 IgV

<400> 564

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
```

20 25 30

Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg His Gly Glu
35 40 45

Glu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 565
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 IgV

<400> 565

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 566
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v117 IgV

<400> 566

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Ser Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Lys Gln Gly Pro Trp Tyr Ala
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val

100 105 110

Asp Ile Trp Leu
115

<210> 567
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v118 IgV

<400> 567

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 568
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v119 IgV

<400> 568

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Trp Tyr Ala
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Val Phe Gly Leu Arg Ala Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 569
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 IgV

<400> 569

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 570
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 IgV

<400> 570

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35   40   45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 571
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 IgV

<400> 571

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 572
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v26 IgV

<400> 572

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 573

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v27 IgV

<400> 573

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 574
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 IgV

<400> 574

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 575
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v29 IgV

<400> 575

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 576
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v30 IgV

<400> 576

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 577
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 IgV

<400> 577

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 578
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 IgV

<400> 578

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Trp Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 579
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v33 IgV

<400> 579

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Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  580
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v34 IgV

<400>  580

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 581
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 IgV

<400> 581

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 582
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v36 IgV

<400> 582

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gln Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 583
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 IgV

<400> 583

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 584
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v38 IgV

<400> 584

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 585
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v39 IgV

<400> 585

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 586
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v40 IgV

<400> 586

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 587
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v41 IgV

<400> 587

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 588
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 IgV

<400> 588

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 589
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 IgV

<400> 589

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35   40   45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 590
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 IgV

<400> 590

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln

20 25 30

Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 591
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v45 IgV

<400> 591

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
50 55 60

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Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  592
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v46 IgV

<400>  592

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 593
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v47 IgV

<400> 593

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 594
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v48 IgV

<400> 594

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Gln Gly Ser Met Ala Leu Phe His Gln Thr Tyr Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 595
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v49 IgV

<400> 595

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 596
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 IgV

<400> 596

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 597
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 IgV

<400> 597

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  598
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v52 IgV

<400>  598

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Trp Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  599
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<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v53 IgV

<400> 599

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 600
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v54 IgV

<400> 600

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 601
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 IgV

<400> 601

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 602
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v56 IgV

<400> 602

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 603
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 IgV

<400> 603

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 604
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v58 IgV

<400> 604

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 605
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v59 IgV

<400> 605

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Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  606
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v60 IgV

<400>  606

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Val Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 607
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 IgV

<400> 607

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Arg Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 608
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 IgV

<400> 608

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 609
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 IgV

<400> 609

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Leu Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 610
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 IgV

<400> 610

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Cys Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Met Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 611
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v65 IgV

<400> 611

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  612
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v66 IgV

<400>  612

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ala Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
```

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 613
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v67 IgV

<400> 613

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Leu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 614
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 IgV

<400> 614

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Asn Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 615
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v69 IgV

<400> 615

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 616
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v70 IgV

<400> 616

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln

20 25 30

Val Pro Asn Met Glu Val Ala His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

Asn Tyr Leu Glu Ser Lys Arg Leu Gly Phe Val Ala Ala Gly Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 617
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v71 IgV

<400> 617

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

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Asn Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  618
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v72 IgV

<400>  618

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 619
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v73 IgV

<400> 619

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

Asn Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Pro Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 620
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v74 IgV

<400> 620

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 621
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v75 IgV

<400> 621

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 622
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 IgV

<400> 622

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 623
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 IgV

<400> 623

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  624
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v78 IgV

<400>  624

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Arg Gln Gly Pro
    50                  55                  60


His Tyr His Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  625
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<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v79 IgV

<400> 625

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 626
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 IgV

<400> 626

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Ser Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gly Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 627
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v81 IgV

<400> 627

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Pro Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 628
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v82 IgV

<400> 628

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu

85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 629
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 IgV

<400> 629

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Val Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 630
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 IgV

<400> 630

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Ser Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Tyr Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Asn
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 631
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v85 IgV

<400> 631

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Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  632
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v86 IgV

<400>  632

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr His Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 633
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 IgV

<400> 633

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Lys Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 634
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 IgV

<400> 634

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 635
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 IgV

<400> 635

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 636
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 IgV

<400> 636

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Asp
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 637
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v91 IgV

<400> 637

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Thr Phe His Gln Ser Gln Gly Pro
50 55 60

Tyr Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 638
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v92 IgV

<400> 638

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 639
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v93 IgV

<400> 639

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Met Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 640
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 IgV

<400> 640

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Met Gln Gly Pro
    50   55   60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 641
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v95 IgV

<400> 641

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Ala Gly Gln Leu Gly Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120
```

<210> 642
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 IgV

<400> 642

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val His Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Ile Trp Ala Arg
35 40 45

His Gly Glu Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro
50 55 60

Asp Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 643
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v97 IgV

<400> 643

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Val Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Leu His Gln Thr Gln Gly Pro
50 55 60

```
Ser Tyr Trp Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  644
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v98 IgV

<400>  644

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ile Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 645
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v99 IgV

<400> 645

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Gly Gln Leu Gly Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Ala Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 646
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v100 IgV

<400> 646

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val His Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr Arg Val Gly Gln Leu Ile Trp Ala Arg
35 40 45

His Gly Glu Thr Arg His Met Ala Leu Phe Glu Gln Ser Gln Gly Pro
50 55 60

Asp Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Tyr Phe Leu Thr His Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 647
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v101 IgV

<400> 647

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Val Val Thr His Val Gly Gln Leu Gly Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Asn Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 648
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 IgV

<400> 648

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 649
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 IgV

<400> 649

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 650
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v104 IgV

<400> 650

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Leu Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Gly Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 651

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v105 IgV

<400> 651

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asn Ile Trp Leu Arg Val Leu
115 120

<210> 652
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 IgV

<400> 652

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln

1 5 10 15

Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Met Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Ser
65 70 75 80

Pro Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 653
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v107 IgV

<400> 653

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Thr Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  654
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v108 IgV

<400>  654

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Arg Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Tyr Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Pro Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Gly Gly Ser Met Ala Ala Phe His Gln Thr Met Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
```

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 655
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 IgV

<400> 655

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Tyr Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 656
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 IgV

<400> 656

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
50 55 60

Thr Tyr Ser Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Gly Ser Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asn Ile Trp Leu Arg Val Leu
115 120

<210> 657
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v111 IgV

<400> 657

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Pro Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Gly Gln Gly Pro
    50                  55                  60


His Tyr Glu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asn Ile Trp Leu Arg Val Leu
        115                 120


<210>  658
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v112 IgV

<400>  658

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
```

35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
50 55 60

Thr Tyr Ser Glu Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Ala Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 659
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 IgV

<400> 659

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr Thr Met Ser Gln Leu Thr Trp Val Arg
35 40 45

His Gly Glu Gln Gly Ser Met Ala Val Phe His Gln Thr Leu Gly Pro
50 55 60

Thr Tyr Ser Gly Ser Lys Arg Leu Arg Phe Val Ala Ala Arg Leu Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Gly Ser Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  660
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v114 IgV

<400>  660

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
        35                  40                  45


His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
```

115 120

<210> 661
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 IgV

<400> 661

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Pro Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Gln Trp Ala Arg
35 40 45

His Gly Glu Glu Gly Ser Met Ala Val Phe His Gln Thr Phe Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 662
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 IgV

<400> 662

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 663
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v117 IgV

<400> 663

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ser Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Lys Gln Gly Pro
    50                  55                  60


Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  664
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v118 IgV

<400>  664

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
```

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 665
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v119 IgV

<400> 665

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Val Phe Gly Leu Arg Ala Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 666
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD112 IgV

<400> 666

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 667
<211> 329
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v1 ECD

<400> 667

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Asp Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe

180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 668
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v2 ECD

<400> 668

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

```
Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Gly
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Gly
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Ser Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220
```

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 669
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v3 ECD

<400> 669

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe

260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 670
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v4 ECD

<400> 670

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
85 90 95

```
His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ile
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300
```

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 671
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v5 ECD

<400> 671

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln

130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 672

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v6 ECD

<400> 672

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175
```

```
Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 673
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v7 ECD

<400> 673

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
```

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
```

210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 674
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v8 ECD

<400> 674

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn Tyr
35 40 45

```
Gln Asn Val Ala Ala Ser His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255
```

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 675
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 ECD

<400> 675

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val

290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 676
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 ECD

<400> 676

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Ser Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

```
Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 677
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 ECD

<400> 677

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr

165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 678
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v12 ECD

<400> 678

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205
```

```
Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  679
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v13 ECD

<400>  679

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser

245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 680
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v14 ECD

<400> 680

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

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Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Thr Pro
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285
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Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  681
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v15 ECD

<400>  681

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Ser Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
```

115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly

325

<210> 682
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v16 ECD

<400> 682

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

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Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 683
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v17 ECD

<400> 683

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Ser Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
```

195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 684
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v18 ECD

<400> 684

Gln Asp Val Arg Val Gln Val Leu Ser Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Ser His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240
```

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 685
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v19 ECD

<400> 685

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys His Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser

```
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
```

275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 686
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v20 ECD

<400> 686

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Leu Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

```
Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320
```

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 687
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v21 ECD

<400> 687

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Asp Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro

145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 688
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v22 ECD

<400> 688

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Pro Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190
```

```
Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  689
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v23 ECD

<400>  689

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
```

```
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Ala Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
```

225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 690
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v24 ECD

<400> 690

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Ser Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270
```

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 691
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 ECD

<400> 691

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val

100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn

305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 692
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v26 ECD

<400> 692

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

```
Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325

<210>  693
<211>  329
<212>  PRT
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<213> Artificial Sequence

<220>
<223> CD112 v27 ECD

<400> 693

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65                  70                  75                  80


Thr Gly Gln Gly Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Ser Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
```

180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 694
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v28 ECD

<400> 694

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

```
Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45

Gln Asn Val Ala Ala Leu His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220
```

```
Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  695
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v29 ECD

<400>  695

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
```

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe

260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 696
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v30 ECD

<400> 696

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
85 90 95

```
His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300
```

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 697
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v31 ECD

<400> 697

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln

130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 698

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v32 ECD

<400> 698

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175
```

```
Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  699
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v33 ECD

<400>  699

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
```

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Met Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
```

210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 700
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 ECD

<400> 700

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255
```

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 701
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 ECD

<400> 701

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Ser Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val

290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 702
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 ECD

<400> 702

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys Arg Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Gly Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

```
Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 703
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 ECD

<400> 703

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr

165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 704
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v38 ECD

<400> 704

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205
```

```
Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  705
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v39 ECD

<400>  705

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
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        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
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245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 706
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v40 ECD

<400> 706

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

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Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Ile Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285
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Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  707
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v41 ECD

<400>  707

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
```

115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly

325

<210> 708
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v42 ECD

<400> 708

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

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Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 709
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v43 ECD

<400> 709

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Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
```

195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 710
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v44 ECD

<400> 710

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

```
Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240
```

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 711
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v45 ECD

<400> 711

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val

275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 712
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v46 ECD

<400> 712

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Ile Cys Glu Phe Val
100 105 110

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Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320
```

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 713
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v47 ECD

<400> 713

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Leu Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro

145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 714
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v1 IgV

<400> 714

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Asp Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 715
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v2 IgV

<400> 715

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Gly
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Gly
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Ser Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 716
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v3 IgV

<400> 716

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  717
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v4 IgV

<400>  717

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ile
```

100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 718
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v5 IgV

<400> 718

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 719
<211> 125
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v6 IgV

<400> 719

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 720
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v7 IgV

<400> 720

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 721
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v8 IgV

<400> 721

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn Tyr
        35   40   45

Gln Asn Val Ala Ala Ser His Pro Lys Met Gly Pro Ser Phe Pro Ser

```
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125
```

<210> 722
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 IgV

<400> 722

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95
```

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 723
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 IgV

<400> 723

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Ser Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 724

<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 IgV

<400> 724

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 725
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v12 IgV

<400> 725

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  726
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v13 IgV

<400>  726

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45
```

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125
```

<210> 727
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v14 IgV

<400> 727

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Thr Pro
```

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 728
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v15 IgV

<400> 728

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Ser Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 729
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v16 IgV

<400> 729

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 730
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v17 IgV

<400> 730

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Ser Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  731
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v18 IgV

<400>  731

Gln Asp Val Arg Val Gln Val Leu Ser Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Ser His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 732
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v19 IgV

<400> 732

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys His Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  733
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v20 IgV

<400>  733

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Leu Pro Val Pro Gly Pro
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
```

115 120 125

<210> 734
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v21 IgV

<400> 734

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Asp Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 735
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v22 IgV

<400> 735

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Pro Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 736
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v23 IgV

<400> 736

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

```
Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Ala Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  737
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v24 IgV

<400>  737

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Ser Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 738
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 IgV

<400> 738

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 739
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v26 IgV

<400> 739

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 740
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v27 IgV

<400> 740

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65   70   75   80

Thr Gly Gln Gly Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Ser Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 741
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v28 IgV

<400> 741

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Leu His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 742
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v29 IgV

<400> 742

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  743
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v30 IgV

<400>  743

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
```

100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 744
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v31 IgV

<400> 744

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 745
<211> 125
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v32 IgV

<400> 745

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 746
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v33 IgV

<400> 746

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Met Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 747
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 IgV

<400> 747

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 748
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 IgV

<400> 748

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Ser Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 749
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 IgV

<400> 749

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys Arg Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Gly Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 750

<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 IgV

<400> 750

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 751
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v38 IgV

<400> 751

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

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1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  752
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v39 IgV

<400>  752

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45
```

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  753
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v40 IgV

<400>  753

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
```

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Ile Thr Trp Leu
115 120 125

<210> 754
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v41 IgV

<400> 754

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 755
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v42 IgV

<400> 755

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 756
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v43 IgV

<400> 756

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  757
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v44 IgV

<400>  757

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 758
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v45 IgV

<400> 758

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  759
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v46 IgV

<400>  759

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Ile Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
```

115 120 125

<210> 760
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v47 IgV

<400> 760

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Leu Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 761
<211> 127
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> CD112 IgV Wildtype

<400> 761

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 762
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v1 IgV

<400> 762

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Asp Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 763
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v2 IgV

<400> 763

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Gly
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Gly
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Ser Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  764
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v3 IgV

<400>  764

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
```

100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 765
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v4 IgV

<400> 765

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ile
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 766
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v5 IgV

<400> 766

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 767
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v6 IgV

<400> 767

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 768
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v7 IgV

<400> 768

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 769
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v8 IgV

<400> 769

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn Tyr
35 40 45

Gln Asn Val Ala Ala Ser His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 770
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 IgV

<400> 770

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 771

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 IgV

<400> 771

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Ser Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 772
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 IgV

<400> 772

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  773
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v12 IgV

<400>  773

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45
```

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 774
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v13 IgV

<400> 774

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 775
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v14 IgV

<400> 775

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Thr Pro
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 776
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v15 IgV

<400> 776

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Ser Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 777
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v16 IgV

<400> 777

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Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  778
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v17 IgV

<400>  778

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Ser Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 779
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v18 IgV

<400> 779

Gln Asp Val Arg Val Gln Val Leu Ser Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Ser His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  780
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v19 IgV

<400>  780

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys His Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
```

115 120 125

<210> 781
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v20 IgV

<400> 781

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Leu Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 782
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v21 IgV

<400> 782

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Asp Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 783
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v22 IgV

<400> 783

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
His Ile Pro Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  784
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v23 IgV

<400>  784

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Ser Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Ala Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 785
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v24 IgV

<400> 785

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Ser Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 786
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 IgV

<400> 786

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 787
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v26 IgV

<400> 787

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 788
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v27 IgV

<400> 788

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu

20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65 70 75 80

Thr Gly Gln Gly Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Ser Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 789
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v28 IgV

<400> 789

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Leu His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  790
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v29 IgV

<400>  790

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
```

100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 791
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v30 IgV

<400> 791

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Val Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 792
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v31 IgV

<400> 792

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 793
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v32 IgV

<400> 793

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 794
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v33 IgV

<400> 794

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Met Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 795
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 IgV

<400> 795

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 796
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 IgV

<400> 796

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Ala Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Ser Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 797

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 IgV

<400> 797

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys Arg Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Asn Trp Gln Arg Pro Gly Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 798
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 gV

<400> 798

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  799
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v38 gV

<400>  799

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45
```

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  800
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v39 gV

<400>  800

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
```

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 801
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v40 gV

<400> 801

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Ile Thr Trp Leu Arg Val
115 120 125

<210> 802
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v41 gV

<400> 802

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 803
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v42 gV

<400> 803

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  804
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v43 gV

<400>  804

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 805
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v44 gV

<400> 805

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Ser Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  806
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v45 IgV

<400>  806

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Ala Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
```

115 120 125

<210> 807
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v46 IgV

<400> 807

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Ile Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 808
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v47 IgV

<400> 808

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Leu Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 809
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v48 ECD

<400> 809

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

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Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240
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Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  810
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v49 ECD

<400>  810

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Arg Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Thr Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val

275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 811
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v50 ECD

<400> 811

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

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Thr Tyr Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320
```

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 812
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v51 ECD

<400> 812

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro

145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 813
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v52 ECD

<400> 813

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Ala Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190
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```
Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  814
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v53 ECD

<400>  814

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

```
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
```

225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 815
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v54 ECD

<400> 815

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270
```

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 816
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v55 ECD

<400> 816

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala

100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn

305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 817
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v56 ECD

<400> 817

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

```
Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325

<210>  818
<211>  329
<212>  PRT
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<213> Artificial Sequence

<220>
<223> CD112 v57 ECD

<400> 818

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe

180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 819
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v58 ECD

<400> 819

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

```
Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220
```

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 820
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 ECD

<400> 820

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Ala Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe

260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 821
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v60 ECD

<400> 821

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

```
His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300
```

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 822
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 ECD

<400> 822

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Met Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln

130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 823

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v62 ECD

<400> 823

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175
```

```
Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 824
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v63 ECD

<400> 824

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
```

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
```

210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 825
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v64 ECD

<400> 825

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255
```

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 826
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v65 ECD

<400> 826

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Ser Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val

290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 827
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v66 ECD

<400> 827

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Glu Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

```
Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 828
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v67 ECD

<400> 828

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Ala Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr

165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 829
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v68 ECD

<400> 829

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205
```

```
Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  830
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v69 ECD

<400>  830

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

```
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
```

245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 831
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 ECD

<400> 831

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285
```

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 832
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v71 ECD

<400> 832

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile

115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly

325

<210> 833
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 ECD

<400> 833

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Ser Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

```
Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 834
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 ECD

<400> 834

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
```

195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 835
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v74 ECD

<400> 835

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240
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Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  836
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v75 ECD

<400>  836

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

```
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
```

275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 837
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v76 ECD

<400> 837

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Met Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

```
Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320
```

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 838
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v77 ECD

<400> 838

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Ala Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro

145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 839
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v78 ECD

<400> 839

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190
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```
Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  840
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v79 ECD

<400>  840

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Gly Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn

225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 841
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v80 ECD

<400> 841

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270
```

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 842
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v81 ECD

<400> 842

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala

100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn

305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 843
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v82 ECD

<400> 843

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Asp Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

```
Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 844
<211> 329
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v83 ECD

<400> 844

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Ser Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe

180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 845
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v84 ECD

<400> 845

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

```
Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Ser Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220
```

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 846
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 ECD

<400> 846

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

```
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
```

260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 847
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v86 ECD

<400> 847

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

```
His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300
```

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 848
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 ECD

<400> 848

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln

130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 849

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v88 ECD

<400> 849

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175
```

```
Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  850
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v48 IgV

<400>  850

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
```

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  851
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v49 IgV

<400>  851

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Arg Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45
```

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Thr Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  852
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v50 IgV

<400>  852

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
```

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Tyr Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 853
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v51 IgV

<400> 853

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 854
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v52 IgV

<400> 854

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Ala Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 855
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v53 IgV

<400> 855

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  856
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v54 IgV

<400>  856

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 857
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v55 IgV

<400> 857

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  858
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v56 IgV

<400>  858

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Gly Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
```

115 120 125

<210> 859
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v57 IgV

<400> 859

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 860
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v58 IgV

<400> 860

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 861
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 IgV

<400> 861

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Ala Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  862
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v60 IgV

<400>  862

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 863
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 IgV

<400> 863

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Met Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 864
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v62 IgV

<400> 864

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 865
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v63 IgV

<400> 865

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 866
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v64 IgV

<400> 866

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 867
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v65 IgV

<400> 867

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Ser Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  868
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v66 IgV

<400>  868

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Ala
```

100 105 110

Thr Phe Pro Glu Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 869
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v67 IgV

<400> 869

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Ala Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 870
<211> 125
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v68 IgV

<400> 870

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 871
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v69 IgV

<400> 871

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 872
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 IgV

<400> 872

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 873
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v71 IgV

<400> 873

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 874
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 IgV

<400> 874

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Ser Met Thr Trp Leu
115 120 125

<210> 875

<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 IgV

<400> 875

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 876
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v74 IgV

<400> 876

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  877
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v75 IgV

<400>  877

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45
```

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115   120   125

<210> 878
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v76 IgV

<400> 878

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Met Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 879
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v77 IgV

<400> 879

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Ala Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 880
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v78 IgV

<400> 880

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 881
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v79 IgV

<400> 881

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Gly Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  882
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v80 IgV

<400>  882

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 883
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v81 IgV

<400> 883

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  884
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v82 IgV

<400>  884

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Asp Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
```

115 120 125

<210> 885
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v83 IgV

<400> 885

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Ser Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 886
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v84 IgV

<400> 886

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Ser Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 887
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 IgV

<400> 887

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  888
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v86 IgV

<400>  888

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 889
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 IgV

<400> 889

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 890
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v88 IgV

<400> 890

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 891
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v48 IgV

<400> 891

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125
```

<210> 892
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v49 IgV

<400> 892

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

20 25 30

Tyr Ile Ser Leu Val Thr Trp Arg Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Thr Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 893
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v50 IgV

<400> 893

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Tyr Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  894
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v51 IgV

<400>  894

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Arg Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
```

100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 895
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v52 IgV

<400> 895

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Ala Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 896
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v53 IgV

<400> 896

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 897
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v54 IgV

<400> 897

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 898
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v55 IgV

<400> 898

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Arg Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 899
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v56 IgV

<400> 899

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Gly Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 900
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v57 IgV

<400> 900

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 901

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v58 IgV

<400> 901

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 902
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 IgV

<400> 902

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

1 5 10 15

Gly Ala Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 903
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v60 IgV

<400> 903

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Val Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 904
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 IgV

<400> 904

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Met Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 905
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v62 IgV

<400> 905

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 906
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v63 IgV

<400> 906

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 907
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v64 IgV

<400> 907

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  908
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v65 IgV

<400>  908

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Ser Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Met Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 909
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v66 IgV

<400> 909

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Ala Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Glu Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  910
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v67 IgV

<400>  910

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Ala Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
```

115 120 125

<210> 911
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v68 IgV

<400> 911

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 912
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v69 IgV

<400> 912

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 913
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 IgV

<400> 913

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  914
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v71 IgV

<400>  914

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 915
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 IgV

<400> 915

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Ser Met Thr Trp Leu Arg Val
        115   120   125

<210> 916
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 IgV

<400> 916

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 917
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v74 IgV

<400> 917

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125
```

<210> 918
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v75 IgV

<400> 918

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 919
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v76 IgV

<400> 919

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Met Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  920
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v77 IgV

<400>  920

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Pro
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Ala Cys Glu Phe Ala
```

100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 921
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v78 IgV

<400> 921

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 922
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v79 IgV

<400> 922

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Gly Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 923
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v80 IgV

<400> 923

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 924
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v81 IgV

<400> 924

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 925
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v82 IgV

<400> 925

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Asp Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 926
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v83 IgV

<400> 926

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Ser Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 927

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v84 IgV

<400> 927

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Ser Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 928
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 IgV

<400> 928

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 929
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v86 IgV

<400> 929

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 930
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 IgV

<400> 930

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 931
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v88 IgV

<400> 931

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 932
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 ECD

<400> 932

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr

165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 933
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 ECD

<400> 933

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Phe Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

```
Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  934
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v124 ECD

<400>  934

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
```

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 935
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v125 ECD

<400> 935

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Thr Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 936
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v126 ECD

<400> 936

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Arg

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 937

<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v127 ECD

<400> 937

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 938
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 ECD

<400> 938

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Arg Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn

130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 939
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v130 ECD

<400> 939

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Val Val Leu Thr Met Met Ser Gly Asp Thr Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 940
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v131 ECD

<400> 940

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Val Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn

50 55 60

Leu Ser Ile Val Ile Pro Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Thr Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 941
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v132 ECD

<400> 941

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

```
Gly His Asn Val Ser Ile Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 942
<211> 208
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v133 ECD

<400> 942

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Gly Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
```

180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 943
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v134 ECD

<400> 943

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Thr Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

```
Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  944
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v135 ECD

<400>  944

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Met Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
```

100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 945
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v136 ECD

<400> 945

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

```
Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  946
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v137 ECD

<400>  946

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
```

20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Ser Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 947
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v138 ECD

<400> 947

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Pro Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190
```

```
Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  948
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v139 ECD

<400>  948

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Pro Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
```

145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 949
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v140 ECD

<400> 949

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Ser Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

```
Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  950
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v141 ECD

<400>  950

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Thr Val Ile Leu Ala Leu Arg Ser Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Gly Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Asp His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 951
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 ECD

<400> 951

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

```
Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 952
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 ECD

<400> 952

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Ala Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Asn Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
```

195 200 205

<210> 953
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v144 ECD

<400> 953

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Lys Cys Val Val Leu Lys Tyr Glu Lys Asp Ser Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 954
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v145 ECD

<400> 954

Val Ile His Val Thr Lys Glu Val Lys Glu Val Val Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys

115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 955
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v146 ECD

<400> 955

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Glu Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 956
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 ECD

<400> 956

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ala Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 957
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v148 ECD

<400> 957

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 958
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v149 ECD

<400> 958

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
```

165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 959
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 ECD

<400> 959

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Arg Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Ala Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 960
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v151 ECD

<400> 960

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Glu Lys Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 961
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v152 ECD

<400> 961

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val His
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  962
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v153 ECD

<400>  962

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
```

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Ala Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 963

<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v154 ECD

<400> 963

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175
```

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 964
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v155 ECD

<400> 964

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Ser Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn

130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 965
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v156 ECD

<220>
<221> VARIANT
<222> (24)..(24)
<223> X is a stop codon

<400> 965

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Xaa Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Arg Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Asn Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Val Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr

65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 966
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v157 ECD

<400> 966

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

```
Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  967
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v158 ECD
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<400> 967

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
```

195 200 205

<210> 968
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v159 ECD

<400> 968

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Ile Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 969
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 ECD

<400> 969

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Ala Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys

115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 970
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v161 ECD

<400> 970

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 971
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v162 ECD

<400> 971

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ile Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 972
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v163 ECD

<400> 972

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 973
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v164 ECD

<400> 973

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr

165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 974
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 ECD

<400> 974

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 975
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 ECD

<400> 975

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 976
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v167 ECD

<400> 976

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Leu Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  977
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v168 ECD

<400>  977

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
```

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 978

<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 ECD

<400> 978

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Val Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175
```

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 979
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 ECD

<400> 979

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn

130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 980
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v171 ECD

<400> 980

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 981
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v172 ECD

<400> 981

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn

50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 982
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v173 ECD

<400> 982

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

```
Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 983
<211> 208
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v174 ECD

<400> 983

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Pro Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Gln Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
```

180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 984
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v175 ECD

<400> 984

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

```
Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  985
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v176 ECD

<400>  985

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Leu Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Gln Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
```

100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 986
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v177 ECD

<400> 986

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

```
Leu Ser Ile Val Phe Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Ile Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  987
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v178 ECD

<400>  987

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
```

20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 988
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v179 ECD

<400> 988

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15


Gly Tyr Asn Val Ser Val Glu Glu Leu Thr Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190
```

```
Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  989
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v180 ECD

<400>  989

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
```

145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 990
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v181 ECD

<400> 990

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Asp Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Val Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Val Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

```
Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  991
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v182 ECD

<400>  991

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Met Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 992
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v183 ECD

<400> 992

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

```
Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Ile Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Phe Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 993
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v184 ECD

<400> 993

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
```

195 200 205

<210> 994
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v185 ECD

<400> 994

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 995
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 ECD

<400> 995

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Val Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys

115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 996
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v187 ECD

<400> 996

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 997
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 ECD

<400> 997

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Gly Glu Leu Ser Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn

```
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Asn Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  998
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v189 ECD

<400>  998
```

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Thr Thr Leu Ser Cys
1               5                  10                  15

Gly His Asn Val Ser Val Glu Asp Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Val His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 999
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v190 ECD

<400> 999

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser His Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr

165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 1000
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v191 ECD

<400> 1000

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Glu Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

```
Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175


Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190


Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  1001
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v192 ECD

<400>  1001

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
```

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 1002
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v193 ECD

<400> 1002

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Glu Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205


<210>  1003
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v194 ECD

<400>  1003

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
```

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Glu Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145 150 155 160

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
165 170 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 1004

<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 ECD

<400> 1004

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile His Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Leu Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Arg Trp Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Thr Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140


Gly Glu Glu Leu Ser Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu
145                 150                 155                 160


Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175
```

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
180 185 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
195 200 205

<210> 1005
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT IgV

<400> 1005

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1006
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 IgV

<400> 1006

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1007
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 IgV

<400> 1007

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Phe Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1008
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v124 IgV

<400> 1008

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1009
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v125 IgV

<400> 1009

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Thr Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1010
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v126 IgV

<400> 1010

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Arg
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1011
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v127 IgV

<400>  1011

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
```

50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1012
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 IgV

<400> 1012

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Arg Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1013
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v130 IgV

<400> 1013

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Val Val Leu Thr Met Met Ser Gly Asp Thr Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1014
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v131 IgV

<400> 1014

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Val Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Thr Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1015
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v132 IgV

<400> 1015

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Ile Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr

65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1016
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v133 IgV

<400> 1016

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Gly Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1017
<211> 101
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v134 IgV

<400> 1017

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Thr Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1018
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v135 IgV

<400> 1018

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Met Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1019
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v136 IgV

<400> 1019

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

85 90 95

Leu Ala Glu Val Thr
100

<210> 1020
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v137 IgV

<400> 1020

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Ser Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1021
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v138 IgV

<400> 1021

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Pro Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1022
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v139 IgV

<400> 1022

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Pro Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1023
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v140 IgV

<400>  1023

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Ser Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
```

100

<210> 1024
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v141 IgV

<400> 1024

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Thr Val Ile Leu Ala Leu Arg Ser Ser Asp Glu Gly Thr Tyr
65 70 75 80

Gly Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Asp His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1025
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 IgV

<400> 1025

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1026
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 IgV

<400> 1026

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Ala Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Asn Thr Asn Asn
50 55 60

```
Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1027
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v144 IgV

<400>  1027

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Lys Cys Val Val Leu Lys Tyr Glu Lys Asp Ser Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1028
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<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v145 IgV

<400> 1028

Val Ile His Val Thr Lys Glu Val Lys Glu Val Val Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1029
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v146 IgV

<400> 1029

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Glu Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1030
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 IgV

<400> 1030

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ala Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1031
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v148 IgV

<400> 1031

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1032
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v149 IgV

<400> 1032

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1033
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 IgV

<400> 1033

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Arg Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Ala Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1034
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v151 IgV

<400> 1034

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Glu Lys Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1035
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v152 IgV

<400> 1035

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val His
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1036
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v153 IgV

<400> 1036

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Ala Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1037
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v154 IgV

<400>  1037

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
```

50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1038
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v155 IgV

<400> 1038

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Ser Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1039
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v156 IgV

<220>
<221> VARIANT
<222> (24)..(24)
<223> X is a stop codon

<400> 1039

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Xaa Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Arg Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Asn Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Val Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1040
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v157 IgV

<400> 1040

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1041
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v158 IgV

<400> 1041

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1042
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v159 IgV

<400>  1042

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Ile Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
```

100

<210> 1043
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 IgV

<400> 1043

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Ala Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1044
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v161 IgV

<400> 1044

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1045
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v162 IgV

<400> 1045

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ile Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1046
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v163 IgV

<400> 1046

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1047

<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v164 IgV

<400> 1047

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1048
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 IgV

<400> 1048

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1049
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 IgV

<400> 1049

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1050
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v167 IgV

<400> 1050

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Leu Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1051
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v168 IgV

<400> 1051

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100
```

<210> 1052
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 IgV

<400> 1052

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Val Met Ser Gly Asp Ile Asn
```

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1053
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 IgV

<400> 1053

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1054
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v171 IgV

<400> 1054

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1055
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v172 IgV

<400> 1055

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1056
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v173 IgV

<400>  1056

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
```

50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1057
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v174 IgV

<400> 1057

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Pro Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1058
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v175 IgV

<400> 1058

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1059
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v176 IgV

<400> 1059

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

```
Gly His Asn Val Ser Val Glu Glu Leu Ala Leu Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Gln Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1060
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v177 IgV

<400>  1060

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Phe Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Glu Cys Ile Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1061
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v178 IgV

<400> 1061

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1062
<211> 101
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v179 IgV

<400> 1062

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly Tyr Asn Val Ser Val Glu Glu Leu Thr Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1063
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v180 IgV

<400> 1063

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

```
Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1064
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v181 IgV

<400>  1064

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Asp Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Val Ile Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Val Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
```

85 90 95

Leu Ala Glu Val Thr
100

<210> 1065
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v182 IgV

<400> 1065

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Met Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1066
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v183 IgV

<400> 1066

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Ile Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Phe Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1067
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v184 IgV

<400> 1067

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  1068
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v185 IgV

<400>  1068

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
```

100

<210> 1069
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 IgV

<400> 1069

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Val Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1070
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v187 IgV

<400> 1070

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1071
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 IgV

<400> 1071

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Gly Glu Leu Ser Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Asn Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1072
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v189 IgV

<400> 1072

Val Ile His Val Thr Lys Glu Val Lys Glu Val Thr Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Asp Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Val His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1073

<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v190 IgV

<400> 1073

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser His Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1074
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v191 IgV

<400> 1074

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Glu Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1075
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v192 IgV

<400> 1075

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1076
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v193 IgV

<400> 1076

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Glu Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1077
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v194 IgV

<400> 1077

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Glu Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 1078
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 IgV

<400> 1078

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile His Trp
            20   25   30

Gln Lys Asp Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Leu Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Arg Trp Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 1079
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT IgV

<400> 1079

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1080
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 IgV

<400> 1080

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1081
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 IgV

<400> 1081

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Phe Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105


<210>  1082
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v124 IgV

<400>  1082

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
```

50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1083
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v125 IgV

<400> 1083

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Thr Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1084
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v126 IgV

<400> 1084

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Arg
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1085
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v127 IgV

<400> 1085

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

```
Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105
```

<210> 1086
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 IgV

<400> 1086

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Glu Arg Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1087
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v130 IgV

<400> 1087

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Val Val Leu Thr Met Met Ser Gly Asp Thr Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1088
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v131 IgV

<400> 1088

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Val Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Pro Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Thr Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100   105

<210> 1089
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v132 IgV

<400> 1089

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Ile Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100   105

<210> 1090
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v133 IgV

<400> 1090

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Gly Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1091
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v134 IgV

<400> 1091

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Thr Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1092
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v135 IgV

<400> 1092

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asp Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Met Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1093
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v136 IgV

<400> 1093

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

```
Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105


<210>  1094
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v137 IgV

<400>  1094

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Pro Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Ser Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
```

100 105

<210> 1095
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v138 IgV

<400> 1095

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Pro Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1096
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v139 IgV

<400> 1096

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Pro Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1097
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v140 IgV

<400> 1097

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Ser Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asn Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1098
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v141 IgV

<400> 1098

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Thr Val Ile Leu Ala Leu Arg Ser Ser Asp Glu Gly Thr Tyr
65 70 75 80

Gly Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Asp His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1099

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 IgV

<400> 1099

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1100
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 IgV

<400> 1100

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Ala Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Asn Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1101
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v144 IgV

<400> 1101

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Lys Cys Val Val Leu Lys Tyr Glu Lys Asp Ser Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1102
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v145 IgV

<400> 1102

Val Ile His Val Thr Lys Glu Val Lys Glu Val Val Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1103
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v146 IgV

<400> 1103

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Glu Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105
```

<210> 1104
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 IgV

<400> 1104

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
```

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ala Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1105
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v148 IgV

<400> 1105

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1106
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v149 IgV

<400> 1106

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1107
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 IgV

<400> 1107

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Gln Lys Glu Arg Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Ala Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105


<210>  1108
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v151 IgV

<400>  1108

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30


Glu Lys Glu Lys Lys Met Val Leu Ala Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
```

50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1109
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v152 IgV

<400> 1109

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val His
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1110
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v153 IgV

<400> 1110

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Ala Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1111
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v154 IgV

<400> 1111

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

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Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Pro Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105


<210>  1112
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v155 IgV

<400>  1112

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Asp Leu Ser Pro Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1113
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v156 IgV

<220>
<221> VARIANT
<222> (24)..(24)
<223> X is a stop codon

<400> 1113

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Xaa Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Arg Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Asn Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Val Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp

100 105

<210> 1114
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v157 IgV

<400> 1114

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1115
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v158 IgV

<400> 1115

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1116
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v159 IgV

<400> 1116

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Ile Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1117
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 IgV

<400> 1117

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Ala Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1118

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v161 IgV

<400> 1118

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1119
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v162 IgV

<400> 1119

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Ile Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1120
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v163 IgV

<400> 1120

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1121
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v164 IgV

<400> 1121

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 IgV

<400> 1122

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1123
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 IgV

<400> 1123

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1124
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v167 IgV

<400> 1124

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Leu Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1125
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v168 IgV

<400> 1125

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala His Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Ile Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1126
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 IgV

<400> 1126

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Arg Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Val Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 IgV

<400> 1127

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn

50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1128
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v171 IgV

<400> 1128

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1129
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v172 IgV

<400> 1129

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1130
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v173 IgV

<400> 1130

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

```
Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Met Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105
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<210> 1131
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v174 IgV

<400> 1131

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Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15

Gly His Asn Val Ser Val Glu Glu Leu Pro Gln Thr Arg Ile Tyr Trp
            20                  25                  30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
        35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
```

65 70 75 80

Glu Cys Val Val Gln Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1132
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v175 IgV

<400> 1132

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1133
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v176 IgV

<400> 1133

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Leu Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Ile Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
    50   55   60

Leu Ser Ile Val Ile Gln Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Lys Tyr Asp Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100   105

<210> 1134
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v177 IgV

<400> 1134

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Val Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Phe Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Ile Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1135
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v178 IgV

<400> 1135

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ala Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v179 IgV

<400> 1136

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Thr Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1137
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v180 IgV

<400> 1137

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v181 IgV

<400> 1138

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Asp Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Val Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Val Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1139
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v182 IgV

<400> 1139

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Met Ile Met Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Lys His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp

100 105

<210> 1140
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v183 IgV

<400> 1140

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Ile Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Phe Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1141
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v184 IgV

<400> 1141

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys

1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1142
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v185 IgV

<400> 1142

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Ile Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1143
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 IgV

<400> 1143

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly Tyr Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Val Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1144

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v187 IgV

<400> 1144

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Ile Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1145
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 IgV

<400> 1145

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Gly Glu Leu Ser Gln Thr Arg Ile Tyr Trp

20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Asn Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Val Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Met Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1146
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v189 IgV

<400> 1146

Val Ile His Val Thr Lys Glu Val Lys Glu Val Thr Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Asp Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Val Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Val Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Val His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1147
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v190 IgV

<400> 1147

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Leu Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Leu Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Gly Leu Arg Pro Ser His Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1148
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v191 IgV

<400> 1148

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Gly Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Glu Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1149
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v192 IgV

<400> 1149

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn

35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Gln Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1150
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v193 IgV

<400> 1150

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Glu Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Asp Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Leu Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Gln Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1151
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v194 IgV

<400> 1151

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Glu Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Asp Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 1152
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 IgV

<400> 1152

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1               5                   10                  15


Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile His Trp
            20                  25                  30


Gln Lys Asp Lys Lys Met Val Leu Ser Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Leu Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Arg Trp Glu His
                85                  90                  95


Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
            100                 105


<210>  1153
<211>  232
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Knob Fc

<400>  1153

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
```

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1154
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Hole Fc

<400> 1154

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
            180                 185                 190
```

```
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly Lys
225                 230


<210>  1155
<211>  232
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Stack Fc (homodimeric)

<400>  1155

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
```

```
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly Lys
225                 230


<210>  1156
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Stuffer

<400>  1156

His Met Ser Ser Val Ser Ala Gln
1               5


<210>  1157
<211>  232
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fc (C5S (C220S), R77C, (R292C),  N82G (N297G), V87C (V302C))
```

<400> 1157

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
65                  70                  75                  80

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
```

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1158
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc with C220S/L234A/L235E/G237A

<400> 1158

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1159
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc with C220S/E233P/L234V/L235A/G236del/S267K

<400> 1159

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

Asp Val Lys His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65 70 75 80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
100 105 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
130 135 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145 150 155 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
210 215 220

Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1160
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19z chimeric antigen receptor

<400> 1160

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110


Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125


Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140


Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160


Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175


Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190
```

```
Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ala Ala Lys Pro Thr Thr Thr Pro Ala Pro
                245                 250                 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
            260                 265                 270

Arg Pro Glu Ala Ser Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
        275                 280                 285

Gly Leu Asp Phe Ala Ser Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
    290                 295                 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
305                 310                 315                 320

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
                325                 330                 335

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            340                 345                 350

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        355                 360                 365

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    370                 375                 380

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
385                 390                 395                 400
```

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
405 410 415

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
420 425 430

<210> 1161
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8-derived signal sequence

<400> 1161

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 1162
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8-derived signal sequence

<400> 1162

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser
20

<210> 1163
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD19 scFv

<400> 1163

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110


Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125


Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140


Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160


Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175


Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190


Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
```

195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser
245

<210> 1164
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8-derived hinge and transmembrane domain

<400> 1164

Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
1 5 10 15

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
20 25 30

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
50 55 60

Ser Leu Val Ile Thr
65

<210> 1165
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB-derived costimulatory domain

<400> 1165

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 1166
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1166

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
1 5 10 15

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
20 25 30

Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 1167
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1167

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro

20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 1168
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1168

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
1 5 10 15

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
20 25 30

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 1169
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A protein

<400> 1169

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
1 5 10 15

Asn Pro Gly Pro
20

<210> 1170
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Blue fluorescent protein

<400> 1170

```
Ser Glu Leu Ile Lys Glu Asn Met His Met Lys Leu Tyr Met Glu Gly
1               5                  10                  15


Thr Val Asp Asn His His Phe Lys Cys Thr Ser Glu Gly Glu Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Thr Gln Thr Met Arg Ile Lys Val Val Glu Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Thr Ser Phe Leu Tyr Gly
    50                  55                  60


Ser Lys Thr Phe Ile Asn His Thr Gln Gly Ile Pro Asp Phe Phe Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Val Thr Thr Tyr Glu
                85                  90                  95


Asp Gly Gly Val Leu Thr Ala Thr Gln Asp Thr Ser Leu Gln Asp Gly
            100                 105                 110


Cys Leu Ile Tyr Asn Val Lys Ile Arg Gly Val Asn Phe Thr Ser Asn
        115                 120                 125


Gly Pro Val Met Gln Lys Lys Thr Leu Gly Trp Glu Ala Phe Thr Glu
    130                 135                 140


Thr Leu Tyr Pro Ala Asp Gly Gly Leu Glu Gly Arg Asn Asp Met Ala
145                 150                 155                 160


Leu Lys Leu Val Gly Gly Ser His Leu Ile Ala Asn Ile Lys Thr Thr
                165                 170                 175


Tyr Arg Ser Lys Lys Pro Ala Lys Asn Leu Lys Met Pro Gly Val Tyr
            180                 185                 190
```

Tyr Val Asp Tyr Arg Leu Glu Arg Ile Lys Glu Ala Asn Asn Glu Thr
195 200 205

Tyr Val Glu Gln His Glu Val Ala Val Ala Arg Tyr Cys Asp Leu Pro
210 215 220

Ser Lys Leu Gly His Lys Leu Asn
225 230

<210> 1171
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> 2nd Gen CAR

<400> 1171

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys

115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro
245 250 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
260 265 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
275 280 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
290 295 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Met His Lys Arg
305 310 315 320

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro

325 330 335

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
340 345 350

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
355 360 365

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
370 375 380

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
385 390 395 400

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
405 410 415

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
420 425 430

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
435 440 445

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
450 455 460

His Met Gln Ala Leu Pro Pro Arg
465 470

<210> 1172
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> 2nd Gen CAR

<400> 1172

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

```
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220
```

```
Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro
                245                 250                 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
            260                 265                 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
        275                 280                 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
    290                 295                 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Met His Lys Arg
305                 310                 315                 320

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
                325                 330                 335

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
            340                 345                 350

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
        355                 360                 365

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
    370                 375                 380

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
385                 390                 395                 400

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
                405                 410                 415

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
            420                 425                 430
```

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
435 440 445

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
450 455 460

His Met Gln Ala Leu Pro Pro Arg Gly Gly Arg Ser Gly Glu Gly Arg
465 470 475 480

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Ser
485 490 495

Arg

<210> 1173
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> 2nd Gen CAR with CD28-derived costimulatory domain

<400> 1173

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr

85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro
245 250 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
260 265 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
275 280 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly

290 295 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Met His Arg Ser
305 310 315 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
325 330 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
340 345 350

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
355 360 365

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
370 375 380

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
385 390 395 400

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
405 410 415

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
420 425 430

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
435 440 445

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
450 455 460

Met Gln Ala Leu Pro Pro Arg
465 470

<210> 1174
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD19 scFv

<400> 1174

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110


Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125


Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140


Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160


Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175


Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190
```

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Ala Ala Ala
245

<210> 1175
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> antiCD19x8z chimeric antigen receptor nucleotide

<400> 1175
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120

accatcagtt gcagggcaag tcaggacatt agtaaatatt taaattggta tcagcagaaa 180

ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240

tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag 300

caagaagata ttgccactta cttttgccaa cagggtaata cgcttccgta cacgttcgga 360

gggggggacta agttggaaat aacaggctcc acctctggat ccggcaagcc cggatctggc 420

gagggatcca ccaagggcga ggtgaaactg caggagtcag gacctggcct ggtggcgccc 480

tcacagagcc tgtccgtcac atgcactgtc tcaggggtct cattacccga ctatggtgta 540

agctggattc gccagcctcc acgaaagggt ctggagtggc tgggagtaat atggggtagt 600

gaaaccacat actataattc agctctcaaa tccagactga ccatcatcaa ggacaactcc 660

aagagccaag ttttcttaaa aatgaacagt ctgcaaactg atgacacagc catttactac 720

tgtgccaaac attattacta cggtggtagc tatgctatgg actactgggg tcaaggaacc 780

tcagtcaccg tctcctcagc ggccgcaaag cccaccacga cgccagcgcc gcgaccacca 840

acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gagccggcca 900

gcggcggggg gcgcagtgca cacgaggggg ctggacttcg ccagtgatat ctacatctgg 960

gcgcccctgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cctttactgc 1020

agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 1080

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1140

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1200

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1260

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1320

tacgacgccc ttcacatgca ggccctgccc cctcgc 1356

<210> 1176
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> T2A
Nucleotide

<400> 1176
ggcagtggcg agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctggc 60

cca 63

<210> 1177
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A
Protein

<400> 1177

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro

20

<210> 1178
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v1 ECD

<400> 1178

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Val Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Val Pro Leu Ala Pro
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Gly Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
115

<210> 1179
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v2 ECD

<400> 1179

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Val Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
115

<210> 1180
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v3 ECD

<400> 1180

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Val Pro Leu Ala Ser
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
115

<210> 1181
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v4 ECD

<400> 1181

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Pro
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val

65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
115

<210> 1182
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v5 ECD

<400> 1182

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Gly Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu Gly
        115

<210> 1183
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 WT IgC-like

<400> 1183

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1   5   10   15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
            20   25   30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
        35   40   45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
    50   55   60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65   70   75   80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
                85   90   95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
            100   105

<210> 1184
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v1 IgC-like

<400> 1184

```
Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1               5                   10                  15


Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Val Ala Ile
            20                  25                  30


Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
        35                  40                  45


Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Val Pro Leu Ala Pro
    50                  55                  60


Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65                  70                  75                  80


Arg Gly His Asp Ala Gly Ile Tyr Val Cys Arg Val Glu Val Leu Gly
                85                  90                  95


Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
            100                 105


<210>  1185
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NKp30 v2 IgC-like

<400>  1185

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1               5                   10                  15


Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Val Ala Ile
            20                  25                  30


Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
        35                  40                  45


Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
```

50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
100 105

<210> 1186
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v3 IgC-like

<400> 1186

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Val Pro Leu Ala Ser
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
100 105

<210> 1187
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v4 IgC-like

<400> 1187

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Pro
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
100 105

<210> 1188
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v5 IgC-like

<400> 1188

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile
            20   25   30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
        35   40   45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser
    50   55   60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65   70   75   80

Arg Gly His Asp Ala Gly Ile Tyr Val Cys Arg Val Glu Val Leu Gly
                85   90   95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val
            100   105

<210> 1189
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Nkp30 stack

<400> 1189

Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu
1   5   10   15

Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val
            20   25   30

Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His
        35   40   45

Ile Pro Gln His Ser Ser Leu Glu Tyr Val Asp Ser Arg Tyr Arg Asn
    50   55   60

Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu

65 70 75 80

Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu
85 90 95

Val Leu Ser Pro Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val
100 105 110

Thr Leu His Val Ala Ala Asn Phe Ser Val Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Trp Val Ser Gln Pro Pro
130 135 140

Glu Ile Arg Thr Leu Glu Gly Ser Ser Ala Phe Leu Pro Cys Ser Phe
145 150 155 160

Asn Ala Ser Gln Gly Arg Val Ala Ile Gly Ser Val Thr Trp Phe Arg
165 170 175

Asp Glu Val Val Pro Gly Lys Glu Val Arg Asn Gly Thr Pro Glu Phe
180 185 190

Arg Gly Arg Leu Val Pro Leu Ala Pro Ser Arg Phe Leu His Asp His
195 200 205

Gln Ala Glu Leu His Ile Arg Asp Val Arg Gly His Asp Ala Gly Ile
210 215 220

Tyr Val Cys Arg Val Glu Val Leu Gly Leu Gly Val Gly Thr Gly Asn
225 230 235 240

Gly Thr Arg Leu Val Val Glu Lys Glu His Pro Gln Leu Gly Gly Gly
245 250 255

Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala Glu Pro Lys
260 265 270

<210> 1190

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v1 IgC-like (long)

<400> 1190

Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly Ser Ser
1 5 10 15

Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Val Ala Ile
20 25 30

Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val
35 40 45

Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Val Pro Leu Ala Pro
50 55 60

Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val
65 70 75 80

Arg Gly His Asp Ala Gly Ile Tyr Val Cys Arg Val Glu Val Leu Gly
85 90 95

Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu
100 105 110

His Pro Gln Leu
115

<210> 1191
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v1 ECD

<400> 1191

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro

```
1               5                   10                  15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
            20                  25                  30

Phe Trp His Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
        35                  40                  45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile Leu His Lys Lys Pro Thr Gly
                85                  90                  95

Met Ile Arg Ile His His Met Asn Ser Glu Leu Ser Val Leu Ala Asn
            100                 105                 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
        115                 120                 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
    130                 135                 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145                 150                 155                 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
                165                 170                 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
            180                 185                 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
        195                 200                 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
```

210 215 220

<210> 1192
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v2 ECD

<400> 1192

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp His Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
50 55 60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65 70 75 80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
85 90 95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn
100 105 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
115 120 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
130 135 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145 150 155 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
165 170 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
180 185 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
195 200 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
210 215 220

<210> 1193
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v3 ECD

<400> 1193

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
50 55 60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65 70 75 80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile Leu His Lys Lys Pro Thr Gly
85 90 95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn

100 105 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
115 120 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
130 135 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145 150 155 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
165 170 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
180 185 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
195 200 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
210 215 220

<210> 1194
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v4 ECD

<400> 1194

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

```
Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
                85                  90                  95

Met Ile Arg Ile His His Met Asn Ser Glu Leu Ser Val Leu Ala Asn
            100                 105                 110

Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val
        115                 120                 125

Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys
    130                 135                 140

Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp
145                 150                 155                 160

Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val
                165                 170                 175

Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr
            180                 185                 190

Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro
        195                 200                 205

Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro
    210                 215                 220


<210>  1195
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD86 WT IgV
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<400> 1195

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
50 55 60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65 70 75 80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
85 90 95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
100 105

<210> 1196
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v1 IgV

<400> 1196

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp His Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

```
Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60


Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80


Asp Lys Gly Leu Tyr Gln Cys Ile Ile Leu His Lys Lys Pro Thr Gly
                85                  90                  95


Met Ile Arg Ile His His Met Asn Ser Glu Leu Ser
            100                 105


<210>  1197
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD86 v2 IgV

<400>  1197

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1               5                   10                  15


Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
            20                  25                  30


Phe Trp His Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
        35                  40                  45


Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
    50                  55                  60


Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65                  70                  75                  80


Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
                85                  90                  95


Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
```

100 105

<210> 1198
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v3 IgV

<400> 1198

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro
1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
50 55 60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65 70 75 80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile Leu His Lys Lys Pro Thr Gly
85 90 95

Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
100 105

<210> 1199
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v4 IgV

<400> 1199

Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro

1 5 10 15

Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val
20 25 30

Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly
35 40 45

Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser
50 55 60

Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys
65 70 75 80

Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly
85 90 95

Met Ile Arg Ile His His Met Asn Ser Glu Leu Ser
100 105

<210> 1200
<211> 229
<212> PRT
<213> artificial sequence

<220>
<223> IgG4 Fc

<400> 1200

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 1201
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 Fc S228P

<400> 1201

```
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1               5                  10                  15


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45


Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65                  70                  75                  80


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100                 105                 110


Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115                 120                 125


Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150                 155                 160


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165                 170                 175


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190


Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
```

195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 1202
<211> 232
<212> PRT
<213> artificial Sequence

<220>
<223> IgG1 Fc C220S

<400> 1202

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

```
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly Lys
225                 230


<210>  1203
<211>  98
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 IgV

<400>  1203

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1               5                   10                  15


Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20                  25                  30


Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35                  40                  45


His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
```

50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1204
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v1

<400> 1204

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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
        195                 200


<210>  1205
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v2

<400>  1205

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 Asp 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
195 200

<210> 1206
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v3

<400> 1206

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 Asp 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
        195                 200


<210>  1207
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v4
```

<400> 1207

```
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 Asp 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
```

195 200

<210> 1208
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v5

<400> 1208

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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1209
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v6

<400> 1209

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 Gly 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 Arg 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
195 200

<210> 1210
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v7

<400> 1210

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 Ile 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 Asp 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
        195                 200


<210>  1211
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v8

<400>  1211

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 Leu 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 Asp 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
        195                 200


<210>  1212
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v9

<400>  1212
```

```
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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80

Tyr Gln Cys Ile Phe 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
        195                 200
```

<210> 1213
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v10

<400> 1213

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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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1214
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v11

<400> 1214

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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

Arg 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
195 200

<210> 1215
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v12

<400> 1215

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 His Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1216
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v13

<400> 1216

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Gly 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
        195                 200


<210>  1217
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v14

<400>  1217

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe 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
195 200

<210> 1218

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v15

<400> 1218

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Arg 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
195 200

<210> 1219
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v16

<400> 1219

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1220
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v17

<400> 1220

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Ser 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 Thr 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
        195                 200


<210>  1221
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v18

<400>  1221

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Thr 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
195 200

<210> 1222
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v19

<400> 1222

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Gly Asp Glu Gly Gln
65                  70                  75                  80

Tyr Gln Cys Ile Phe 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
        195                 200
```

<210> 1223
<211> 201
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 ECD v20

<400> 1223

```
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 Asp 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 Asp Ala Arg 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
195 200

<210> 1224
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v21

<400> 1224

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Leu 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 Asp 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
        195                 200


<210>  1225
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v22

<400>  1225

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1226
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v23

<400> 1226

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Thr 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
        195                 200


<210>  1227
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v24

<400>  1227

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Asp 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 Asp 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
195 200

<210> 1228
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v25

<400> 1228

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Ile Leu Gln Lys Val Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1229
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v26

<400> 1229

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1230
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v27

<400> 1230

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr 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
        195                 200


<210>  1231
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v28

<400>  1231

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Gly Asp Glu Gly Gln
```

65 70 75 80

Tyr Gln Cys Ile Phe 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
195 200

<210> 1232
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v29

<400> 1232

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Gly Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1233
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v30
```

<400> 1233

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Phe 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
```

195 200

<210> 1234
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v31

<400> 1234

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1235
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v32

<400> 1235

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 His Val Gln Val Gly 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
195 200

<210> 1236
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v33

<400> 1236

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 His Val Gln Val Gly 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
        195                 200


<210>  1237
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v34

<400>  1237

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Asp 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe 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
195 200

<210> 1238
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v35

<400> 1238

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Leu 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 Asp 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
        195                 200
```

<210> 1239
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v36

<400> 1239

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1               5                   10                  15


Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asp
            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 Leu 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 Asp 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
195 200

<210> 1240
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v37

<400> 1240

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 Asp
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 Leu 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 Asp 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
195 200

<210> 1241
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v38

<400> 1241

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1242
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v39

<400> 1242

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 His Val Arg Val Gly Asp Glu Gly Gln
65                  70                  75                  80

Tyr Gln Cys Ile Ile Thr 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
        195                 200
```

<210> 1243
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v40

<400> 1243

```
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 Val 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1244

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v41

<400> 1244

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ile Leu Gln Lys Val Asp 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 Leu 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
        195                 200


<210>  1245
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v42

<400>  1245

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 Asp 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 Leu Phe His Ile Pro His Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1246
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v43

<400> 1246

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Asp 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
        195                 200


<210>  1247
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v44

<400>  1247

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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
195 200

<210> 1248
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v45

<400> 1248

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Arg 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
        195                 200
```

<210> 1249
<211> 201
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 ECD v46

<400> 1249

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Asp 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
195 200

<210> 1250
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v47

<400> 1250

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1251
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v48

<400>  1251

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1252
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v49

<400> 1252

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Met 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1253
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v50

<400>  1253

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Arg 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
195 200

<210> 1254
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v51

<400> 1254

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1               5                   10                  15


Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Ala Asn
            20                  25                  30


Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Ser 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1255
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v52

<220>
<221> VARIANT
<222> (65)..(65)
<223> X is a stop codon

<400> 1255

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly
1 5 10 15

Ser Asn Val Ala 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 Ala Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Xaa Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1256
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v53

<400> 1256

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1257
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v54

<400> 1257

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Leu Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200
```

<210> 1258
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v55

<400> 1258

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Val Val Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1259

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v56

<400> 1259

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Gly Asn Glu Gly Gln
65                  70                  75                  80


Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1260
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v57

<400> 1260

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1261
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v58

<400> 1261

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1262
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v59

<400>  1262

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1               5                   10                  15


Ser Asn Val Thr Leu Glu Cys Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1263
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> PD-L2 IgV wildtype

<400> 1263

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
100

<210> 1264
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v61

<400> 1264

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Val Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Leu 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 Asp 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
        195                 200


<210>  1265
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v62

<400>  1265

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Arg Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1266
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v63

<400> 1266

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1               5                  10                  15


Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
            20                  25                  30


Pro Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Leu Phe His Ile Ser Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1267
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v64

<400> 1267

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1268
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v65

<400> 1268

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1269
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v66

<400>  1269

Leu Leu Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Glu Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
```

65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1270
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v67

<400> 1270

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

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Phe Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1271
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v68
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<400> 1271

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Gly Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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

195 200

<210> 1272
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v69

<400> 1272

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Ser 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1273
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v70

<400>  1273

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Val Asn Asp Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1274
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v71

<400> 1274

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asp 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 Ala 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 His Ala Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Asp 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
195 200

<210> 1275
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v72

<400> 1275

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Cys

35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1276
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v73

<400> 1276

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1               5                  10                  15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
            20                  25                  30

His 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200
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<210> 1277
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v74

<400> 1277

```
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80


Tyr Gln Cys Ile Ile Thr 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
195 200

<210> 1278
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v75

<400> 1278

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile Leu Gln Lys Val Asp 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 His Val Gln Gly Gly Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1279
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v76

<400> 1279

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
195 200

<210> 1280
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v77

<400> 1280

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp 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
        195                 200


<210>  1281
<211>  98
<212>  PRT
<213>  Artificial Seqeunce

<220>
<223>  PD-L2 IgV v1

<400>  1281

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
```

1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1282
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v2

<400> 1282

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asp Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1283
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v3

<400> 1283

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1284

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v4

<400> 1284

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1285
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v5

<400> 1285

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu

20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1286
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v6

<400> 1286

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Gly Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1287
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v7

<400> 1287

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1288
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v8

<400> 1288

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1289
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v9

<400> 1289

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro

35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1290
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v10

<400> 1290

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1291
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v11

<400> 1291

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Arg
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1292
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v12

<400> 1292

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1293
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v13

<400> 1293

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys

50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1294
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v14

<400> 1294

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1295
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v15

<400> 1295

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1296
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v16

<400> 1296

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1297
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v17

<400> 1297

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Ser Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr

65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1298
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v18

<400> 1298

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1299
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v19

<400> 1299

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1300
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v20

<400> 1300

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Arg Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1301
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v21

<400> 1301

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr

85 90 95

Leu Lys

<210> 1302
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v22

<400> 1302

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1303
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v23

<400> 1303

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1304
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v24

<400> 1304

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1305
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v25

<400> 1305

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1306
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v26

<400> 1306

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1307
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v27

<400> 1307

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser

1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1308
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v28

<400> 1308

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1309
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v29

<400> 1309

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1310

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v30

<400> 1310

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1311
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v31

<400> 1311

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu

20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1312
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v32

<400> 1312

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1313
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v33

<400> 1313

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1314
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v34

<400> 1314

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65   70   75   80

Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1315
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v35

<400> 1315

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Glu Asn Asp Thr Ser Pro

35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1316
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v36

<400> 1316

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asp Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1317
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v37

<400> 1317

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asp Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1318
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v38

<400> 1318

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1319
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v39

<400> 1319

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys

50 55 60

Ala Ser Phe His Ile Pro His Val Arg Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1320
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v40

<400> 1320

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Val Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1321
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v41

<400> 1321

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1322
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v42

<400> 1322

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Leu Phe His Ile Pro His Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1323
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v43

<400> 1323

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr

65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1324
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v44

<400> 1324

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1325
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v45

<400> 1325

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1326
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v46

<400> 1326

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1327
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v47

<400> 1327

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr

85 90 95

Leu Lys

<210> 1328
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v48

<400> 1328

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1329
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v49

<400> 1329

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Met Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1330
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v50

<400> 1330

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1331
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v51

<400> 1331

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Ala Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Ser Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1332
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v52

<220>
<221> VARIANT
<222> (64)..(64)
<223> X is a stop codon

<400> 1332

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly Ser
1   5   10   15

Asn Val Ala Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Xaa
    50   55   60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1333
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v53

<400> 1333

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Ser Phe Leu Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1334
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v54

<400> 1334

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro

35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe Leu Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1335
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v55

<400> 1335

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Val Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1336
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v56

<400> 1336

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asn Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1337
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v57

<400> 1337

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1338
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v58

<400> 1338

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys

50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1339
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v60

<400> 1339

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asp Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1340
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v61

<400> 1340

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Val Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1341
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v62

<400> 1341

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Arg
    50   55   60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1342
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v63

<400> 1342

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Pro
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Leu Phe His Ile Ser Gln Val Gln Val Arg Asp Glu Gly Gln Tyr

65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1343
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v64

<400> 1343

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1344
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v65

<400> 1344

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
        35   40   45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
    50   55   60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65   70   75   80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
                85   90   95

Leu Lys

<210> 1345
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v66

<400> 1345

Leu Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1   5   10   15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
            20   25   30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Glu Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1346
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v67

<400> 1346

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Phe
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr

85 90 95

Leu Lys

<210> 1347
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v68

<400> 1347

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Gly Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1348
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v69

<400> 1348

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Ser Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1349
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v70

<400> 1349

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Val Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1350
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v71

<400> 1350

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asp Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Ala Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1351
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v72

<400> 1351

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Ala Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Cys Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1352
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v73

<400> 1352

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser

1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn His
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1353
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v74

<400> 1353

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1354
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v75

<400> 1354

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ile Leu Gln Lys Val Asp Asn Asp Thr Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Ser Phe His Ile Pro His Val Gln Gly Gly Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1355

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v76

<400> 1355

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu
20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1356
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v77

<400> 1356

Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly Ser
1 5 10 15

Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu

20 25 30

Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala Ser Pro
35 40 45

His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys
50 55 60

Ala Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln Tyr
65 70 75 80

Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu Thr
85 90 95

Leu Lys

<210> 1357
<211> 102
<212> PRT
<213> Artificial Seqeunce

<220>
<223> PD-L2 IgV v1

<400> 1357

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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
100

<210> 1358
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v2

<400> 1358

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 Asp 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
100

<210> 1359
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v3

<400> 1359

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 Asp 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
            100

<210> 1360
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v4

<400> 1360

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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1361
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v5

<400> 1361

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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1362
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v6

<400> 1362

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 Gly 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 Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1363
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v7

<400> 1363

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 Ile 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1364
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v8

<400> 1364

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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1365
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v9

<400> 1365

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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1366
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v10

<400> 1366

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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1367
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v11

<400> 1367

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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

Arg 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
            100

<210> 1368
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v12

<400> 1368

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 His Val Gln Val Arg Asp Glu Gly Gln

65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1369
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v13

<400> 1369

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Gly 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
100

<210> 1370
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v14

<400> 1370

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Gly Asp Glu Gly Gln
65   70   75   80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1371
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v15

<400> 1371

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1372
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v16

<400> 1372

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu

85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1373
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v17

<400> 1373

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Ser 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 Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1374
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v18

<400> 1374

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1375
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v19

<400> 1375

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1376
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v20

<400> 1376

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 Asp 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 Asp Ala Arg Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala

100

<210> 1377
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v21

<400> 1377

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1378
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v22

<400> 1378

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1379
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v23

<400> 1379

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1380
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v24

<400> 1380

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Asp 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1381

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v25

<400> 1381

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Ile Leu Gln Lys Val Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1382
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v26

<400> 1382

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1383
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v27

<400> 1383

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1384
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v28

<400> 1384

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1385
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v29

<400> 1385

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Gly Asp Glu Gly Gln
65   70   75   80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1386
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v30

<400> 1386

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1387
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v31

<400> 1387

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1388
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v32

<400> 1388

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 His Val Gln Val Gly 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
100

<210> 1389
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v33

<400> 1389

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 His Val Gln Val Gly 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
            100

<210> 1390
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v34

<400> 1390

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Asp 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 Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Phe Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1391
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v35

<400> 1391

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile 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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1392
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v36

<400> 1392

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asp
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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1393
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v37

<400> 1393

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 Asp
            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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1394
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v38

<400> 1394

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln

65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1395
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v39

<400> 1395

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 His Val Arg Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1396
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v40

<400> 1396

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 Val 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 His Val Gln Val Gly Asp Glu Gly Gln
65   70   75   80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1397
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v41

<400> 1397

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ile Leu Gln Lys Val Asp 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 Leu 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
100

<210> 1398
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v42

<400> 1398

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 Asp 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 Leu Phe His Ile Pro His Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu

85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1399
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v43

<400> 1399

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1400
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v44

<400> 1400

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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
100

<210> 1401
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v45

<400> 1401

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1402
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v46

<400> 1402

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala

100

<210> 1403
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v47

<400> 1403

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1404
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v48

<400> 1404

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1405
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v49

<400> 1405

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Met 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1406
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v50

<400> 1406

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1407

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v51

<400> 1407

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Ala Asn
20 25 30

Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Ser 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1408
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v52

<220>
<221> VARIANT
<222> (65)..(65)
<223> X is a stop codon

<400> 1408

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu His Gly
1   5   10   15

Ser Asn Val Ala 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 Ala Ser
        35   40   45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
    50   55   60

Xaa Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65   70   75   80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1409
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v53

<400> 1409

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1410
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v54

<400> 1410

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Leu Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1411
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v55

<400> 1411

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Val Val Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1412
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v56

<400> 1412

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Gly Asn Glu Gly Gln
65   70   75   80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1413
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v57

<400> 1413

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Gly Asp Glu Gly Gln

65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1414
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v58

<400> 1414

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1415
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v60

<400> 1415

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1   5   10   15

Ser Asn Val Thr Leu Glu Cys Asp 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1416
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v61

<400> 1416

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Val Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Leu 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 Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1417
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v62

<400> 1417

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Arg Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu

85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1418
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v63

<400> 1418

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

Pro Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Leu Phe His Ile Ser Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1419
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v64

<400> 1419

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1420
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v65

<400> 1420

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80


Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85                  90                  95


Thr Leu Lys Val Lys Ala
            100


<210>  1421
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 IgV v66

<400>  1421

Leu Leu Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Glu Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65                  70                  75                  80


Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85                  90                  95


Thr Leu Lys Val Lys Ala
```

100

<210> 1422
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v67

<400> 1422

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

Phe Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1423
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v68

<400> 1423

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala Ser
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Gly Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1424
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v69

<400> 1424

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Ser 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1425
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v70

<400> 1425

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Val Asn Asp Ala 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 Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1426

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v71

<400> 1426

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asp 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 Ala 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 His Ala Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1427
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v72

<400> 1427

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala Ala Ser Leu Gln Lys Val Asp Asn Asp Thr Cys
35 40 45

Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
50 55 60

Lys Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1428
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v73

<400> 1428

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln Gly
1 5 10 15

Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
20 25 30

His 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1429
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v74

<400> 1429

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Gln Cys Ile Ile Thr Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1430
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v75

<400> 1430

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ile Leu Gln Lys Val Asp 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 His Val Gln Gly Gly Asp Glu Gly Gln
65   70   75   80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95

Thr Leu Lys Val Lys Ala
            100

<210> 1431
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v76

<400> 1431

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu Gln 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 Ala 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 Leu Phe His Ile Pro Gln Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1432
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v77

<400> 1432

Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Val Glu Gln 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 Ala 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 Leu Phe His Ile Pro His Val Gln Val Gly Asp Glu Gly Gln
65 70 75 80

Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr Lys Tyr Leu
85 90 95

Thr Leu Lys Val Lys Ala
100

<210> 1433
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 ECD

<400> 1433

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro

145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1434
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 ECD

<400> 1434

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Met Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190
```

```
Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  1435
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v91 ECD

<400>  1435

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

```
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
```

225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1436
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v92 ECD

<400> 1436

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270
```

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1437
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 ECD

<400> 1437

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala

100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn

305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1438
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v94 ECD

<400> 1438

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

```
Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 1439
<211> 329
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v95 ECD

<400> 1439

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                  10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Ala Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175


Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
```

180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1440
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v96 ECD

<400> 1440

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

```
Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220
```

```
Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  1441
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v97 ECD

<400>  1441

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
```

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Pro Ala Lys Gln Ser
65 70 75 80

Ile Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe

260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1442
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v98 ECD

<400> 1442

Gln Asp Val Arg Val Gln Val Leu Arg Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Val Leu Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Met Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Phe Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Val Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

```
His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Ala Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300
```

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1443
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v99 ECD

<400> 1443

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln

130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1444

<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 ECD

<400> 1444

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Ala Pro Gly Pro
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175
```

```
Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190


Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205


Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  1445
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v101 ECD

<400>  1445

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
```

```
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
```

210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1446
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 ECD

<400> 1446

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255
```

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1447
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 ECD

<400> 1447

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu

85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val

290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1448
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v104 ECD

<400> 1448

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Leu Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

```
Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 1449
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v105 ECD

<400> 1449

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Ala Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125


Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140


Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160


Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
```

165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1450
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v106 ECD

<400> 1450

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Pro Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205
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```
Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220


Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240


Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255


Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270


Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285


Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  1451
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v107 ECD

<400>  1451

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Leu Asp Ala Pro Ala Lys His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser

245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1452
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v108 ECD

<400> 1452

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Ser Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Leu Val
            100                 105                 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285
```

```
Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300


Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320


Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325


<210>  1453
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v109 ECD

<400>  1453

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Thr Ala Arg Gly Met Thr Trp Leu Arg Val Ile
```

115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly

325

<210> 1454
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 ECD

<400> 1454

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

```
Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
                245                 250                 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
            260                 265                 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
        275                 280                 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
    290                 295                 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305                 310                 315                 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
                325
```

<210> 1455
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v111 ECD

<400> 1455

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Leu Leu Arg Val Ile
115 120 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
130 135 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145 150 155 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
165 170 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
180 185 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys

195 200 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
210 215 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225 230 235 240

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1456
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v112 ECD

<400> 1456

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

```
Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
        115                 120                 125

Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
    130                 135                 140

Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
145                 150                 155                 160

Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
                165                 170                 175

Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
            180                 185                 190

Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
        195                 200                 205

Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
    210                 215                 220

Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
225                 230                 235                 240
```

Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
245 250 255

Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
260 265 270

Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
275 280 285

Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
290 295 300

Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
305 310 315 320

Thr Ala Gly Ala Gly Ala Thr Gly Gly
325

<210> 1457
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 IgV

<400> 1457

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser

65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1458
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 IgV

<400> 1458

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Met Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1459
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v91 IgV

<400> 1459

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1460
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v92 IgV

<400> 1460

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Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125
```

<210> 1461
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 IgV

<400> 1461

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
```

20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1462
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v94 IgV

<400> 1462

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

```
Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  1463
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v95 IgV

<400>  1463

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Ala Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
```

100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1464
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v96 IgV

<400> 1464

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1465
<211> 125
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v97 IgV

<400> 1465

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Pro Ala Lys Gln Ser
65 70 75 80

Ile Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1466
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v98 IgV

<400> 1466

Gln Asp Val Arg Val Gln Val Leu Arg Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Val Leu Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Met Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Phe Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Val Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Ala
        115   120   125

<210> 1467
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v99 IgV

<400> 1467

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

```
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
        115                 120                 125
```

<210> 1468
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1468

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Ala Pro Gly Pro
            20                  25                  30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95
```

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1469
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v101 IgV

<400> 1469

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1470

<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 IgV

<400> 1470

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1471
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 IgV

<400> 1471

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1472
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v104 IgV

<400> 1472

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Leu Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  1473
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v105 IgV

<400>  1473

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Ala Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
```

85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1474
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v106 IgV

<400> 1474

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Pro Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1475
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v107 IgV

<400> 1475

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Leu Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1476
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v108 IgV

<400> 1476

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Ser Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Leu Val
            100                 105                 110


Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  1477
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v109 IgV

<400>  1477

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Ala Arg Gly Met Thr Trp Leu
115 120 125

<210> 1478
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1478

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

```
Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu
        115                 120                 125


<210>  1479
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v111 IgV

<400>  1479

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Leu Leu
```

115 120 125

<210> 1480
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v112 IgV

<400> 1480

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu
115 120 125

<210> 1481
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 IgV

<400> 1481

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1482
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 IgV

<400> 1482

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Met Pro Gly Leu
20 25 30

```
His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  1483
<211>  127
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v91 IgV

<400>  1483

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
```

65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1484
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v92 IgV

<400> 1484

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 1485
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 IgV

<400> 1485

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 1486
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v94 IgV

<400> 1486

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 1487
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v95 IgV

<400> 1487

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu

20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Ala Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1488
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v96 IgV

<400> 1488

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1489
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v97 IgV

<400> 1489

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Pro Ala Lys Gln Ser
65 70 75 80

Ile Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Tyr Tyr Thr Cys Glu Phe Val

100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1490
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v98 IgV

<400> 1490

Gln Asp Val Arg Val Gln Val Leu Arg Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Val Leu Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Met Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Phe Glu Arg Leu Ser Leu Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Val Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Ala Arg Val
115 120 125

<210> 1491
<211> 127
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v99 IgV

<400> 1491

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
            100   105   110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 1492
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1492

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Ala Pro Gly Pro
            20   25   30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50   55   60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65   70   75   80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85   90   95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
            100   105   110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115   120   125

<210> 1493
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v101 IgV

<400> 1493

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1   5   10   15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20   25   30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35   40   45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser

50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1494
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 IgV

<400> 1494

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Trp Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Arg Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1495
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 IgV

<400> 1495

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1496

<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v104 IgV

<400> 1496

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Leu Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1497
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v105 IgV

<400> 1497

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly

1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Ala Trp Gln Arg Pro Asp Ala Pro Thr Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1498
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v106 IgV

<400> 1498

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Ser Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

```
Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Pro Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110

Thr Phe Pro Lys Gly Tyr Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  1499
<211>  127
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v107 IgV

<400>  1499

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30

His Ile Ser Leu Val Thr Trp Gln Arg Leu Asp Ala Pro Ala Lys His
        35                  40                  45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
```

85 90 95

His Gly Leu Thr Met Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1500
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v109 IgV

<400> 1500

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Lys His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Ser Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Lys Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Leu Val
100 105 110

Thr Phe Pro Lys Gly Thr Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1501
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v109 IgV

<400> 1501

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Thr Ala Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1502
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1502

```
Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
        35                  40                  45


Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
    50                  55                  60


Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65                  70                  75                  80


Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
                85                  90                  95


His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
            100                 105                 110


Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
        115                 120                 125


<210>  1503
<211>  127
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v111 IgV

<400>  1503

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1               5                   10                  15


Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
            20                  25                  30


His Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
```

35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Met Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
100 105 110

Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Leu Leu Arg Val
115 120 125

<210> 1504
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v112 IgV

<400> 1504

Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly
1 5 10 15

Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu
20 25 30

Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His
35 40 45

Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
50 55 60

Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
65 70 75 80

Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
85 90 95

His Gly Leu Thr Val Glu Asp Glu Gly Ile Tyr Thr Cys Glu Phe Val
100 105 110

Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val
115 120 125

<210> 1505
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 IgV

<400> 1505

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Gly Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser Trp Ser Val
100 105 110

Asp Ile Trp Leu

115

<210> 1506
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v121 IgV

<400> 1506

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Gly Ala Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asp
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Leu Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1507
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 IgV

<400> 1507

Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Leu Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Lys Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1508
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 IgV

<400> 1508

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

```
Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Arg Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1509
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v124 IgV

<400>  1509

Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
```

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1510
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v125 IgV

<400> 1510

Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Arg Met Ala Val Phe His Pro Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 1511
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 IgV

<400> 1511

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1512
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v127 IgV

<400> 1512

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115
```

<210> 1513
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 IgV

<400> 1513

```
Pro Gly Thr Gly Gly Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
```

20 25 30

Ile Glu Ala Thr His Val Ser Gln Leu Thr Trp Ala Arg Gln Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Glu Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser Trp Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1514
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v129 IgV

<400> 1514

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Ser Phe Pro Gln Gly Ser Trp Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1515
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v130 IgV

<400> 1515

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val

100 105 110

Asp Ile Trp Leu
115

<210> 1516
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v131 IgV

<400> 1516

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Asp Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1517
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v132 IgV

<400> 1517

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Arg Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Asp Gly
                85   90   95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1518
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v133 IgV

<400> 1518

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Leu Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1519
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v134 IgV

<400> 1519

Pro Gly Thr Gly Asp Ile Val Val Lys Ala Pro Thr Gln Val Phe Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1520
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v135 IgV

<400> 1520

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1521
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 IgV

<400> 1521

Pro Gly Thr Gly Asp Ile Ile Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Ser Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Tyr Pro Gln Arg Val Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1522

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 IgV

<400> 1522

Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Leu Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Ser Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1523
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v138 IgV

<400> 1523

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Cys Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1524
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 IgV

<400> 1524

Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1525
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 IgV

<400> 1525

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Leu Ser Gly Leu Arg Ala Glu Asp Glu Gly

85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1526
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v141 IgV

<400> 1526

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Glu
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly Thr Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1527
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 IgV

<400> 1527

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Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115
```

<210> 1528
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 IgV

<400> 1528

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Gly Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser
            100                 105                 110


Trp Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1529
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v121 IgV

<400>  1529

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Gly Ala Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
```

35 40 45

Leu Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1530
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 IgV

<400> 1530

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Leu Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Lys Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1531
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 IgV

<400> 1531

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 1532
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v124 IgV

<400> 1532

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1533
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v125 IgV

<400> 1533

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Arg Met Ala Val Phe His Pro Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1534
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 IgV

<400> 1534

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1535
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v127 IgV

<400>  1535

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
```

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1536
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 IgV

<400> 1536

Trp Pro Pro Pro Gly Thr Gly Gly Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Ile Glu Ala Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Gln Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Glu Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser
100 105 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1537
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v129 IgV

<400> 1537

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ser Phe Pro Gln Gly Ser
            100   105   110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1538
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v130 IgV

<400> 1538

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1539
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v131 IgV

<400> 1539

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Phe Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln

20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Asp Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1540
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v132 IgV

<400> 1540

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Arg Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

```
Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Asp Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1541
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v133 IgV

<400>  1541

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1542
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v134 IgV

<400> 1542

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Lys Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1543
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v135 IgV

<400> 1543

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1544
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 IgV

<400> 1544

Trp Pro Pro Pro Gly Thr Gly Asp Ile Ile Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Ser Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Tyr Pro Gln Arg Val
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1545
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 IgV

<400> 1545

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Ser Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1546
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v138 IgV

<400> 1546

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Cys Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1547
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 IgV

<400> 1547

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1548

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 IgV

<400> 1548

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Leu Ser Gly Leu Arg Ala Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1549
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v141 IgV

<400> 1549

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Glu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly
65 70 75 80

Thr Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1550
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 IgV

<400> 1550

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1551
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 ECD

<400> 1551

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Gly Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser
100 105 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1552
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v121 ECD

<400> 1552

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Gly Ala Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Leu Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 1553
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 ECD

<400> 1553

```
Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Leu Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Lys Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Glu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1554
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 ECD

<400> 1554

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Asp Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1555
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v124 ECD

<400> 1555

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg

35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1556
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v125 ECD

<400> 1556

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Arg Met Ala Val Phe His Pro Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

```
Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1557
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 ECD

<400> 1557

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1558
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v127 ECD

<400> 1558

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1559
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 ECD

<400> 1559

```
Trp Pro Pro Pro Gly Thr Gly Gly Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Ile Glu Ala Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


Gln Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Glu Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ala Phe Pro Gln Gly Ser
            100                 105                 110


Trp Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1560
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v129 ECD

<400> 1560

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Ser Phe Pro Gln Gly Ser
            100                 105                 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

```
Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
               245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1561
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v130 ECD

<400>  1561

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
```

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1562
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v131 ECD

<400> 1562

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Asp Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Asp Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 1563
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v132 ECD

<400> 1563

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Arg Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Asp Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1564
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v133 ECD

<400> 1564

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Ala Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1565
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v134 ECD

<400>  1565

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Lys Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1566
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v135 ECD

<400> 1566

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

```
Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1567
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 ECD

<400> 1567

Trp Pro Pro Pro Gly Thr Gly Asp Ile Ile Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Ser Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Tyr Pro Gln Arg Val

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 1568
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 ECD

<400> 1568

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Ser Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 1569
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v138 ECD

<400> 1569

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Cys Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Val Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1570
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 ECD

<400> 1570

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Thr Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1571
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 ECD

<400> 1571

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Leu Ser Gly Leu Arg Ala Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1572
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v141 ECD

<400> 1572

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Glu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly
65 70 75 80

Thr Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1573
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 ECD

<400> 1573

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1574

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v143 ECD

<400> 1574

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1575
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v143 IgV

<400>  1575

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
```

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Trp Tyr Ala
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1576
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v143 IgV

<400> 1576

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1577
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 ECD

<400> 1577

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Asp Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Asn Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Gln Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Tyr Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1578
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v145 ECD

<400> 1578

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Leu Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 1579
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v146 ECD

<400> 1579

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr Gln Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Lys Lys Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Val Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1580
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v147 ECD

<400> 1580

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Arg
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Ala Phe Pro Gln Gly Ser
            100                 105                 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1581
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v148 ECD

<400> 1581

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val His Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Ser Ser Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg

35 40 45

His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Thr Arg Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1582
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v149 ECD

<400> 1582

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Pro Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Gln Gly Glu Ser Gly Ser Met Ala Val Tyr His Arg Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1583
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v150 ECD

<400> 1583

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Cys Ala Arg
35 40 45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Thr Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Thr Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1584
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v151 ECD

<400> 1584

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Thr Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Gly Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Trp Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1585
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v152 ECD
```

<400> 1585

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Phe Val Gln Ala Pro Ser Gln
1               5                   10                  15


Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Gln
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Met Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1586
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v153 ECD

<400> 1586

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Met Gly Asp Ser Val Thr Leu Pro Cys Phe Leu Gln
20 25 30

```
Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65                  70                  75                  80

Ala Glu Leu Trp Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Gly Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1587
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v154 ECD

<400> 1587

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Val Ser Gly Gly Met Ala Val Phe His Arg Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly

65 70 75 80

Ala Gly Leu Arg Asn Ala Thr Leu Arg Ile Ser Arg Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1588
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v155 ECD

<400> 1588

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr His
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 1589
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 ECD

<400> 1589

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Ala Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1590
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v157 ECD

<400> 1590

```
Trp Pro Pro Pro Gly Thr Gly Gly Ile Val Ala Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Ala Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Leu Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Ala Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1591
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 ECD

<400> 1591

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln

```
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg
        35                  40                  45

His Ser Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
```

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1592
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v159 ECD

<400> 1592

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

```
Ser Tyr Ser Glu Pro Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1593
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v160 ECD

<400> 1593

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Pro Gly Arg Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 1594
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 ECD

<400> 1594

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asn Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Asn Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 1595
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v162 ECD

<400> 1595

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Ser Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Val Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1596
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v163 ECD

<400> 1596

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

```
Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe Asn Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Ala Ala Ala Arg Pro Gly
65                  70                  75                  80

Thr Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1597
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 ECD

<400> 1597

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Arg Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro

50 55 60

Ser Tyr Ser Asp Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Gly Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala

260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1598
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v165 ECD

<400> 1598

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Lys Val Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Thr Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300
```

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1599
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v166 ECD

<400> 1599

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Leu Ala Val Phe His Gln Arg Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Ile Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala

130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1600

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 ECD

<400> 1600

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Met Pro Phe Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Leu Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Ser Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175
```

```
Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 1601
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v168 ECD

<400> 1601

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
```

```
1               5                   10                  15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Glu Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
```

210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1602
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 ECD

<400> 1602

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Ile Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg
35 40 45

```
His Gly Lys Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255
```

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1603
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 ECD

<400> 1603

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His His Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Val Ser Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu

290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1604
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v171 ECD

<400> 1604

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Arg Tyr Leu Gln
20 25 30

Val Pro Asp Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ala Tyr Gly Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Arg Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

```
Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 1605
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v172 ECD

<400> 1605

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Arg Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60


Ser Tyr Thr Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
```

165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1606
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v173 ECD

<400> 1606

```
Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205
```

```
Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1607
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v174 ECD

<400>  1607

Trp Pro Pro Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Ser Leu Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly

245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1608
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v175 ECD

<400> 1608

Trp Pro Pro Pro Gly Thr Gly Glu Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Ala Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

```
Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285
```

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1609
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 ECD

<400> 1609

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Ala Ser Gln Leu Thr Trp Ala Arg
35 40 45

Arg Gly Glu Ser Gly Cys Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Ser Gly
65 70 75 80

Ala Glu Leu Arg Tyr Ala Ser Pro Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr

115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1610
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v177 ECD

<400> 1610

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Glu Gln Ala Pro Thr Gln
1               5                   10                  15


Val His Gly Tyr Leu Gly Asp Ser Glu Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160
```

```
Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320

Ser Arg Asn
```

<210> 1611
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 ECD

<400> 1611

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Asp
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Ala Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
```

195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1612
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 ECD

<400> 1612

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Arg Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240
```

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1613
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v180 ECD

<400> 1613

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Met Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Gly Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Met Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr

275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1614
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v181 ECD

<400> 1614

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Tyr Gly Phe Leu Gly Asp Ser Ala Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Gly Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Thr Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

```
Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320
```

Ser Arg Asn

<210> 1615
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v182 ECD

<400> 1615

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Gly Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Gln Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
```

145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1616
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v183 ECD

<400> 1616

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe Arg Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Gly Ala Ser Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125


Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140


Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190
```

```
Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn



<210>  1617
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v184 ECD

<400>  1617

Trp Pro Pro Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

20 25 30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Gly Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn

225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1618
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v185 ECD

<400> 1618

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ala Gly Ser Met Ala Ala Phe His Arg Thr Lys Gly Pro
50 55 60

```
Cys Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Thr Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Tyr Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270
```

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1619
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v186 ECD

<400> 1619

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Asp Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser

100 105 110

Arg Asn Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile

305 310 315 320

Ser Arg Asn

<210> 1620
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 ECD

<400> 1620

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Thr Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

```
Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160


Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175


Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190


Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205


Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220


Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225                 230                 235                 240


Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
                245                 250                 255


Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
            260                 265                 270


Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
        275                 280                 285


Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
    290                 295                 300


Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305                 310                 315                 320


Ser Arg Asn
```

<210> 1621
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v188 ECD

<400> 1621

Trp Pro Pro Pro Gly Thr Gly Asp Asp Val Met Leu Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Val Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Arg Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Gln Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
115 120 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
130 135 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145 150 155 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
165 170 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser

180 185 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
195 200 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
210 215 220

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1622
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v189 ECD

<400> 1622

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ser Gln
1 5 10 15

```
Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys His Leu Leu
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Ala Lys Pro Gln Asn Thr
        115                 120                 125

Ala Glu Val Gln Lys Val Gln Leu Thr Gly Glu Pro Val Pro Met Ala
    130                 135                 140

Arg Cys Val Ser Thr Gly Gly Arg Pro Pro Ala Gln Ile Thr Trp His
145                 150                 155                 160

Ser Asp Leu Gly Gly Met Pro Asn Thr Ser Gln Val Pro Gly Phe Leu
                165                 170                 175

Ser Gly Thr Val Thr Val Thr Ser Leu Trp Ile Leu Val Pro Ser Ser
            180                 185                 190

Gln Val Asp Gly Lys Asn Val Thr Cys Lys Val Glu His Glu Ser Phe
        195                 200                 205

Glu Lys Pro Gln Leu Leu Thr Val Asn Leu Thr Val Tyr Tyr Pro Pro
    210                 215                 220
```

Glu Val Ser Ile Ser Gly Tyr Asp Asn Asn Trp Tyr Leu Gly Gln Asn
225 230 235 240

Glu Ala Thr Leu Thr Cys Asp Ala Arg Ser Asn Pro Glu Pro Thr Gly
245 250 255

Tyr Asn Trp Ser Thr Thr Met Gly Pro Leu Pro Pro Phe Ala Val Ala
260 265 270

Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys Pro Ile Asn Thr
275 280 285

Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala Arg Gln Ala Glu
290 295 300

Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu His Ser Gly Ile
305 310 315 320

Ser Arg Asn

<210> 1623
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 IgV

<400> 1623

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Asp
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Asn Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser

```
    50                  55                  60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Gln
65                  70                  75                  80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95

Asn Tyr Thr Cys Leu Phe Val Met Tyr Pro Gln Gly Ser Arg Ser Val
            100                 105                 110

Asp Ile Trp Leu
        115


<210>  1624
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v145 IgV

<400>  1624

Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Leu Gly
1               5                   10                  15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45

Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60

Glu Leu Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Glu Glu Leu
65                  70                  75                  80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95
```

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1625
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v146 IgV

<400> 1625

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr Gln Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Lys Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Val Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1626

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v147 IgV

<400> 1626

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Arg Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Ala Phe Pro Gln Gly Ser Trp Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1627
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v148 IgV

<400> 1627

Pro Gly Thr Gly Asp Val Val Val His Ala Pro Thr Gln Val Thr Gly

1 5 10 15

Phe Ser Ser Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Ala Phe His Gln Thr Arg Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1628
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v149 IgV

<400> 1628

Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Pro Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Gln Gly Glu
35 40 45

```
Ser Gly Ser Met Ala Val Tyr His Arg Thr Lys Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1629
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v150 IgV

<400>  1629

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Cys Ala Arg Arg Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Thr Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Thr Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
```

85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1630
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v151 IgV

<400> 1630

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Thr Gln Leu Thr Trp Ala Arg His Gly Gly
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Trp Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1631
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v152 IgV

<400> 1631

Pro Gly Thr Gly Asp Val Phe Val Gln Ala Pro Ser Gln Val Leu Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Gln His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Met
            100   105   110

Asp Ile Trp Leu
        115

<210> 1632
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v153 IgV

<400> 1632

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Met Gly Asp Ser Val Thr Leu Pro Cys Phe Leu Gln Val Pro Asp
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65                  70                  75                  80


Trp Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Gly Ile Trp Leu
        115


<210>  1633
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v154 IgV

<400>  1633

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Val
```

35 40 45

Ser Gly Gly Met Ala Val Phe His Arg Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly Ala Gly Leu
65 70 75 80

Arg Asn Ala Thr Leu Arg Ile Ser Arg Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1634
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v155 IgV

<400> 1634

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr His Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1635
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 IgV

<400> 1635

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro Ser Tyr Leu
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Ala
100 105 110

Asp Ile Trp Leu

115

<210> 1636
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v157 IgV

<400> 1636

Pro Gly Thr Gly Gly Ile Val Ala Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Ala Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Leu Phe Pro Gln Gly Ser Arg Ser Ala
100 105 110

Asp Ile Trp Leu
115

<210> 1637
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 IgV

<400> 1637

Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg His Ser Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1638
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v159 IgV

<400> 1638

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

```
Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Pro Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1639
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v160 IgV

<400>  1639

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Pro Gly Arg Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
```

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1640
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 IgV

<400> 1640

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asn Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Asn Val
100 105 110

Asp Ile Trp Leu
        115

<210> 1641
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v162 IgV

<400> 1641

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Ser Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Val
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1642
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v163 IgV

<400> 1642

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe Asn Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Ala Ala Ala Arg Pro Gly Thr Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115
```

<210> 1643
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 IgV

<400> 1643

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
```

20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Arg Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Asp Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Gly Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1644
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v165 IgV

<400> 1644

Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ala Tyr Val
50 55 60

```
Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Lys Val Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Thr Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1645
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v166 IgV

<400>  1645

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Leu Ala Val Phe His Gln Arg Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Ile Met Phe Pro Gln Gly Ser Arg Ser Val
```

100 105 110

Asp Ile Trp Leu
115

<210> 1646
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 IgV

<400> 1646

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Met Pro Phe
20 25 30

Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Leu Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Ser Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1647
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v168 IgV

<400> 1647

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Glu Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Trp Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1648
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 IgV

<400> 1648

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Phe Gly
1   5   10   15

Ile Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg His Gly Lys
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1649
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 IgV

<400> 1649

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1   5   10   15

Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His His Thr Gln Gly Pro Ser Tyr Ser

50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Val Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1650
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v171 IgV

<400> 1650

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Gly Ser Val Thr Leu Pro Arg Tyr Leu Gln Val Pro Asp
20 25 30

Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro Ala Tyr Gly
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Arg Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1651
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v172 IgV

<400> 1651

Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Arg Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Thr
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1652

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v173 IgV

<400> 1652

Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Arg Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1653
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v174 IgV

<400> 1653

Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln Val Phe Gly

1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Ser Leu Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1654
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v175 IgV

<400> 1654

Pro Gly Thr Gly Glu Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Ala Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1655
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 IgV

<400> 1655

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Ala Ser Gln Leu Thr Trp Ala Arg Arg Gly Glu
35 40 45

Ser Gly Cys Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Ser Gly Ala Glu Leu
65 70 75 80

Arg Tyr Ala Ser Pro Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly

85 90 95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1656
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v177 IgV

<400> 1656

Pro Gly Thr Gly Asp Val Val Glu Gln Ala Pro Thr Gln Val His Gly
1 5 10 15

Tyr Leu Gly Asp Ser Glu Thr Leu Pro Cys Tyr Leu Gln Val Pro Ser
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg Arg Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Arg Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1657
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 IgV

<400> 1657

Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln Val Phe Gly
1 5 10 15

Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Asp Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Ala Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1658
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 IgV

<400> 1658

```
Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Arg Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1659
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v180 IgV

<400>  1659

Pro Gly Thr Gly Asp Leu Val Met Gln Ala Pro Thr Gln Val Ser Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Ser
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
```

35 40 45

Ser Gly Gly Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Met
100 105 110

Asp Ile Trp Leu
115

<210> 1660
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v181 IgV

<400> 1660

Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln Val Tyr Gly
1 5 10 15

Phe Leu Gly Asp Ser Ala Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Gly Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Thr Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1661
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v182 IgV

<400> 1661

Pro Gly Thr Gly Asp Val Gly Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Gln Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu

115

<210> 1662
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v183 IgV

<400> 1662

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe Arg Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Gly Ala Ser Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1663
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v184 IgV

<400> 1663

Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln Val Ser Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Gly Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile Arg Ser Val
100 105 110

Asp Ile Trp Leu
115

<210> 1664
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v185 IgV

<400> 1664

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
20 25 30

```
Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35                  40                  45


Ala Gly Ser Met Ala Ala Phe His Arg Thr Lys Gly Pro Cys Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65                  70                  75                  80


Arg Asn Ala Ser Leu Arg Met Thr Gly Leu Arg Val Glu Asp Glu Gly
                85                  90                  95


Tyr Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100                 105                 110


Asp Ile Trp Leu
        115


<210>  1665
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v186 IgV

<400>  1665

Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln Val Phe Gly
1               5                   10                  15


Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asp
            20                  25                  30


Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg His Gly Glu
        35                  40                  45


Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro Ser Tyr Ser
    50                  55                  60


Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
```

65 70 75 80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Asp
85 90 95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Asn Val
100 105 110

Asp Ile Trp Leu
115

<210> 1666
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 IgV

<400> 1666

Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln Val Thr Gly
1 5 10 15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Ser
20 25 30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
35 40 45

Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser
50 55 60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65 70 75 80

Arg Asn Ala Thr Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
85 90 95

Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val
100 105 110

Asp Ile Trp Leu
        115

<210> 1667
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v188 IgV

<400> 1667

Pro Gly Thr Gly Asp Asp Val Met Leu Ala Pro Thr Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn
            20   25   30

Met Val Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Ile Ala Val Phe His Arg Thr Gln Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Gln Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1668
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v189 IgV

<400> 1668

Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ser Gln Val Ser Gly
1   5   10   15

Phe Leu Gly Asp Ser Val Thr Leu Pro Cys His Leu Leu Val Pro Asn
            20   25   30

Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu
        35   40   45

Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro Ser Tyr Ser
    50   55   60

Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly Ala Glu Leu
65   70   75   80

Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu Asp Glu Gly
                85   90   95

Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser Arg Ser Val
            100   105   110

Asp Ile Trp Leu
        115

<210> 1669
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 IgV

<400> 1669

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Asp Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln

20 25 30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Asn Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Gln Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Tyr Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1670
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v145 IgV

<400> 1670

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

```
Ser Tyr Ser Glu Leu Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Glu Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1671
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v146 IgV

<400>  1671

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr Gln Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Lys Lys Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Val Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1672
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v147 IgV

<400> 1672

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Arg
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Ala Phe Pro Gln Gly Ser
100 105 110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1673
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v148 IgV

<400> 1673

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val His Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Ser Ser Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Ala Phe His Gln Thr Arg Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1674
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v149 IgV

<400> 1674

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1   5   10   15

```
Val Ser Gly Phe Leu Gly Asp Pro Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

Gln Gly Glu Ser Gly Ser Met Ala Val Tyr His Arg Thr Lys Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120
```

<210> 1675
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v150 IgV

<400> 1675

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Cys Ala Arg
        35                  40                  45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
```

50 55 60

Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Thr Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Thr Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1676
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v151 IgV

<400> 1676

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Thr Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Gly Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Trp Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1677
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v152 IgV

<400> 1677

Trp Pro Pro Pro Gly Thr Gly Asp Val Phe Val Gln Ala Pro Ser Gln
1 5 10 15

Val Leu Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Gln
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Met Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1678

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v153 IgV

<400> 1678

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Met Gly Asp Ser Val Thr Leu Pro Cys Phe Leu Gln
20 25 30

Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Trp Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Gly Ile Trp Leu Arg Val Leu
115 120

<210> 1679
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v154 IgV

<400> 1679

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln

1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Val Ser Gly Gly Met Ala Val Phe His Arg Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Gln Gly
65 70 75 80

Ala Gly Leu Arg Asn Ala Thr Leu Arg Ile Ser Arg Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1680
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v155 IgV

<400> 1680

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr His
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1681
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 IgV

<400> 1681

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Arg Thr Gln Gly Pro
    50   55   60

Ser Tyr Leu Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Ala Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1682
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v157 IgV

<400> 1682

Trp Pro Pro Pro Gly Thr Gly Gly Ile Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Pro Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Ala Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Leu Phe Pro Gln Gly Ser
100 105 110

Arg Ser Ala Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1683
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 IgV

<400> 1683

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg
35 40 45

His Ser Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Gly Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1684
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v159 IgV

<400> 1684

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Pro Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1685
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v160 IgV

<400>  1685

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg
```

35 40 45

His Gly Glu Pro Gly Arg Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1686
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 IgV

<400> 1686

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asn Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Asn Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1687
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v162 IgV

<400> 1687

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Ser Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Val Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 1688
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v163 IgV

<400> 1688

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe Asn Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Ala Ala Ala Arg Pro Gly
65 70 75 80

Thr Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1689
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 IgV

<400> 1689

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Arg Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Asp Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Gly Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1690
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v165 IgV

<400> 1690

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Ala Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ala Tyr Val Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Lys Val Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Thr Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1691
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v166 IgV

<400>  1691

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Leu Ala Val Phe His Gln Arg Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
```

65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Ile Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1692
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 IgV

<400> 1692

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ile Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Met Pro Phe Met Glu Val Ser His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Leu Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Ser Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1693
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v168 IgV

<400> 1693

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Glu Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Glu Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100   105   110

Trp Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1694
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 IgV

<400> 1694

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Ile Leu Gly Asp Ser Val Met Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Val Arg
        35                  40                  45


His Gly Lys Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120
```

<210> 1695
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 IgV

<400> 1695

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln
```

20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His His Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Val Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1696
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v171 IgV

<400> 1696

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Gly Ser Val Thr Leu Pro Arg Tyr Leu Gln
20 25 30

Val Pro Asp Met Gly Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

```
Ala Tyr Gly Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Gly Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Arg Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1697
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v172 IgV

<400>  1697

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Glu Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Arg Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
    50                  55                  60


Ser Tyr Thr Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
```

100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1698
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v173 IgV

<400> 1698

Trp Pro Pro Pro Gly Thr Gly Asp Ile Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asp Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1699
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v174 IgV

<400> 1699

Trp Pro Pro Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Ser Leu Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1700
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v175 IgV

<400> 1700

Trp Pro Pro Pro Gly Thr Gly Glu Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35   40   45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Ala Gln Gly Pro
    50   55   60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65   70   75   80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85   90   95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100   105   110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115   120

<210> 1701
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 IgV

<400> 1701

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1   5   10   15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20   25   30

Val Pro Asn Met Glu Val Thr His Ala Ser Gln Leu Thr Trp Ala Arg
        35   40   45

Arg Gly Glu Ser Gly Cys Met Ala Val Phe His Gln Thr Gln Gly Pro

```
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Ser Gly
65                  70                  75                  80

Ala Glu Leu Arg Tyr Ala Ser Pro Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120
```

<210> 1702
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v177 IgV

<400> 1702

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Glu Gln Ala Pro Thr Gln
1               5                   10                  15

Val His Gly Tyr Leu Gly Asp Ser Glu Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30

Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45

Arg Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95
```

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1703
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 IgV

<400> 1703

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Phe Gly Phe Leu Gly Ala Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Asp
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Ala Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1704

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 IgV

<400> 1704

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Arg Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120
```

<210> 1705
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v180 IgV

<400> 1705

```
Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Met Gln Ala Pro Thr Gln
```

1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Gly Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Met Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1706
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v181 IgV

<400> 1706

Trp Pro Pro Pro Gly Thr Gly Asp Leu Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Tyr Gly Phe Leu Gly Asp Ser Ala Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Gly Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

```
His Gly Glu Ser Gly Ser Val Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Thr Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Ile Ser Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Thr Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1707
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v182 IgV

<400>  1707

Trp Pro Pro Pro Gly Thr Gly Asp Val Gly Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
    50                  55                  60


Ser Tyr Ser Glu Ser Lys Arg Gln Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
```

85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1708
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v183 IgV

<400> 1708

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe Arg Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Gly Ala Ser Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1709
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v184 IgV

<400> 1709

Trp Pro Pro Pro Gly Thr Gly Asp Ala Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Thr Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Gly Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Thr Phe Val Thr Phe Pro Gln Arg Ile
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1710
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v185 IgV

<400> 1710

```
Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1               5                   10                  15


Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
        35                  40                  45


His Gly Glu Ala Gly Ser Met Ala Ala Phe His Arg Thr Lys Gly Pro
    50                  55                  60


Cys Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65                  70                  75                  80


Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Thr Gly Leu Arg Val Glu
                85                  90                  95


Asp Glu Gly Tyr Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
            100                 105                 110


Arg Ser Val Asp Ile Trp Leu Arg Val Leu
        115                 120


<210>  1711
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v186 IgV

<400>  1711

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1               5                   10                  15


Val Phe Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
            20                  25                  30


Val Pro Asp Met Glu Val Thr His Val Ser Gln Leu Thr Trp Glu Arg
```

35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Lys Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Asp Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Asn Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1712
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 IgV

<400> 1712

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Ala Gln Ala Pro Thr Gln
1 5 10 15

Val Thr Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Ser Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Thr Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Thr Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1713
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v188 IgV

<400> 1713

Trp Pro Pro Pro Gly Thr Gly Asp Asp Val Met Leu Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Val Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Ile Ala Val Phe His Arg Thr Gln Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Gln Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Met Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu

115 120

<210> 1714
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v189 IgV

<400> 1714

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Ser Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys His Leu Leu
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Arg Gly Pro
50 55 60

Ser Tyr Ser Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Pro Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Ser Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Leu Phe Val Met Phe Pro Gln Gly Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu
115 120

<210> 1715
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Stack Fc Lysine removed (homodimeric)

<400> 1715

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
```

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly
225 230

<210> 1716
<211> 494
<212> PRT
<213> Artificial Seqeuence

<220>
<223> PD-L1/CD155 Stack 1 Fc fusion

<400> 1716

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
100 105 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly Ser Gly
115 120 125

```
Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
    130                 135                 140

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
145                 150                 155                 160

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                165                 170                 175

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            180                 185                 190

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        195                 200                 205

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    210                 215                 220

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
225                 230                 235                 240

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                245                 250                 255

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            260                 265                 270

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        275                 280                 285

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    290                 295                 300

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
305                 310                 315                 320

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                325                 330                 335
```

```
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            340                 345                 350


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
        355                 360                 365


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Thr Val Thr Val
    370                 375                 380


Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
385                 390                 395                 400


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
                405                 410                 415


Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
            420                 425                 430


Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
        435                 440                 445


Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
    450                 455                 460


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
465                 470                 475                 480


Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val Asn Ala
                485                 490


<210>  1717
<211>  494
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1/CD155 Stack 2 Fc fusion

<400>  1717

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110

Val Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
        115                 120                 125

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
```

210 215 220

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
355 360 365

Gly Gly Gly Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln
370 375 380

Ala Pro Thr Gln Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro
385 390 395 400

Cys Tyr Leu Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu
405 410 415

Thr Trp Ala Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln

420 425 430

Thr Gln Gly Pro Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala
435 440 445

Ala Arg Leu Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly
450 455 460

Leu Arg Val Glu Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe
465 470 475 480

Pro Gln Arg Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu
485 490

<210> 1718
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD155 Stack 3 Fc fusion

<400> 1718

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
1 5 10 15

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
20 25 30

Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
35 40 45

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
50 55 60

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
65 70 75 80

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
85 90 95

```
Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
            100                 105                 110

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Thr Val Thr Val Pro Lys
    130                 135                 140

Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys
145                 150                 155                 160

Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp
                165                 170                 175

Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu Glu Asp
            180                 185                 190

Gln Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys
        195                 200                 205

Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys
    210                 215                 220

Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Gly
225                 230                 235                 240

Ala Asp Tyr Lys Arg Ile Thr Val Lys Val Asn Ala Gly Gly Gly Gly
                245                 250                 255

Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
            260                 265                 270

Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe
        275                 280                 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    290                 295                 300
```

```
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
305                 310                 315                 320

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                325                 330                 335

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            340                 345                 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        355                 360                 365

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    370                 375                 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385                 390                 395                 400

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
```

<210> 1719
<211> 494
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1/CD155 Stack 4 Fc fusion

<400> 1719

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
100 105 110

Val Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro
130 135 140

Thr Gln Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr
145 150 155 160

Leu Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp
165 170 175

Ala Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln

180 185 190

Gly Pro Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg
195 200 205

Leu Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg
210 215 220

Val Glu Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln
225 230 235 240

Arg Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
260 265 270

Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe
275 280 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
290 295 300

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
305 310 315 320

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
325 330 335

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
340 345 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
355 360 365

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
370 375 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

385 390 395 400

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
405 410 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
420 425 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
435 440 445

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
450 455 460

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465 470 475 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 1720
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD155 Stack 5 Fc fusion

<400> 1720

His Met Ser Ser Val Ser Ala Gln Glu Pro Lys Ser Ser Asp Lys Thr
1 5 10 15

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser
20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
50 55 60

```
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
65                  70                  75                  80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                85                  90                  95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            100                 105                 110

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        115                 120                 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    130                 135                 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
145                 150                 155                 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                165                 170                 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            180                 185                 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        195                 200                 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    210                 215                 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Trp
                245                 250                 255

Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln Val
            260                 265                 270
```

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Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln Val
        275                 280                 285

Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg His
    290                 295                 300

Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro Trp
305                 310                 315                 320

Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly Ala
                325                 330                 335

Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu Asp
            340                 345                 350

Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser Arg
        355                 360                 365

Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly Ser Gly Gly
    370                 375                 380

Gly Gly Ser Gly Gly Gly Gly Ser Phe Thr Val Thr Val Pro Lys Asp
385                 390                 395                 400

Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe
                405                 410                 415

Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu
            420                 425                 430

Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu Glu Asp Gln
        435                 440                 445

Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp
    450                 455                 460

Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu
465                 470                 475                 480
```

Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Gly Ala
485 490 495

Asp Tyr Lys Arg Ile Thr Val Lys Val Asn Ala
500 505

<210> 1721
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD155 Stack 6 Fc fusion

<400> 1721

His Met Ser Ser Val Ser Ala Gln Glu Pro Lys Ser Ser Asp Lys Thr
1 5 10 15

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser
20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
100 105 110

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
115 120 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

130 135 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
145 150 155 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
165 170 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
180 185 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
195 200 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
210 215 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe
245 250 255

Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn
260 265 270

Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala
275 280 285

Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe
290 295 300

Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg Gln
305 310 315 320

Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu
325 330 335

Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met

340 345 350

Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
355 360 365

Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr
385 390 395 400

Gln Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu
405 410 415

Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala
420 425 430

Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly
435 440 445

Pro Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu
450 455 460

Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val
465 470 475 480

Glu Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg
485 490 495

Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu
500 505

<210> 1722
<211> 635
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD112/CD155 Stack 1 Fc fusion

<400> 1722

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110

Val Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro
    130                 135                 140

Thr Gln Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr
145                 150                 155                 160

Leu Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp
                165                 170                 175

Ala Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln
            180                 185                 190

Gly Pro Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg
        195                 200                 205
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Leu Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg
    210                 215                 220

Val Glu Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln
225                 230                 235                 240

Arg Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly
                245                 250                 255

Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
            260                 265                 270

Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe
        275                 280                 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    290                 295                 300

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
305                 310                 315                 320

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                325                 330                 335

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            340                 345                 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        355                 360                 365

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    370                 375                 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385                 390                 395                 400

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
                485                 490                 495

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Val Arg
            500                 505                 510

Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly Thr Val Glu
        515                 520                 525

Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr Ile Ser Leu
    530                 535                 540

Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln Asn Val Ala
545                 550                 555                 560

Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro Lys Pro Gly
                565                 570                 575

Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr Gly Gln Asp
            580                 585                 590

Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His Gly Leu Thr
        595                 600                 605

Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr Phe Pro Lys
    610                 615                 620
```

Gly Phe Val Arg Gly Met Thr Trp Leu Arg Val
625 630 635

<210> 1723
<211> 635
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD112/CD155 Stack 2 Fc fusion

<400> 1723

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
100 105 110

Val Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro
130 135 140

Thr Gln Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr

145 150 155 160

Leu Gln Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp
165 170 175

Ala Arg His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln
180 185 190

Gly Pro Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg
195 200 205

Leu Gly Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg
210 215 220

Val Glu Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln
225 230 235 240

Arg Ser Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Asp Val Arg Val Gln
260 265 270

Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly Thr Val Glu Leu Pro
275 280 285

Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr Ile Ser Leu Val Thr
290 295 300

Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln Asn Val Ala Ala Phe
305 310 315 320

His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro Lys Pro Gly Ser Glu
325 330 335

Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr Gly Gln Asp Thr Glu
340 345 350

Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His Gly Leu Thr Val Glu

355 360 365

Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr Phe Pro Lys Gly Phe
370 375 380

Val Arg Gly Met Thr Trp Leu Arg Val Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
405 410 415

Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro
420 425 430

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
435 440 445

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
450 455 460

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
465 470 475 480

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
485 490 495

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
500 505 510

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
515 520 525

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
530 535 540

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
545 550 555 560

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

565 570 575

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
580 585 590

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
595 600 605

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
610 615 620

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
625 630 635

<210> 1724
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1/CD112/CD155 Stack 3 Fc fusion

<400> 1724

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110

Val Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gln Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln
    130                 135                 140

Leu Gly Gly Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro
145                 150                 155                 160

Gly Leu Tyr Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala
                165                 170                 175

Asn His Gln Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe
            180                 185                 190

Pro Ser Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys
        195                 200                 205

Gln Ser Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu
    210                 215                 220

Ala Leu His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu
225                 230                 235                 240

Phe Ala Thr Phe Pro Lys Gly Phe Val Arg Gly Met Thr Trp Leu Arg
                245                 250                 255

Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            260                 265                 270

Trp Pro Pro Pro Gly Thr Gly Asp Val Val Val Gln Ala Pro Thr Gln
        275                 280                 285

Val Ser Gly Phe Leu Gly Asp Ser Val Thr Leu Pro Cys Tyr Leu Gln
    290                 295                 300
```

```
Val Pro Asn Met Glu Val Thr His Val Ser Gln Leu Thr Trp Ala Arg
305                 310                 315                 320

His Gly Glu Ser Gly Ser Met Ala Val Phe His Gln Thr Gln Gly Pro
                325                 330                 335

Trp Tyr Ala Glu Ser Lys Arg Leu Glu Phe Val Ala Ala Arg Leu Gly
            340                 345                 350

Ala Glu Leu Arg Asn Ala Ser Leu Arg Met Phe Gly Leu Arg Val Glu
        355                 360                 365

Asp Glu Gly Asn Tyr Thr Cys Gln Phe Val Thr Phe Pro Gln Arg Ser
    370                 375                 380

Arg Ser Val Asp Ile Trp Leu Arg Val Leu Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                405                 410                 415

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
            420                 425                 430

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        435                 440                 445

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    450                 455                 460

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
465                 470                 475                 480

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                485                 490                 495

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            500                 505                 510
```

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
515 520 525

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
530 535 540

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
545 550 555 560

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
565 570 575

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
580 585 590

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
595 600 605

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
610 615 620

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
625 630 635

<210> 1725
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v66

<400> 1725

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
100 105 110

Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp
115 120 125

Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro
130 135 140

Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly
145 150 155 160

Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val
165 170 175

Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys
180 185 190

Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val
195 200 205

Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1726
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV 66

<400> 1726

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Leu Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
        35   40   45

Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
                85   90   95

Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105

<210> 1727
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v66

<400> 1727

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
100 105 110

Val Asn Ala
115

<210> 1728
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Wildtype PD-L1 ECD

<400> 1728

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1729
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v67

<400> 1729

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1730
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v68

<400> 1730

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Leu Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1731
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v69

<400> 1731

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Ser Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1732
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v70

<400> 1732

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ser Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Gln
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Phe Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1733
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v71

<400> 1733

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Arg Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Leu Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Gln
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Asn Asn Gln Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Leu
210 215 220

<210> 1734
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v72

<400> 1734

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Leu Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Phe Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1735
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v73

<400> 1735

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Ser Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Arg Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Ser Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1736
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v74

<400>  1736

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
```

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Val Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His His Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1737
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v75

<400> 1737

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Ile Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1738
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v76

<400> 1738

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1739
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v77

<400> 1739

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Thr Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Phe Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1740
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v78

<400>  1740

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Gln
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1741

<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v79

<400> 1741

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1742
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v80

<400> 1742

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Val Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1743
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v81

<400> 1743

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1744
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v82

<400>  1744

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Gly Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
```

210 215 220

<210> 1745
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v83

<400> 1745

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn Gln Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1746
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v84

<400>  1746

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1747
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v85

<400> 1747

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1748
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v86

<400> 1748

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1749
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v87

<400> 1749

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1750
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v88

<400>  1750

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Thr Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1751
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v89

<400> 1751

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Ala Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Leu Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1752
<211> 221
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v90

<400> 1752

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Ser Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Ser Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
```

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1753
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v91

<400> 1753

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Arg Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Ala
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Ala Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1754
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v92

<400>  1754

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Val Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Gly Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Glu Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1755
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v93

<400> 1755

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Thr Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1756
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v94

<400> 1756

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1757
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v95

<400> 1757

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1758
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v96

<400> 1758

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His His Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Ser Arg Arg Leu Asp Pro Glu Glu Tyr His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1759
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v97

<400> 1759

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1760
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v98

<400> 1760

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Pro Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1761
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v99

<400> 1761

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Ile Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Gly Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Gly Glu Asn His Thr Ala Glu Leu Ala Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1762
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v100

<400> 1762

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Thr Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1763
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v101

<400> 1763

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Asn
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1764
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v102

<400> 1764

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1765
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v103

<400> 1765

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1766
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v104

<400>  1766

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1767

<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v105

<400> 1767

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

```
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn Gln Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1768
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v106

<400>  1768

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
```

115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1769
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v107

<400> 1769

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Ala Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1770
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v108

<400>  1770

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
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```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Glu Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
```

210 215 220

<210> 1771
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v109

<400> 1771

Phe Thr Val Thr Val Pro Lys Asp Leu Phe Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Arg Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Ala Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1772
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v110

<400>  1772

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1773
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v111

<400> 1773

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Met
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1774
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v112
```

<400> 1774

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1775
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v113

<400> 1775

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1776
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v114

<400> 1776

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1777
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v115

<400> 1777

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1778
<211> 221
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v116

<400> 1778

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
```

180 185 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1779
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v117

<400> 1779

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Phe Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1780
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v118

<400>  1780

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Asp Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1781
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v119

<400> 1781

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1782
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v120

<400> 1782

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Thr Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Tyr Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Ser Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1783
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v121

<400> 1783

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Gly Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Pro Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1784
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v122

<400> 1784

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Ile Asn Val Thr
165 170 175

Cys Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1785
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v123

<400> 1785

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1786
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v124

<400> 1786

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Thr Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1787
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v125

<400> 1787

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Tyr Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1788
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v126

<400>  1788

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
```

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Tyr Ser Lys Arg Glu Gly Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1789
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v127

<400> 1789

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Val Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1790
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v128

<400> 1790

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Phe Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1791
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v129

<400> 1791

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1792
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v131

<400>  1792

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Thr Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1793

<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 1793

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Asp Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

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Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Val Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1794
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v132

<400>  1794

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
```

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Tyr Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Ile Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Ser Asp Pro Glu Glu Asn His Ala Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1795
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v133

<400> 1795

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Ser Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1796
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v134

<400> 1796

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Asp Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Trp Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
```

210 215 220

<210> 1797
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v135

<400> 1797

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Val Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Leu Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1798
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v136

<400>  1798

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1799
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v137

<400> 1799

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Thr Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Val Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1800
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v138
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<400> 1800

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Ser Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1801
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v139

<400> 1801

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Arg Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Ala Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1802
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v140

<400> 1802

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Ile Thr Asn Ser Arg Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1803
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v141

<400> 1803

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Ile Phe Tyr Cys Ser
            180                 185                 190

Phe Gly Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1804
<211> 221
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v142

<400> 1804

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Thr Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1805
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v143

<400> 1805

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Ala Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1806
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v144

<400>  1806

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Ala Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1807
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v145

<400> 1807

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Ala Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Ile Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1808
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v146

<400> 1808

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Thr Arg Glu Glu Lys Leu Phe Asn Val Thr

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1809
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v147

<400> 1809

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Arg Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Ile Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1810
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v148

<400>  1810

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
```

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Arg Thr Ser Ser Asp His Gln Val Leu Gly Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1811
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v149

<400> 1811

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Arg Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Val Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1812
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v150

<400> 1812

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Arg Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Asn Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Thr Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1813
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v151

<400> 1813

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1814
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v152

<400> 1814

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1815
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v153

<400> 1815

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Leu Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Leu Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Gly Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1816
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v154

<400> 1816

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1817
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v155

<400> 1817

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Glu Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1818
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v156

<400>  1818

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Pro Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1819

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v67

<400> 1819

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1820
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v68

<400> 1820

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Leu Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1821
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v69

<400> 1821

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Ser Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1822
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v70

<400>  1822

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ser Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Gln
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Phe Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
```

210 215 220

<210> 1823
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v72

<400> 1823

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Leu Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Phe Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1824
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v73

<400>  1824

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Ser Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Arg Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Ser Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1825
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v74

<400> 1825

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Val Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His His Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1826
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v75

<400> 1826

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Ile Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1827
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v76

<400> 1827

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1828
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v77

<400>  1828

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Thr Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Lys Asn Gln Thr Ala Glu Phe Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1829
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v78

<400> 1829

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Gln
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1830
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v79

<400> 1830

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr

180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1831
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v80

<400> 1831

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Val Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1832
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v81

<400>  1832

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1833
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v82

<400> 1833

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Gly Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1834
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v83

<400> 1834

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn Gln Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1835
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v84

<400> 1835

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

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Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1836
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v85

<400>  1836

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
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    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1837
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v86

<400>  1837
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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Ala Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1838
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v87

<400> 1838

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1839
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v88

<400> 1839

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Thr Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1840
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v89

<400> 1840

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln

35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Ala Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Leu Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1841
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v90

<400> 1841

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Ser Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Ser Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
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Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1842
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v91

<400> 1842

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Arg Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Ala
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Ala Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1843
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v92

<400> 1843

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Val Ile Gln
35 40 45

Phe Val His Gly Glu Glu Gly Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Glu Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1844
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v93

<400>  1844

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Thr Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1845

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v94

<400> 1845

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1846
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v95

<400> 1846

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1847
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v96

<400> 1847

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His His Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Ser Arg Arg Leu Asp Pro Glu Glu Tyr His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1848
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v97

<400>  1848

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg

210 215 220

<210> 1849
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v98

<400> 1849

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Pro Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1850
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v99

<400>  1850

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Ile Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Gly Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Gly Glu Asn His Thr Ala Glu Leu Ala Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1851
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v100

<400> 1851

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Thr Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1852
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v101
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<400> 1852

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Asn
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1853
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v102

<400> 1853

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1854
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v103

<400>  1854

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1855
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v104

<400> 1855

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1856
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v105

<400> 1856

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
```

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn Gln Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1857
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v106

<400> 1857

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1858
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v107

<400>  1858

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Ala Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1859
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v108

<400> 1859

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Glu Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1860
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v109

<400> 1860

```
Phe Thr Val Thr Val Pro Lys Asp Leu Phe Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Val Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Arg Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Ala Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1861
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v110

<400> 1861

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1862
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v111

<400> 1862

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Met
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1863
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v112

<400> 1863

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1864
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v113

<400> 1864

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1865
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v114

<400> 1865

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1866
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v115

<400>  1866

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
```

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1867
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v116

<400> 1867

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1868
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v117

<400> 1868

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Phe Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1869
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v118

<400> 1869

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Asp Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1870
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v119

<400>  1870

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1871

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v120

<400> 1871

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Thr Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Tyr Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Ser Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1872
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v121

<400> 1872

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Gly Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Pro Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1873
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v122

<400> 1873

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Ile Asn Val Thr
                165                 170                 175


Cys Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1874
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v123

<400>  1874

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

```
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
```

210 215 220

<210> 1875
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v124

<400> 1875

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Thr Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1876
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v125

<400>  1876

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Tyr Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1877
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v126

<400> 1877

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Tyr Ser Lys Arg Glu Gly Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1878
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v127

<400> 1878

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Val Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1879
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v128

<400> 1879

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Phe Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1880
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v129

<400>  1880

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
```

85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1881
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 1881

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Thr Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1882
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 1882

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Asp Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Val Phe Tyr Cys Thr
```

180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1883
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v132

<400> 1883

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Tyr Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Ile Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Ser Asp Pro Glu Glu Asn His Ala Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1884
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v133

<400>  1884

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
```

65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Ser Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1885
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v134

<400> 1885

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Asp Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Trp Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
```

<210> 1886
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v135

<400> 1886

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Val Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Leu Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
```

165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1887
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v136

<400> 1887

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1888
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v137

<400>  1888

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
```

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Thr Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Val Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1889
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v138

<400> 1889

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Ser Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1890
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v139

<400> 1890

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Arg Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys

145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Ala Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1891
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v140

<400> 1891

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Ile Thr Asn Ser Arg Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1892
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v141

<400>  1892

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
```

35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Ala Thr Thr Asn Glu Ile Phe Tyr Cys Ser
180 185 190

Phe Gly Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1893
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v142

<400> 1893

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Thr Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1894
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v143

<400> 1894

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Ala Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu

130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1895
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v144

<400> 1895

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Ala Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1896
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v145

<400>  1896

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Ala Glu Lys Gln Leu Asp Leu
```

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Ile Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1897

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v146

<400> 1897

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Thr Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1898
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v147

<400> 1898

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Asn Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Arg Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro

115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Ile Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1899
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v148

<400> 1899

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Arg Thr Ser Ser Asp His Gln Val Leu Gly Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Thr Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1900
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v149

<400>  1900

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
```

1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Arg Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Val Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Ser Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg

210 215 220

<210> 1901
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v150

<400> 1901

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Arg Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Asp Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Asn Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Thr Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1902
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v151

<400>  1902

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
```

100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1903
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v152

<400> 1903

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
35 40 45

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1904
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v153
```

<400> 1904

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Leu Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Leu Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Gly Ser Glu Glu Asn His Thr Ala Glu Leu Val Ile
```

195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1905
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v154

<400> 1905

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Val Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220


<210>  1906
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v155

<400>  1906

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Glu Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
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85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Gly Leu Asp Pro Glu Glu Asp His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 1907
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v156

<400> 1907

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

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Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Ser Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Glu
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Pro Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Gly Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
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<210> 1908
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v67

<400> 1908

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35   40   45

Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50   55   60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65   70   75   80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Gly Tyr Gly
                85   90   95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105

<210> 1909
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v75

<400> 1909

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1   5   10   15

Cys Lys Phe Pro Val Glu Ile Gln Leu Asp Leu Ala Ala Leu Ile Val
            20   25   30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Gly Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1910
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v80

<400> 1910

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Val Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Gly Tyr Gly

85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1911
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v81

<400> 1911

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105

<210> 1912
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v82

<400> 1912

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Gly Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Gly Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1913
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v87

<400> 1913

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ser Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

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Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105


<210>  1914
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v94

<400>  1914

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1               5                   10                  15


Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
            20                  25                  30


Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
        35                  40                  45


Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
    50                  55                  60


Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65                  70                  75                  80


Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Ser Tyr Gly
                85                  90                  95


Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
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100 105

<210> 1915
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v98

<400> 1915

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Pro Ser Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105

<210> 1916
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v100

<400> 1916

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Thr Thr Ile Glu

1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Thr Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105

<210> 1917
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v102

<400> 1917

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Gly Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1918
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v103

<400> 1918

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asp Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Leu Ile Gly Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1919

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v110

<400> 1919

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1920
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v118

<400> 1920

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val

20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Asp Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1921
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v127

<400> 1921

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys Met Val Ser Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1922
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v152

<400> 1922

Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser Asn Met Thr Ile Glu
1 5 10 15

Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu Ala Ala Leu Ile Val
20 25 30

Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln Phe Val His Gly Glu
35 40 45

Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser Gln Arg Ala Arg Leu
50 55 60

Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp
65 70 75 80

Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Gly Tyr Gly
85 90 95

Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105

<210> 1923
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v67

<400> 1923

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 1924
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v75

<400> 1924

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Ile Gln Leu Asp Leu

20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1925
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v80

<400> 1925

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Val Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1926
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v81

<400> 1926

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val

100 105 110

Asn Ala

<210> 1927
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v82

<400> 1927

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Gly Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1928
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v87

<400> 1928

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110

Asn Ala

<210> 1929
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v94

<400> 1929

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
            100   105   110

Asn Ala

<210> 1930
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v98

<400> 1930

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1   5   10   15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30

Ala Ala Pro Ser Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg

50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala

<210> 1931
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v100

<400> 1931

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Thr Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asn Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Glu Val
100 105 110

Asn Ala

<210> 1932
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v102

<400> 1932

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1933

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v103

<400> 1933

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Leu Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1934
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v110

<400> 1934

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser

1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1935
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v118

<400> 1935

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Asp Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1936
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v127

<400> 1936

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys

85 90 95

Met Val Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1937
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v152

<400> 1937

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Ser
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala

<210> 1938
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc (C5S (C220S), R77C, (R292C), N82G (N297G), V87C (V302C), L232del (K447del))

<400> 1938

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15


Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
65                  70                  75                  80


Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160
```

```
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly
225                 230


<210>  1939
<211>  231
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fc with C220S/L234A/L235E/G237A/K447del

<400>  1939

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95
```

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly
225                 230


<210>  1940
<211>  230
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fc with C220S/E233P/L234V/L235A/G236del/S267K/K447del

<400>  1940

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15
```

```
Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20                  25                  30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35                  40                  45

Asp Val Lys His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    50                  55                  60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65                  70                  75                  80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85                  90                  95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            100                 105                 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    130                 135                 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        195                 200                 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
```

Leu Ser Leu Ser Pro Gly
225 230

<210> 1941
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 1941

Gly Ser Gly Gly Gly Gly Ser
1 5

<210> 1942
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4GS Linker

<400> 1942

Gly Gly Gly Gly Ser
1 5

<210> 1943
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v1

<400> 1943

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Asn Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
35 40 45

```
Phe Val Asn Gly Glu Glu Asp Leu Glu Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1944
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v2

<400> 1944

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Thr Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1945
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v3

<400> 1945

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Glu Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1946
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v4

<400>  1946

Phe Thr Val Thr Val Ser Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80
```

Leu Gln Thr Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1947
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v5

<400> 1947

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1948
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v6

<400> 1948

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1949
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v7

<400> 1949

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1950
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v8

<400> 1950

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60
```

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1951
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v9

<400>  1951

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15
```

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1952
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v10

<400> 1952

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160
```

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1953
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v11

<400> 1953

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1954
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v12

<400>  1954

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asp Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45
```

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Gly Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1955
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v13

<400> 1955

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Ser Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

```
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1956
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v14

<400>  1956

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140
```

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1957
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v15

<400> 1957

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1958
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v16

<400>  1958

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30
```

```
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
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<210> 1959
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v17

<400> 1959

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Val Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1960
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v18

<400> 1960

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1961
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v19

<400> 1961

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Glu Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1962
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v20

<400> 1962

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15
```

```
Asn Ile Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val Arg Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1963
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v21

<400> 1963

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Glu Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln Arg Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1964
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v22

<400> 1964

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1965
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v23

<400>  1965

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Gly
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60
```

```
Gln Arg Ala Arg Leu Leu Glu Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1966
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v24

<400> 1966

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1967
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v25

<400> 1967

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Arg Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1968
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v26

<400>  1968

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Val Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95
```

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1969
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v27

<400>  1969

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45
```

```
Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1970
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v28

<400> 1970

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Gly Met Glu Val Lys Thr Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1971
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v29

<400> 1971

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Ser Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1972
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v30

<400>  1972

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65                  70                  75                  80
```

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1973
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v31

<400> 1973

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1974
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v32

<400> 1974

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1975
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v33

<400> 1975

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1976
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v34

<400> 1976

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60
```

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1977
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v35

<400>  1977

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15
```

```
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ser Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1978
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v36

<400> 1978

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Met Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160
```

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1979
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v37

<400> 1979

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1980
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v38

<400>  1980

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45
```

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Pro Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1981
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v39

<400> 1981

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1982
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v40

<400> 1982

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Arg Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1983
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v41

<400> 1983

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

```
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1984
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v42

<400>  1984

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30
```

```
Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Val Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1985
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v43

<400> 1985

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Gly Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1986
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v44

<400> 1986

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1987
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v45

<400> 1987

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

```
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1988
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v46

<400>  1988

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15
```

```
Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1989
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v47

<400> 1989

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
```

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1990
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v48

<400> 1990

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1991
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v49

<400> 1991

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
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<210> 1992
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v50

<400> 1992

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1993
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v51

<400> 1993

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

```
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1994
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v52

<400>  1994

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Ala Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val Tyr Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95
```

```
Met Ile Gly Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1995
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v53

<400>  1995

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Thr Ile Ile Gln
        35                  40                  45
```

```
Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 1996
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v54

<400> 1996

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
```

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1997
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v55

<400> 1997

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Thr Val Tyr Trp Glu Met Glu Asp Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

```
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  1998
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v56

<400>  1998

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Gly Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80
```

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 1999
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v57

<400> 1999

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

```
Asp Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Pro Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 2000
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v58

<400> 2000

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 2001
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v59

<400> 2001

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Gly Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Asp Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

```
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 2002
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v60

<400> 2002

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60
```

```
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110


Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp
        115                 120                 125


Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro
    130                 135                 140


Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly
145                 150                 155                 160


Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val
                165                 170                 175


Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys
            180                 185                 190


Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val
        195                 200                 205


Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  2003
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v61

<400>  2003

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15
```

```
Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45

Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 2004
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v62

<400> 2004

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Glu Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160
```

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
210 215 220

<210> 2005
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v63

<400> 2005

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Ile Ile Glu Cys Lys Phe Pro Val Gly Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Ile Ile Ile Gln
35 40 45

Phe Ala His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Lys Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

```
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205


Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  2006
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v64

<400>  2006

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Lys Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45
```

```
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220
```

<210> 2007
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v65

<400> 2007

```
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                  10                  15


Asn Met Thr Ile Glu Cys Arg Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Thr Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Ile Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110


Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125


Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140


Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160


Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175


Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190


Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
```

```
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  2008
<211>  222
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v66

<400>  2008

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1               5                   10                  15


Asn Met Thr Leu Glu Cys Lys Phe Pro Val Glu Glu Gln Leu Asp Leu
            20                  25                  30


Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp Ile Ile Gln
        35                  40                  45


Phe Val His Gly Glu Glu Asp Leu Lys Ala Gln His Ser Ser Tyr Arg
    50                  55                  60


Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80


Leu Gln Ile Thr Asp Val Lys Leu Arg Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95


Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys
            100                 105                 110


Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp
        115                 120                 125


Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro
    130                 135                 140
```

```
Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly
145                 150                 155                 160


Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val
                165                 170                 175


Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys
            180                 185                 190


Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val
        195                 200                 205


Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr
    210                 215                 220


<210>  2009
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Signal Peptide

<400>  2009

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
1               5                   10                  15


Val Ser Ala



<210>  2010
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Flag tag

<400>  2010

Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 2011
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 2011

His His His His His His
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<210> 2012
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Wildtype PD-L1 SIP

<400> 2012

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
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Val Ser Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu
20 25 30

Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln
35 40 45

Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn
50 55 60

Ile Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser
65 70 75 80

Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly
85 90 95

Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val
100 105 110

Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr
115 120 125

Val Lys Val Asn Ala
130

<210> 2013
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 v60 SIP

<400> 2013

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
1 5 10 15

Val Ser Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu
20 25 30

Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln
35 40 45

Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Gly Lys Asp
50 55 60

Ile Ile Gln Phe Val His Gly Glu Glu Asp Gln Lys Ala Gln His Ser
65 70 75 80

Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly
85 90 95

Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val
100 105 110

Tyr Arg Cys Met Ile Ser Tyr Gly Gly Gly Ala Asp Tyr Lys Arg Ile
115 120 125

Thr Val Lys Val Asn Ala
130

<210> 2014
<211> 68
<212> PRT
<213> Artificial Sequence

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<223> CD8 hinge and transmembrane domain

<400> 2014

Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
1 5 10 15

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
20 25 30

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
35 40 45

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
50 55 60

Leu Val Ile Thr
65

<210> 2015
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-2

<400> 2015

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

```
Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro
                245                 250                 255
```

```
Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
            260                 265                 270

Arg Pro Glu Ala Ser Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
        275                 280                 285

Gly Leu Asp Phe Ala Ser Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
    290                 295                 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
305                 310                 315                 320

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
                325                 330                 335

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            340                 345                 350

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        355                 360                 365

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    370                 375                 380

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
385                 390                 395                 400

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                405                 410                 415

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            420                 425                 430
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<210> 2016
<211> 707
<212> PRT
<213> Artificial Sequence

<220>

<223> antiCD19 chimeric antigen receptor CAR-2

<400> 2016

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His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30


Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45


Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60


Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95


Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110


Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125


Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
    130                 135                 140


Lys Gly Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro
145                 150                 155                 160


Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro
                165                 170                 175


Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu
            180                 185                 190
```

```
Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala
        195                 200                 205

Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val
    210                 215                 220

Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr
225                 230                 235                 240

Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp
                245                 250                 255

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr
            260                 265                 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
        275                 280                 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Ser Arg Pro Ala Ala Gly Gly
    290                 295                 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Ser Asp Ile Tyr Ile Trp
305                 310                 315                 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
                325                 330                 335

Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
            340                 345                 350

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
        355                 360                 365

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
    370                 375                 380

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
385                 390                 395                 400
```

```
Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
                405                 410                 415

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
            420                 425                 430

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
        435                 440                 445

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
    450                 455                 460

Gly Asp Val Glu Glu Asn Pro Gly Pro Ser Arg Ser Glu Leu Ile Lys
465                 470                 475                 480

Glu Asn Met His Met Lys Leu Tyr Met Glu Gly Thr Val Asp Asn His
                485                 490                 495

His Phe Lys Cys Thr Ser Glu Gly Glu Gly Lys Pro Tyr Glu Gly Thr
            500                 505                 510

Gln Thr Met Arg Ile Lys Val Val Glu Gly Gly Pro Leu Pro Phe Ala
        515                 520                 525

Phe Asp Ile Leu Ala Thr Ser Phe Leu Tyr Gly Ser Lys Thr Phe Ile
    530                 535                 540

Asn His Thr Gln Gly Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu
545                 550                 555                 560

Gly Phe Thr Trp Glu Arg Val Thr Thr Tyr Glu Asp Gly Gly Val Leu
                565                 570                 575

Thr Ala Thr Gln Asp Thr Ser Leu Gln Asp Gly Cys Leu Ile Tyr Asn
            580                 585                 590

Val Lys Ile Arg Gly Val Asn Phe Thr Ser Asn Gly Pro Val Met Gln
        595                 600                 605
```

Lys Lys Thr Leu Gly Trp Glu Ala Phe Thr Glu Thr Leu Tyr Pro Ala
610 615 620

Asp Gly Gly Leu Glu Gly Arg Asn Asp Met Ala Leu Lys Leu Val Gly
625 630 635 640

Gly Ser His Leu Ile Ala Asn Ile Lys Thr Thr Tyr Arg Ser Lys Lys
645 650 655

Pro Ala Lys Asn Leu Lys Met Pro Gly Val Tyr Tyr Val Asp Tyr Arg
660 665 670

Leu Glu Arg Ile Lys Glu Ala Asn Asn Glu Thr Tyr Val Glu Gln His
675 680 685

Glu Val Ala Val Ala Arg Tyr Cys Asp Leu Pro Ser Lys Leu Gly His
690 695 700

Lys Leu Asn
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<210> 2017
<211> 8708
<212> DNA
<213> Artificial Sequence

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<223> anti-CD19 chimeric antigen receptor CAR-2

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tacgatcgtg ccttattagg aaggcaacag acgggtctga catggattgg acgaaccact 180

gaattgccgc attgcagaga tattgtattt aagtgcctag ctcgatacaa taaacgggtc 240

tctctggtta gaccagatct gagcctggga gctctctggc taactaggga acccactgct 300

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ctctggtaac tagagatccc tcagaccctt ttagtcagtg tggaaaatct ctagcagtgg 420

cgcccgaaca gggacttgaa agcgaaaggg aaaccagagg agctctctcg acgcaggact 480

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ccaaacgacg agcgtgacac cacgatgcct gtagcaatgg caacaacgtt gcgcaaacta 7200

ttaactggcg aactacttac tctagcttcc cggcaacaat taatagactg gatggaggcg 7260

gataaagttg caggaccact tctgcgctcg gcccttccgg ctggctggtt tattgctgat 7320

aaatctggag ccggtgagcg tgggtctcgc ggtatcattg cagcactggg gccagatggt 7380

aagccctccc gtatcgtagt tatctacacg acggggagtc aggcaactat ggatgaacga 7440

aatagacaga tcgctgagat aggtgcctca ctgattaagc attggtaact gtcagaccaa 7500

gtttactcat atatacttta gattgattta aaacttcatt tttaatttaa aaggatctag 7560

gtgaagatcc tttttgataa tctcatgacc aaaatccctt aacgtgagtt ttcgttccac 7620

tgagcgtcag accccgtaga aaagatcaaa ggatcttctt gagatccttt ttttctgcgc 7680

gtaatctgct gcttgcaaac aaaaaaacca ccgctaccag cggtggtttg tttgccggat 7740

caagagctac caactctttt tccgaaggta actggcttca gcagagcgca gataccaaat 7800

actgtccttc tagtgtagcc gtagttaggc caccacttca agaactctgt agcaccgcct 7860

acatacctcg ctctgctaat cctgttacca gtggctgctg ccagtggcga taagtcgtgt 7920

cttaccgggt tggactcaag acgatagtta ccggataagg cgcagcggtc gggctgaacg 7980

gggggttcgt gcacacagcc cagcttggag cgaacgacct acaccgaact gagataccta 8040

cagcgtgagc tatgagaaag cgccacgctt cccgaaggga gaaaggcgga caggtatccg 8100

gtaagcggca gggtcggaac aggagagcgc acgagggagc ttccaggggg aaacgcctgg 8160

tatctttata gtcctgtcgg gtttcgccac ctctgacttg agcgtcgatt tttgtgatgc 8220

tcgtcagggg ggcggagcct atggaaaaac gccagcaacg cggccttttt acggttcctg 8280

gccttttgct ggccttttgc tcacatgttc tttcctgcgt tatcccctga ttctgtggat 8340

aaccgtatta ccgcctttga gtgagctgat accgctcgcc gcagccgaac gaccgagcgc 8400

agcgagtcag tgagcgagga agcggaagag cgcccaatac gcaaaccgcc tctccccgcg 8460

cgttggccga ttcattaatg cagctggcac gacaggtttc ccgactggaa agcgggcagt 8520

gagcgcaacg caattaatgt gagttagctc actcattagg caccccaggc tttacacttt 8580

atgcttccgg ctcgtatgtt gtgtggaatt gtgagcggat aacaatttca cacaggaaac 8640

agctatgacc atgattacgc caagcgcgca attaaccctc actaaaggga acaaaagctg 8700

gagctgca 8708

<210> 2018
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-1

<400> 2018

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

```
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro
                245                 250                 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
            260                 265                 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
        275                 280                 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
    290                 295                 300
```

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Arg Val Lys Phe
305 310 315 320

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
325 330 335

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
340 345 350

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
355 360 365

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
370 375 380

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
385 390 395 400

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
405 410 415

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
420 425

<210> 2019
<211> 706
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-1

<400> 2019

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser
20 25 30

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45

```
Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
    50                  55                  60

Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
65                  70                  75                  80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
                85                  90                  95

Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln
            100                 105                 110

Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
        115                 120                 125

Ile Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
    130                 135                 140

Ser Thr Lys Gly Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val
145                 150                 155                 160

Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser
                165                 170                 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly
            180                 185                 190

Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn
        195                 200                 205

Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser
    210                 215                 220

Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile
225                 230                 235                 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
                245                 250                 255
```

```
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Ala Lys
            260                 265                 270

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305                 310                 315                 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

Val Ile Thr Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
            340                 345                 350

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
        355                 360                 365

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
    370                 375                 380

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
385                 390                 395                 400

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
                405                 410                 415

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
            420                 425                 430

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
        435                 440                 445

Pro Pro Arg Gly Gly Arg Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
    450                 455                 460
```

```
Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Ser Arg Ser Glu Leu Ile
465                 470                 475                 480

Lys Glu Asn Met His Met Lys Leu Tyr Met Glu Gly Thr Val Asp Asn
                485                 490                 495

His His Phe Lys Cys Thr Ser Glu Gly Glu Gly Lys Pro Tyr Glu Gly
            500                 505                 510

Thr Gln Thr Met Arg Ile Lys Val Val Glu Gly Gly Pro Leu Pro Phe
        515                 520                 525

Ala Phe Asp Ile Leu Ala Thr Ser Phe Leu Tyr Gly Ser Lys Thr Phe
    530                 535                 540

Ile Asn His Thr Gln Gly Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro
545                 550                 555                 560

Glu Gly Phe Thr Trp Glu Arg Val Thr Thr Tyr Glu Asp Gly Gly Val
                565                 570                 575

Leu Thr Ala Thr Gln Asp Thr Ser Leu Gln Asp Gly Cys Leu Ile Tyr
            580                 585                 590

Asn Val Lys Ile Arg Gly Val Asn Phe Thr Ser Asn Gly Pro Val Met
        595                 600                 605

Gln Lys Lys Thr Leu Trp Glu Ala Phe Thr Glu Thr Leu Tyr Pro Ala
    610                 615                 620

Asp Gly Gly Leu Glu Gly Arg Asn Asp Met Ala Leu Lys Leu Val Gly
625                 630                 635                 640

Gly Ser His Leu Ile Ala Asn Ile Lys Thr Thr Tyr Arg Ser Lys Lys
                645                 650                 655

Pro Ala Lys Asn Leu Lys Met Pro Gly Val Tyr Tyr Val Asp Tyr Arg
            660                 665                 670
```

Leu Glu Arg Ile Lys Glu Ala Asn Asn Glu Thr Tyr Val Glu Gln His
675 680 685

Glu Val Ala Ala Arg Tyr Cys Asp Leu Pro Ser Lys Leu Gly His Lys
690 695 700

Leu Asn
705

<210> 2020
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Blue fluorescent protein

<400> 2020

Ser Arg Ser Glu Leu Ile Lys Glu Asn Met His Met Lys Leu Tyr Met
1 5 10 15

Glu Gly Thr Val Asp Asn His His Phe Lys Cys Thr Ser Glu Gly Glu
20 25 30

Gly Lys Pro Tyr Glu Gly Thr Gln Thr Met Arg Ile Lys Val Val Glu
35 40 45

Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Thr Ser Phe Leu
50 55 60

Tyr Gly Ser Lys Thr Phe Ile Asn His Thr Gln Gly Ile Pro Asp Phe
65 70 75 80

Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Val Thr Thr
85 90 95

Tyr Glu Asp Gly Gly Val Leu Thr Ala Thr Gln Asp Thr Ser Leu Gln
100 105 110

Asp Gly Cys Leu Ile Tyr Asn Val Lys Ile Arg Gly Val Asn Phe Thr
115 120 125

Ser Asn Gly Pro Val Met Gln Lys Lys Thr Leu Trp Glu Ala Phe Thr
130 135 140

Glu Thr Leu Tyr Pro Ala Asp Gly Gly Leu Glu Gly Arg Asn Asp Met
145 150 155 160

Ala Leu Lys Leu Val Gly Gly Ser His Leu Ile Ala Asn Ile Lys Thr
165 170 175

Thr Tyr Arg Ser Lys Lys Pro Ala Lys Asn Leu Lys Met Pro Gly Val
180 185 190

Tyr Tyr Val Asp Tyr Arg Leu Glu Arg Ile Lys Glu Ala Asn Asn Glu
195 200 205

Thr Tyr Val Glu Gln His Glu Val Ala Ala Arg Tyr Cys Asp Leu Pro
210 215 220

Ser Lys Leu Gly His Lys Leu Asn
225 230

<210> 2021
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A

<400> 2021

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 2022
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> EAAAK Linker

<400> 2022

Glu Ala Ala Ala Lys
1   5

<210> 2023
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3x EAAAK Linker

<400> 2023

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1   5   10   15

<210> 2024
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 5x EAAAK Linker

<400> 2024

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1   5   10   15

Ala Ala Ala Lys Glu Ala Ala Ala Lys
            20   25

<210> 2025
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS

<400> 2025

```
Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
1               5                   10                  15


Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
            20                  25                  30


Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro
        35                  40                  45


Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala
    50                  55                  60


Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
65                  70                  75                  80


Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
                85                  90                  95


Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
            100                 105                 110


Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro
        115                 120                 125


Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala
    130                 135                 140


Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
145                 150                 155                 160


Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
                165                 170                 175


Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
            180                 185                 190


Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro
        195                 200                 205
```

```
Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala
    210                 215                 220

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
225                 230                 235                 240

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
                245                 250                 255

Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
            260                 265                 270

Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro
        275                 280                 285

Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala
    290                 295                 300

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
305                 310                 315                 320

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
                325                 330                 335

Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
            340                 345                 350

Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala Ala Pro Ala Pro
        355                 360                 365

Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Ala Ser Pro Ala
    370                 375                 380

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
385                 390                 395                 400
```

<210> 2026
<211> 22

<212> PRT
<213> Artificial Sequence

<220>
<223> P2A

<400> 2026

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1   5   10   15

Glu Glu Asn Pro Gly Pro
            20

<210> 2027
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> eGFP

<400> 2027

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1   5   10   15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
            20   25   30

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
        35   40   45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr
    50   55   60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
65   70   75   80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
                85   90   95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
            100   105   110

```
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
        115                 120                 125


Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
    130                 135                 140


Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
145                 150                 155                 160


Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
                165                 170                 175


Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
            180                 185                 190


Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
        195                 200                 205


Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
    210                 215                 220


Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235


<210>  2028
<211>  237
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Green fluorescent protein

<400>  2028

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1               5                   10                  15


Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
            20                  25                  30
```

```
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
        35                  40                  45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
    50                  55                  60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
65                  70                  75                  80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
                85                  90                  95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
            100                 105                 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
        115                 120                 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
    130                 135                 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
145                 150                 155                 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
                165                 170                 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
            180                 185                 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
        195                 200                 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
    210                 215                 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
```

<210> 2029
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> eGFP

<400> 2029

```
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                  10                  15


Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30


Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45


Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60


Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80


Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95


Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110


Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125


Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140


Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160


Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175
```

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 2030
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT IgV

<400> 2030

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp
100 105

<210> 2031
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> GS(G4S)3 linker

<400> 2031

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser

<210> 2032
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> GS(G4S)5 linker

<400> 2032

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25