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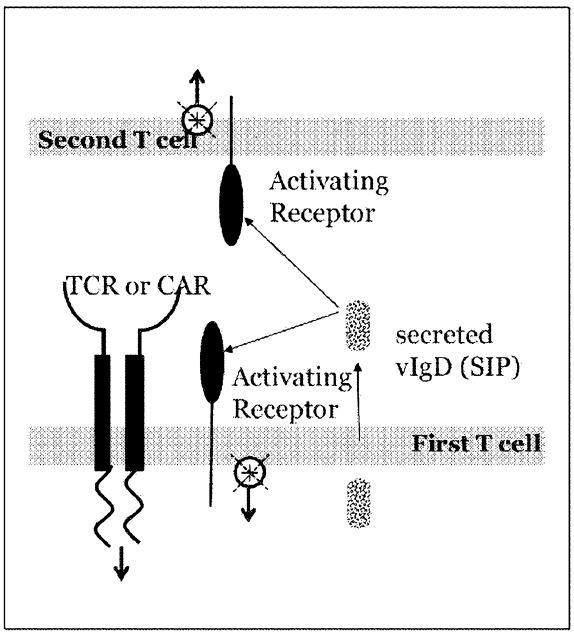
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(54) Title: SECRETABLE VARIANT IMMUNOMODULATORY PROTEINS AND ENGINEERED CELL THERAPY

(57) Abstract: Provided are immunomodulatory proteins, nucleic acids encoding such immunomodulatory proteins, cells engineered to express the immunomodulatory proteins and infections agents containing nucleic acid encoding the immunomodulatory proteins. In some embodiments, the immunomodulatory proteins are secretable. In some embodiments, the immunomodulatory proteins are transmembrane proteins that are surface expressed. The immunomodulatory proteins, engineered cells and infectious agents provide therapeutic utility for a variety of immunological and oncological conditions. Compositions and methods for making and using such proteins are provided.

FIG. 4A



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[Continued on next page]

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SECRETABLE VARIANT IMMUNOMODULATORY PROTEINS AND ENGINEERED CELL THERAPY

Cross-Reference to Related Applications

[0001] This application claims priority from U.S. provisional application No. 62/410,827, filed October 20, 2016, entitled "Secretable Variant Immunomodulatory Proteins and Engineered Cell Therapy," U.S. provisional application No. 62/475,210 filed March 22, 2017, entitled "Secretable Variant Immunomodulatory Proteins and Engineered Cell Therapy, " and U.S. provisional application No. 62/537,921 filed July 27, 2017, entitled "Secretable Variant Immunomodulatory Proteins and Engineered Cell Therapy," 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 761612001440SeqList.TXT, created October 19, 2017 which is 3,524,332 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 provides immunomodulatory proteins, nucleic acids encoding such immunomodulatory proteins, cells engineered to express the immunomodulatory proteins and infections agents containing nucleic acid encoding the immunomodulatory proteins. In some embodiments, the immunomodulatory proteins are secretable. In some embodiments, the immunomodulatory proteins are transmembrane proteins that are surface expressed. The immunomodulatory proteins, engineered cells and infectious agents provide therapeutic utility for a variety of immunological and oncological conditions. Compositions and methods for making and using such proteins are provided.

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. Currently, biologics used to enhance or suppress immune responses have generally been limited to immunoglobulins (e.g., anti-PD-1 mAbs) or soluble receptors (e.g., Fc-CTLA4). Soluble receptors, in some cases, suffer from a number of deficiencies. While useful for antagonizing interactions between proteins, soluble receptors often lack the ability to agonize such interactions. Antibodies have proven less limited in this regard and examples of both agonistic and antagonistic antibodies are known in the art. Nevertheless, both soluble receptors and antibodies lack important attributes that are critical to function in the IS. 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 same cell (cis) as well as a protein on the associated cell (trans), likely at the same time. Although some agents are known that can modulate the IS, improved therapeutics are needed. Provided are embodiments that meet such needs.

Summary

[0005] In one aspect, there is provided an immunomodulatory protein comprising at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; the immunomodulatory protein does not comprise a transmembrane domain; and the immunomodulatory protein is not conjugated to a half-life extending moiety. In some embodiments, the half-life extending moiety is a multimerization domain. In some embodiments, the half-life extending moiety is an Fc domain.

[0006] In some embodiments, the immunomodulatory protein further comprises a signal peptide. In some embodiments, the signal peptide is a native signal peptide from the corresponding wild-type IgSF member. In some embodiments, the signal peptide is a non-native signal peptide. In some embodiments, the signal peptide is a signal peptide from an immunoglobulin antibody molecule (e.g. an IgG-kappa signal peptide), an IL-2 signal peptide,

or a CD33 signal peptide or other signal peptide known or described. Exemplary signal peptides are set forth in any of SEQ ID NOS: 413-430.

[0007] In some embodiments of the immunomodulatory protein, the at least one cell surface cognate binding partner is expressed on a mammalian cell. In some embodiments, the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte. In some embodiments, the mammalian cell is a T-cell. In some embodiments, the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

[0008] In some embodiments of the immunomodulatory protein, at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain.

[0009] In some embodiments of the immunomodulatory protein, specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

[0010] In some embodiments of the immunomodulatory protein, the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family. In some embodiments, the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2,

CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8. In some embodiments, the wild-type IgSF domain is a human IgSF domain. In some embodiments, at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408. In some embodiments, the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS:28-54 and 410 or to a specific binding fragment thereof containing an IgSF domain. In some embodiments, the wild-type IgSF domain is a member of the B7 family. In some embodiments, the wild-type IgSF domain is a domain of CD80, CD86 or ICOSL.

[0011] In some embodiments of the immunomodulatory protein, the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell, and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor. In some embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when secreted from a cell, increases immunological activity of the T-cell. In some embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when secreted from a cell, decreases immunological activity of the T-cell. In some embodiments, the stimulatory receptor is CD28, ICOS, or CD226. In some embodiments, the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

[0012] In some embodiments of the immunomodulatory protein, the at least one cell surface cognate binding partner is an inhibitory receptor expressed on a T-cell, and the at least one affinity-modified IgSF domain has increased binding affinity to the inhibitor receptor compared to the binding affinity of the wild-type IgSF domain to the inhibitor receptor. In some embodiments, binding of the affinity-modified IgSF domain to the inhibitory receptor, such as

when secreted from a cell, increases immunological activity of the T-cell. In some embodiments, binding of the affinity-modified IgSF domain to the inhibitor receptor, such as when secreted from a cell, decreases immunological activity of the T-cell. In some embodiments of the immunomodulatory protein, the inhibitory receptor comprises an ITIM signaling domain. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA VSIG3 or VSIG8 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3 or VSIG8, respectively. In some embodiments, the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively. In some embodiments, the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-L1 or an affinity-modified IgSF of PD-L2. In some embodiments, the inhibitory receptor is TIGIT and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of CD112 or CD155.

[0013] In some embodiments of the immunomodulatory protein, the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner. In some embodiments, the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

[0014] In some embodiments of the immunomodulatory protein, the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners. In some embodiments, the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell. In some embodiments, binding of the affinity-modified domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3 VSIG3, or VSIG8; or the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9 or VISTA. In some embodiments, the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28. In some embodiments, the inhibitory ligand is PD-L1 and the inhibitory receptor is PD-1. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to

CTLA-4 compared to the wild-type IgSF domain. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4.

[0015] In some embodiments of the immunomodulatory protein, the affinity modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226. In some embodiments, the affinity-modified IgSF domain retains or exhibits increased binding to TIGIT or CD112R compared to the binding affinity of the wild-type IgSF domain to TIGIT or CD112R.

[0016] In some embodiments of the immunomodulatory protein, the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen. In some embodiments, the tumor specific antigen is B7-H6. In some embodiments, the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

[0017] In some embodiments of the immunomodulatory protein, the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more different amino acid substitutions in the same wild-type IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

[0018] In some embodiments of the immunomodulatory protein, the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor in which the inhibitory receptor comprises an ITIM signaling domain. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively. In some embodiments, the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1,

GAL9 or VISTA, respectively. In some embodiments, the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-L1 or PD-L2. In some embodiments, the inhibitory receptor is TIGIT and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of CD112 or CD155.

[0019] In some embodiments of the immunomodulatory proteins, the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain. In some embodiments, the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

[0020] In some embodiments of the immunomodulatory protein, the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

[0021] In some embodiments of the immunomodulatory protein, the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

[0022] In some embodiments of the immunomodulatory protein, the immunomodulatory protein has been or is capable of being secreted from an engineered cell. In some embodiments, the engineered cell is an immune cell. In some embodiments, the engineered cell is a primary cell.

[0023] In another aspect, there is provided a recombinant nucleic acid encoding an immunomodulatory protein. In some embodiments, the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein. In some embodiments, the promoter is a constitutively active promoter. In some embodiments, the promoter is an inducible promoter. In some embodiments, the promoter is responsive to an element responsive to T-cell activation signaling. In some embodiments, the promoter comprises a binding site for NFAT or a binding site for NF-κB. In another aspect, there is provided a recombinant expression vector comprising the nucleic acid described.

[0024] In a further aspect, there is provided a recombinant expression vector comprising a nucleic acid encoding an immunomodulatory protein under the operable control of a signal sequence for secretion, wherein: the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the

wild-type IgSF domain; and the encoded immunomodulatory protein is secreted when expressed from a cell. In some embodiments, the immunomodulatory protein does not comprise a transmembrane domain. In some embodiments, the immunomodulatory protein is not conjugated to a half-life extending moiety. In some embodiments, the half-life extending moiety is a multimerization domain. In some embodiments, the half-life extending moiety is an Fc domain. In some embodiments, the signal sequence for secretion encodes a secretory signal peptide. In some embodiments, the signal peptide is a native signal peptide from the corresponding wild-type IgSF member. In some embodiments, the signal peptide is a non-native signal peptide. In some embodiments, the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide or other signal peptides known or described. Exemplary signal peptides are set forth in any of SEQ ID NOS: 413-430.

[0025] In some embodiments of the expression vector, the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein. In some embodiments, the promoter is a constitutively active promoter. In some embodiments, the promoter is an inducible promoter. In some embodiments, the promoter is responsive to an element responsive to T-cell activation signaling. In some embodiments, the promoter comprises a binding site for NFAT or a binding site for NF-κB.

[0026] In some embodiments of the expression vector, the vector is a viral vector. In some embodiments, the viral vector is a retroviral vector. In some embodiments, the viral vector is a lentiviral vector or a gammaretroviral vector.

[0027] In some embodiments of the expression vector, the at least one affinity-modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain.

[0028] In some embodiments of the expression vector, the at least one cell surface cognate binding partner is expressed on a mammalian cell. In some embodiments, the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte. In some embodiments, the mammalian cell is a T-cell. In some embodiments, the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

[0029] In some embodiments of the expression vector, specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein comprising

the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

[0030] In some embodiments of the expression vector, the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family. In some embodiments, the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8. In some embodiments, the wild-type IgSF domain is a human IgSF domain. In some embodiments, the at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408. In some embodiments, the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 28-54 and 410. In some embodiments, the wild-type IgSF domain is a member of the B7 family. In some embodiments, the wild-type IgSF domain is a domain of CD80, CD86 or ICOSL.

[0031] In some embodiments of the expression vector, the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor. In some embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when expressed from a cell containing the expression vector, increases immunological activity

of the T-cell. In some embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when expressed from a cell containing the expression vector, decreases immunological activity of the T-cell. In some embodiments, the stimulatory receptor is CD28, ICOS, or CD226. In some embodiments, the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

[0032] In some embodiments of the expression vector, the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner. In some embodiments, the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

[0033] In some embodiments of the expression vector, the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners. In some embodiments, the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell. In some embodiments, binding of the affinity-modified IgSF domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, VSIG3, or VSIG8; or the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9 or VISTA.

[0034] In some embodiments of the expression vector, the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to CTLA-4 compared to the wild-type IgSF domain. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4. In some embodiments, the inhibitory ligand is PD-L1

and the inhibitory receptor is PD-1. In some embodiments, the inhibitory ligand is PD-L2 and the inhibitory receptor is PD-1.

[0035] In some embodiments of the expression vector, the affinity-modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226. In some embodiments, the affinity-modified IgSF domain retains or exhibits increased binding to TIGIT (T-cell immunoreceptor with Ig and ITIM domains) or CD112R compared to the binding affinity of the wild-type IgSF domain for TIGIT or CD112R.

[0036] In some embodiments of the expression vector, the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen. In some embodiments, the tumor specific antigen is B7-H6. In some embodiments, the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

[0037] In some embodiments of the expression vector, the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more different amino acid substitutions in the same wild-type IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

[0038] In some embodiments of the expression vector, the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor in which the inhibitory receptor comprises an ITIM signaling domain. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively. In some embodiments, the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively. In some embodiments, the inhibitory receptor is PD-1 and the at least one affinity-

modified IgSF domain is an affinity-modified IgSF of PD-L1 or PD-L2. In some embodiments, the affinity-modified IgSF domain has increased binding affinity for a trans surface cognate binding partner compared to the wildtype IgSF domain, whereby the increased binding affinity competitively inhibits binding of the trans surface cognate binding partner to the inhibitory receptor.

[0039] In some embodiments of the expression vector, the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain. In some embodiments, the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

[0040] In some embodiments of the expression vector, the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof, comprising the one or more amino acid substitutions.

[0041] In some embodiments of the expression vector, the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

[0042] In another aspect, there is provided an engineered cell comprising any one or more of the above nucleic acid or the above expression vector. In another aspect, there is provided an engineered cell comprising any one or more of the immunomodulatory protein. In another aspect, there is provided an engineered cell that secretes any one or more of the immunomodulatory protein. In some embodiments, the engineered cell is an immune cell.

[0043] In another aspect, there is provided an engineered immune cell comprising a nucleic acid molecule that encodes an immunomodulatory protein, wherein the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and the engineered cell expresses and secretes the immunomodulatory protein. In some embodiments, the immunomodulatory protein does not comprise a transmembrane domain. In some embodiments, the immunomodulatory protein is not conjugated to a half-life extending moiety. In some embodiments, the half-life extending moiety is a multimerization domain. In some embodiments, the half-life extending moiety is an Fc domain.

[0044] In some embodiments of the engineered cell, the nucleic acid molecule comprises a sequence encoding a secretory signal peptide operably linked to the sequence encoding the immunomodulatory protein. In some embodiments, the signal peptide is the native signal peptide from the corresponding wild-type IgSF member. In some embodiments, the signal peptide is a non-native signal sequence. In some embodiments, the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide or any other signal peptide known in the art. Exemplary signal peptides are set forth in any of SEQ ID NOS: 413-430.

[0045] In some embodiments of the engineered cell, the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein. In some embodiments, the promoter is a constitutively active promoter. In some embodiments, the promoter is an inducible promoter. In some embodiments, the promoter is responsive to an element responsive to T-cell activation signaling. In some embodiments, the promoter comprises a binding site for NFAT or a binding site for NF-κB. In some embodiments, the immunomodulatory protein is expressed and secreted by the engineered cell after the engineered cell is contacted with an inducing agent or after induction of T cell activation signaling, which optionally is induced upon binding of an antigen to a chimeric antigen receptor (CAR) or engineered T-cell receptor (TCR) expressed by the engineered cell. In some embodiments, the cell is a lymphocyte. In some embodiments, the lymphocyte is a T cell, a B cell or an NK cell. In some embodiments, the cell is a T cell. In some embodiments, the T cell is CD4+ or CD8+. In some embodiments, the cell is an antigen presenting cell. In some embodiments, the cell is a primary cell obtained from a subject. In some embodiments, the subject is a human subject.

[0046] In some embodiments of the engineered cell, the at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain. In some embodiments, the at least one cell surface cognate binding partner is expressed on a mammalian cell. In some embodiments, the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte. In some embodiments, the mammalian cell is a T-cell. In some embodiments, the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

[0047] In some embodiments of the engineered cell, specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain

modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain. In some embodiments, specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

[0048] In some embodiments of the engineered cell, the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family. In some embodiments, the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8. In some embodiments, the wild-type IgSF domain is a human IgSF domain. In some embodiments, the at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408. In some embodiments, the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 28-54 and 410.

[0049] In some embodiments of the engineered cell, the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor. In some embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when secreted from the cell, increases immunological activity of the T-cell. In some

embodiments, binding of the affinity-modified IgSF domain to the stimulatory receptor, such as when secreted from the cell, decreases immunological activity of the T-cell. In some embodiments, the stimulatory receptor is CD28, ICOS, or CD226. In some embodiments, the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28. In some embodiments, the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

[0050] In some embodiments of the engineered cell, the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner. In some embodiments, the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

[0051] In some embodiments of the engineered cell, the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners. In some embodiments, the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell. In some embodiments, binding of the affinity-modified domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, VSIG3, or VSIG8; or the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9 or VISTA. In some embodiments, the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28. In some embodiments, the inhibitory ligand is PD-L1 and the inhibitory receptor is PD-1. In some embodiments, the inhibitory ligand is PD-L2 and the inhibitory receptor is PD-1. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to CTLA-4 compared to the wild-type IgSF domain. In some embodiments, the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4.

[0052] In some embodiments of the engineered cell, the affinity modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R. In some embodiments, the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226. In some embodiments, the affinity-modified IgSF domain retains or exhibits increased binding to TIGIT (T-cell immunoreceptor with Ig and ITIM domains) or CD112R compared to the binding affinity of the wild-type IgSF domain for TIGIT or CD112R.

[0053] In some embodiments of the engineered cell, the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen. In some embodiments, the tumor specific antigen is B7-H6. In some embodiments, the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

[0054] In some embodiments of the engineered cell, the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprises one or more different amino acid substitutions in the same wild-type IgSF domain. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

[0055] In some embodiments of the engineered cell, the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor in which the inhibitory receptor comprises an ITIM signaling domain. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively. In some embodiments, the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively. In some embodiments, the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-L1 or PD-L2. In some embodiments,

the inhibitory receptor is TIGIT and the affinity-modified IgSF domain is an affinity-modified IgSF domain of CD155 or CD112.

[0056] In some embodiments of the engineered cell, the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain. In some embodiments, the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

[0057] In some embodiments of the engineered cell, the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

[0058] In some embodiments of the engineered cell, the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

[0059] In some embodiments of the engineered cell further comprises a chimeric antigen receptor (CAR) or an engineered T-cell receptor (TCR).

[0060] In another aspect, there is provided a pharmaceutical composition comprising the above engineered cell and a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical composition is sterile.

[0061] In another aspect, there is provided a method of introducing an immunomodulatory protein into a subject, comprising administering any of the provided engineered cells or the pharmaceutical composition containing the engineered cells to the subject.

[0062] In another aspect, there is provided a method of modulating an immune response in a subject, comprising administering any of the provided engineered cells or a pharmaceutical composition containing any of the provided engineered cells to the subject. In some embodiments, modulating the immune response treats a disease or disorder in the subject. In some embodiments, the modulated immune response is increased. In some embodiments, the disease or disorder is a tumor. In some embodiments, the disease or disorder is a cancer. In some embodiments, the disease or disorder is melanoma, lung cancer, bladder cancer, or a hematological malignancy. In some embodiments, the modulated immune response is decreased. In some embodiments, the disease or disorder is an inflammatory disease or condition. In some embodiments, the disease or condition is Crohn's disease, ulcerative colitis, multiple sclerosis, asthma, rheumatoid arthritis, or psoriasis.

[0063] In some embodiments of the methods, the subject is human. In some embodiments, the cell is autologous to the subject. In some embodiments, the cell is allogenic to the subject. In some embodiments, the engineered cell expresses and secretes the immunomodulatory protein. In some embodiments, the immunomodulatory protein is constitutively expressed by the engineered cell. In some embodiments, the immunomodulatory protein is expressed and secreted by the engineered cell after the engineered cell is contacted with an inducing agent. In some embodiments, the immunomodulatory protein is expressed and secreted by the engineered cell upon T cell activation signaling. In some embodiments, the engineered cell expresses a chimeric antigen receptor (CAR) or an engineered T-cell receptor (TCR) and T cell activation signaling is induced upon binding of an antigen by the CAR or TCR.

[0064] Also provided are any of the infectious agents as described containing a nucleic acid molecule encoding a secretable immunomodulatory protein or a transmembrane immunomodulatory protein.

[0065] Provided are infectious agents containing a nucleic acid molecule encoding a transmembrane immunomodulatory protein (TIP) containing an ectodomain comprising at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitution(s) in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and a transmembrane domain.

[0066] In some embodiments, the at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the reference wild-type IgSF domain.

[0067] In some of any such embodiments, the wild-type IgSF domain is from 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 wild-type IgSF domain is from an IgSF member selected from CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8.

[0068] In some of any such embodiments, the wild-type IgSF domain is a human IgSF member. In some embodiments, the transmembrane immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 381-407 and 409 or to a contiguous portion thereof containing the affinity-modified IgSF domain and a transmembrane domain.

[0069] In some embodiments, the transmembrane immunomodulatory protein is a chimeric receptor, wherein the endodomain is not the endodomain from the wild-type IgSF member comprising the wild-type IgSF domain. In some cases, the endodomain contains at least one ITAM (immunoreceptor tyrosine-based activation motif)-containing signaling domain. In some instances, the endodomain contains a CD3-zeta signaling domain. In some aspects, the endodomain further contains at least one of: a CD28 costimulatory domain, an ICOS signaling domain, an OX40 signaling domain, and a 41BB signaling domain.

[0070] In some of any such embodiments, the affinity modified IgSF domain differs by no more than ten amino acid substitutions or no more than five amino acid substitutions from the wildtype IgSF domain. In some embodiments, the affinity-modified IgSF domain is or contains an affinity modified IgV domain, affinity modified IgC1 domain or an affinity modified IgC2 domain or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

[0071] In some of any such embodiments, the transmembrane domain is the native transmembrane domain from the corresponding wild-type IgSF member. In some cases, the transmembrane domain is not the native transmembrane domain from the corresponding wild-type IgSF member. In some examples, the transmembrane protein is a transmembrane protein derived from CD8.

[0072] In some of any such embodiments, the infectious agent is a bacteria or a virus. In some cases, the virus is an oncolytic virus. In some aspects, 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 embodiments, the virus is a lentiviral vector that is pseudotyped with a modified Sindbis virus envelope product.

[0073] 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 cases, 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 a reprogramming human somatic cells to pluripotency.

Brief Description of the Drawings

[0074] **FIG. 1A** depicts results of a competition binding assay for binding of biotinylated recombinant CD28-Fc fusion protein (rCD28.Fc) to immobilized CD80 variant A91G ECD-Fc fusion molecule in the presence of unlabeled recombinant human PD-L1-His, human CTLA-4-His, or human-PD-L2-Fc fusion protein.

[0075] **FIG. 1B** depicts results of a competition binding assay for binding of biotinylated recombinant human PD-L1-his monomeric protein to immobilized CD80 variant A91G ECD-Fc fusion molecule in the presence of unlabeled recombinant human rCD28.Fc, human CTLA-4.Fc or human PD-L2.Fc

[0076] **FIG. 2A and 2B** depicts the detection of PD-L2 SIP in supernatant of transduced CD19 CAR T cells and in HEK-293 cells, respectively.

[0077] **FIG. 3A** depicts the proliferation studies for T cells transduced with exemplary tested variant PD-L2 SIP.

[0078] **FIG. 3B** depicts levels of IFN-gamma in the supernatant released by T cells transduced with exemplary tested variant PD-L2 SIP as measured by ELISA on day 5 after re-stimulation.

[0079] **FIG. 3C** depicts proliferation of T cells co-transduced with a CAR and an exemplary variant PD-L2 SIP or a wild-type PD-L2 SIP following stimulation with target cells.

[0080] **FIG. 4A** 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 activating receptor, which can be expressed on the first cell (e.g. 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, signaling via the activating receptor is blocked. 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.

[0081] **FIG. 4B** 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, which can be expressed on the first cell (e.g. 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 is blocked. 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.

[0082] **FIG. 5** depicts proliferation studies for T cells transduced with exemplary tested variant PD-L1 SIP.

[0083] **FIG. 6** depicts results of a cell-based assay for detection of SIPs, including variant or wild-type PD-L1 and PD-L2 SIPS, in supernatant of transduced HEK-293 cells.

Detailed Description

[0084] Provided herein are secretable immunomodulatory proteins that can be secreted when expressed in a cell, nucleic acids and vectors encoding the same, and cells, such as immune cells or infectious agents, engineered to express and secrete such immunomodulatory proteins. The immunomodulatory protein contains an affinity-modified IgSF domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain. In some embodiments, the immunomodulatory protein does not include a transmembrane domain and/or a half-life extending moiety.

[0085] Among the provided embodiments are cells, such as immune cells (e.g. T cell), engineered to express and secrete the immunomodulatory proteins, for example by engineering the cells to include an expression vector that encodes the immunomodulatory protein. In some embodiments, the immunomodulatory protein encoded by the expression vector is under the operable control of a signal sequence for secretion, such that when the cell expresses the immunomodulatory protein, the immunomodulatory protein is secreted by the engineered cell. In some embodiments, expression of the immunomodulatory protein is under the operable control of a promotor. The promotor can be, for example, an inducible promoter. In some embodiments, the inducible promoter is responsive to an element responsive to T-cell activation signaling. In some embodiments, the engineered cell (e.g. T cell) also is engineered to express on its surface an antigen receptor, such as a T cell receptor (TCR) or chimeric antigen receptor (CAR), containing an intracellular signaling domain capable of or that does induce or mediate T-cell signaling upon antigen binding. In some aspects, the intracellular signaling domain comprises an immunoreceptor tyrosine-based activation motif (ITAM). Thus, in some embodiments, an engineered immune cell expresses and secretes an immunomodulatory protein only in response to activation of the immune cell, including, in some aspects, in response to recognition of antigen by an engineered antigen receptor.

[0086] Also provided herein are methods of introducing an immunomodulatory protein into a subject, the method comprising administering an engineered cell or infectious agent (or a pharmaceutical composition comprising an engineered cell or infectious agent) into the subject. In another aspect, there is provided a method of modulating an immune response in a subject, the method comprising administering an engineered cell (or a pharmaceutical composition comprising an engineered cell or infectious agent) into the subject. In another aspect, there is provided a method of treating a subject in need of treatment (such as a subject with a disease, such as cancer), the method comprising administering an effective amount of an engineered cell or infectious agent (or a pharmaceutical composition comprising an engineered cell or infectious agent) into the subject. The engineered cell can be a population of cells, such as a cell culture or a plurality of separately engineered cells.

[0087] In some embodiments, the provided engineered cells are administered to a subject and, in response to an induction signal (for example, immune cell activation or administration of an inducing agent) the engineered cells administered to the subject express and secrete the immunomodulatory protein. In some embodiments, the engineered cells constitutively express

and secrete the immunomodulatory protein. In some embodiments, the engineered cells localize to a diseased cell or lesion, such as a cell present in a tumor microenvironment (e.g. tumor cell), which, in some aspects, is mediated by recognition of an antigen by an engineered antigen receptor expressed by the engineered cells, thereby targeting the secreted immunomodulatory proteins to the site of the disease or lesion, e.g. tumor microenvironment.

[0088] In some embodiments, the cognate binding partner of the immunomodulatory protein is a cell surface protein expressed by immune cells that engage with one or more other immune receptors (e.g. on lymphocytes) to induce inhibitory or activating signals. For example, the interaction of certain receptors on lymphocytes with their cell surface cognate binding partners to form an immunological synapse (IS) between antigen-presenting cells (APCs) or target cells and lymphocytes can provide costimulatory or inhibitory signals that can regulate the immune system. In some aspects, the immunomodulatory proteins provided herein (which can be expressed and secreted by an engineered cell) can alter the interaction of cell surface protein ligands with their receptors to modulate immune cells, such as T cell, activity. In some embodiments, the binding of the immunomodulatory protein to a ligand (cognate binding partner) modulates, e.g. induces, enhances or suppresses, immunological immune responses of a cell to which the immunomodulatory protein specifically binds. In some embodiments, the secretable immunomodulatory protein as provided, such as is secreted by the engineered cells, suppresses, such as inhibits or antagonizes, its cognate binding partner.

[0089] 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 (i.e., 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.

[0090] Thus, in some aspects, immunotherapy that alters immune cell activity, such as T cell activity, can treat certain diseases and conditions in which the immune response is dysregulated. Therapeutic approaches that seek to modulate interactions in the IS would benefit from the ability to bind multiple IS targets simultaneously and in a manner that is sensitive to temporal sequence and spatial orientation. Current therapeutic approaches fall short of this goal. Wild-

type receptors and ligands possess low affinities for cognate binding partners, which can preclude their use as soluble therapeutics. Additionally, soluble receptors and antibodies, in some aspects, typically bind no more than a single target protein at a time and/or bind competitively to their targets (e.g., to no more than one target species at a time), and therefore lack the ability to simultaneously bind multiple targets. And while bispecific antibodies, as well as modalities comprising dual antigen binding regions, can bind to more than one target molecule simultaneously, the three-dimensional configuration typical of these modalities often precludes them intervening in key processes occurring in the IS in a manner consistent with their temporal and spatial requirements.

[0091] What is needed is an entirely new class of therapeutic molecules that have the specificity and affinity of antibodies, but also maintain the size, volume, and spatial orientation constraints required in the IS. Further, such therapeutics would have the ability to bind to their targets non-competitively as well as competitively. A molecule with these properties would therefore have novel function in the ability to integrate into multi-protein complexes at IS and generate the desired binding configuration and resulting biological activity.

[0092] To this end, emerging immuno-oncology therapeutic regimes need to safely break tumor-induced T cell tolerance. Current state-of-the-art immuno-therapeutics block PD-1 or CTLA4, central inhibitory molecules of the B7/CD28 family that are known to limit T cell effector function. While antagonistic antibodies against such single targets function to disrupt immune synapse checkpoint signaling complexes, they fall short of simultaneously activating T cells. Conversely, bispecific antibody approaches activate T cells, but fall short of simultaneously blocking inhibitory ligands that regulate the induced signal.

[0093] To address these shortcomings, provided are immunotherapies, such as cell therapies, that can modulate immune cell activities. In some embodiments, the provided immunotherapies can enhance immune cells signaling, such as T-cell activation signaling, and/or can block inhibitory regulation, which, in some cases, can occur simultaneously. In some embodiments, the provided immunotherapies relate to immunoglobulin superfamily (IgSF) components of the immune synapse that are known to have a dual role in both T-cell activation and blocking of inhibitory ligands. In some aspects, IgSF based-cell therapies engineered from immune system ligands, such as human immune system ligands themselves are more likely to retain their ability to normally assemble into key pathways of the immune synapse and maintain normal interactions and regulatory functions in ways that antibodies or next-generation bi-specific

reagents cannot. This is due to the relatively large size of antibodies as well as from the fact they are not natural components of the immune synapse. These unique features of human immune system ligands, and cells engineered to express affinity-modified variants of such ligands, promise to provide a new level of immunotherapeutic efficacy and safety. In particular aspects, the provided engineered cells provide a secretable immunomodulatory platform using affinity-modified native immune ligands to generate immunotherapy biologics that bind with tunable affinities to one or more of their cognate immune receptors in the treatment of a variety of oncological and immunological indications.

[0094] 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.

[0095] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

I. DEFINITIONS

[0096] 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.

[0097] The terms used throughout this specification are defined as follows unless otherwise limited in specific instances. 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 are 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.

[0098] As used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly indicates otherwise.

[0099] 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. 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 wild-type 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, 1: 7930801 (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 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.

[0100] 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.

[0101] 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 immunomodulatory protein (which can be secreted from the engineered cell) and/or chimeric antigen receptor (CAR), which in some cases involves engineering a T-cell or TIL (tumor infiltrating lymphocyte). The engineered cell can then be infused into a patient from which the native T-cell was isolated. In some embodiments, the organism is human or murine.

[0102] 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 cognate binding partner (i.e., 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 an IgSF domain and its cognate binding partner (i.e., its counter-structure). As such, avidity is distinct from affinity, which describes the strength of a single interaction. An increase or attenuation in binding affinity of an affinity-modified IgSF domain to its cognate binding partner is determined relative to the binding affinity of the unmodified IgSF domain (e.g., the native or wild-type IgSF 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).The term "cell surface counter-structure" (alternatively "cognate cell surface binding partner") as used herein is a counter-structure (alternatively is a cognate binding partner) expressed on a mammalian cell. Typically, the cell surface cognate

binding partner is a transmembrane protein. In some embodiments, the cell surface cognate binding partner is a receptor.

[0103] 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 with antigen binding specificity to the patient's tumor is typically engineered to be expressed on a native lymphocyte obtained from the patient. The engineered lymphocyte expressing the CAR is then infused back into the patient. The lymphocyte is thus often an autologous T-cell although allogeneic T-cells 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 an 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 cell on which the CAR is expressed. Thus, for example, upon specific binding by the antigen binding region of the CAR-T to its 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 activation is achieved in some embodiments by the CD3-zeta chain ("CD3-z") which is involved in signal transduction in native mammalian T-cells. CARs can further comprise multiple signaling domains such as CD28, ICOS, 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.

[0104] The terms "cognate binding partner" or "counter-structure" in reference to a protein, such as an IgSF domain or an affinity-modified IgSF domain, refers to at least one molecule (typically a native mammalian protein) to which the referenced protein specifically binds under

specific binding conditions. In some aspects, an affinity-modified IgSF domain specifically binds to the cognate binding partner of the corresponding native or wild-type IgSF domain 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 receptor, to which a native ligand recognizes and specifically binds to under specific binding conditions, is an example of a cognate binding partner of that ligand. In turn, the native ligand is the cognate binding partner of the receptor. For example, ICOSL specifically binds to CD28 and ICOS and thus these proteins are cognate binding partners of ICOSL. In another example, a tumor specific antigen and an affinity-modified IgSF domain to which it specifically binds are each cognate binding partners of the other. In the present invention 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, for example immune cells.

[0105] 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 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) or Forte-Bio Octet experimental systems.

[0106] 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.

[0107] 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. By aligning the sequences, one skilled in the art can identify corresponding residues, for example, using conserved and identical amino acid residues as guides.

[0108] The term "cytokine" includes, e.g., but is not limited to, interleukins, interferons (IFN), chemokines, hematopoietic growth factors, tumor necrosis factors (TNF), and transforming growth factors. In general, these are small molecular weight proteins that regulate maturation, activation, proliferation, and differentiation of cells of the immune system.

[0109] The terms "derivatives" or "derivatized" refer to modification of an immunomodulatory protein by covalently linking it, directly or indirectly, so as to alter such characteristics as half-life, bioavailability, immunogenicity, solubility, toxicity, potency, or efficacy while retaining or enhancing its therapeutic benefit. Derivatives can be made by glycosylation, pegylation, lipidation, or Fc-fusion. In some embodiments, the immunomodulatory protein is not derivatized. In some embodiments, the immunomodulatory protein is not conjugated to a half-life extending moiety, such as an Fc domain.

[0110] 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. 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 (one, two, three or four) longer or shorter.

[0111] The term "ectodomain," "extracellular domain," or "ECD" as used herein refers to the region of a membrane protein, such as a transmembrane protein, that lies outside the vesicular membrane (e.g., the space outside of a cell). Ectodomains often interact with specific ligands or specific cell surface receptors, such as via a binding domain that specifically binds to the ligand or cell surface receptor.

[0112] The terms "effective amount" or "therapeutically effective amount" refer to a quantity and/or concentration of a therapeutic composition of the invention, such as composition containing engineered cells, that when administered ex vivo (by contact with a cell from a patient) or in vivo (by administration into a patient, such as by adoptive transfer) either alone (i.e., as a monotherapy) or in combination with additional therapeutic agents, yields a statistically significant inhibition of disease progression as, for example, by ameliorating or eliminating symptoms and/or the cause of the disease. An effective amount for treating an immune system disease or disorder may be an amount that relieves, lessens, or alleviates at least one symptom or biological response or effect associated with the 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. In some embodiments the patient is a human patient.

[0113] 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.

[0114] The term "enhanced" or "increased" as used herein in the context of increasing immunological activity of a mammalian lymphocyte means to increase one or more activities of the lymphocyte. An increased activity can be one or more of an 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. 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.

[0115] 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 engineered 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 is capable of expressing and secreting an immunomodulatory protein as described herein. In some embodiments, the engineered cell further expresses or contains an engineered T-cell receptor (TCR) or chimeric antigen receptor (CAR).

[0116] 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. In some embodiments, an engineered T-cell is capable of expressing and secreting an immunomodulatory protein as described herein.

[0117] 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.

[0118] A protein "expressed on" a cell is used herein to reference to a protein expressed by a cell and in which at least a portion of the protein is present on the surface of the cell. Proteins expressed on a cell include transmembrane proteins or cell surface receptors. In some embodiments, the protein is conjugated to a small molecule moiety such as a drug or detectable label.

[0119] 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).

[0120] The term "host cell" refers to any 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.

[0121] The term "immunological synapse" or "immune synapse" (abbreviated "IS") 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.

[0122] The term "immunoglobulin" (abbreviated "Ig") as used herein is synonymous with the term "antibody" (abbreviated "Ab") and refers to a mammalian immunoglobulin protein including any of the five human classes: 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 VH and VL, the single chain variable fragment (scFv) containing VH and VL 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.

[0123] 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). An immunoglobulin Fc fusion ("Fc-fusion") 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, in some cases, facilitates effector functions and pharmacokinetics) and the IgSF domain of a wild-type or affinity-modified immunoglobulin superfamily domain ("IgSF"), or other protein or fragment thereof. 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. The IgSF domain mediates recognition of the cognate binding partner (comparable to that of antibody variable region of an antibody for an antigen). An immunoglobulin Fc region may be linked indirectly or directly to one or more polypeptides or small molecules (fusion partners). Various linkers are known in the art and can be used to link an Fc to a fusion partner to generate an Fc-fusion. An Fc-fusion protein can comprise an immunoglobulin Fc region covalently linked, directly or indirectly, to at least one affinity modified IgSF domain. 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 immunomodulatory protein is not conjugated to an Fc domain or any portion thereof.

[0124] 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.

[0125] The terms "IgSF domain" or "immunoglobulin domain" or "Ig domain" as used herein refers 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, IgC1, 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.

[0126] 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.

[0127] The term "immunological activity" as used herein in the context of mammalian lymphocytes refers to one or more cell survival, cell proliferation, cytokine production (e.g. interferon-gamma), or T-cell cytotoxicity activities. Methods to assay the immunological activity of engineered cells, including to evaluate the activity of the 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 51Cr-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). Assays to assess immunological activity of engineered cells can be compared to control non-engineered cells or to cells containing one or more other engineered recombinant receptor (e.g. antigen receptor) with a known activity.

[0128] An "immunomodulatory protein" or "immunomodulatory polypeptide" is a protein that modulates immunological activity. By "modulation" or "modulating" an immune response is meant that immunological activity is either enhanced or suppressed. 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 proteins are within the scope of the defined term. Multimeric proteins can be homomultimeric (of identical polypeptide chains) or heteromultimeric (of different polypeptide chains). Secretable immunomodulatory proteins are a type of immunomodulatory protein.

[0129] 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.

[0130] 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.

[0131] An "inhibitory counter-structure" or "inhibitory cognate binding partner" is a cell membrane protein, often a receptor, which when proximally bound near a separate activating receptor leads to an attenuation in the frequency, duration, magnitude, or intensity of the activating signaling cascade and phenotype mediated by the activating receptor. Examples of inhibitory receptors include PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, and VSIG8. The term "stimulatory counter-structure" or "stimulatory cognate binding partner" is a cell membrane protein, often a receptor, which when activated and signal transduction is thereby induced, leads to an increase in the frequency, duration, or intensity of the phenotype mediated by that receptor. Examples of stimulatory receptors include CD28, ICOS, and CD226.

[0132] 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.

[0133] The terms "mammal," "subject," or "patient" specifically includes reference to at least one of a: human, chimpanzee, rhesus monkey, cynomolgus monkey, dog, cat, mouse, or rat.

[0134] 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".

[0135] 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 decrease, of an existing or potential immune responses that occurs as a result of administration of an immunomodulatory protein or as a result of administration of engineered cells expressing an immunomodulatory protein, such as a secretable immunomodulatory protein of the present invention. Such modulation includes any induction, or alteration in degree or extent, or suppression 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; proliferation, induction, survival 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, perforins, granzymes, 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 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 the wild-type IgSF protein.

[0136] 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 CD80 is an IgSF member and each human CD80 molecule is a species of CD80. 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.

[0137] 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. In some embodiments, the binding occurs under specific binding conditions. 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 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.

[0138] 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. 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.

[0139] 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 protein or engineered cells expressing and/or secreting an immunomodulatory protein of the present invention) and a carrier, excipient, or diluent. The carrier, excipient, or diluent is typically a pharmaceutically acceptable carrier, excipient or diluent, respectively.

[0140] 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 as described herein by well-known organic chemistry techniques.

[0141] 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 such as that described in Example 6. In a preferred embodiment, the assay used is anti-CD3 coimmobilization 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 a mixed lymphocyte reaction (MLR). In this assay, primary T cells are simulated with allogenic 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.

[0142] The term "purified" as applied to nucleic acids, such as encoding a secretable immunomodulatory proteins, or proteins (e.g. immunomodulatory proteins) 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 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).

[0143] 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 (e.g., an immunomodulatory protein) 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 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. The term also refers to the linkage of amino acid sequences in such a manner so that a functional protein is produced and/or transported.

[0144] The term "recombinant expression vector" as used herein refers to a DNA molecule containing a desired coding sequence (e.g., encoding an immunomodulatory protein) and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular 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 so that the expressed protein can be secreted by the recombinant host cell, for more facile 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.

[0145] 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}).

[0146] 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.

[0147] 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.

[0148] The term "species" as used herein in the context of a nucleic acid sequence or a polypeptide sequence refers to an identical collection of such sequences. Slightly truncated

sequences 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.

[0149] 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 10 times as great, but optionally 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 (e.g., its cognate binding partner) 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, an affinity-modified polypeptide of the invention may specifically bind to more than one distinct species of target molecule due to cross-reactivity. Generally, such off-target specific binding is mitigated by reducing affinity or avidity for undesired targets. Solid-phase ELISA immunoassays or Biacore measurements can be used to determine specific binding between two proteins. Generally, interactions between two binding proteins have dissociation constants (Kd) less than about $1x10^{-5}$ M, and often as low as about 1 x 10^{-12} M. In certain aspects of the present disclosure, interactions between two binding proteins have dissociation constants of less than about $1x10^{-6}$ M, $1x10^{-7}$ M, $1x10^{-8}$ M, $1x10^{-9}$ M, $1x10^{-10}$ M, or $1x10^{-11}$ M.

[0150] The term "specific binding fragment" or "fragment" as used herein in reference to a mature (i.e., absent the signal peptide) wild-type IgSF domain, means a polypeptide that is shorter than the full-length mature IgSF domain and that specifically binds in vitro and/or in vivo to the wild-type IgSF domain's native cognate binding partner. In some embodiments, the specific binding fragment is at least 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% the sequence length of the full-length mature wild-type sequence. The specific binding fragment can be altered in sequence to form an affinity modified IgSF domain of the invention. In some embodiments, the specific binding fragment modulates immunological activity of a lymphocyte. The terms "suppress" or "attenuate" or "decrease" as

used herein means to decrease by a statistically significant amount. In some embodiments suppression can be a decrease of at least 10%, and up to 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90%.

[0151] 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.

[0152] 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.

[0153] 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 an immunomodulatory protein or engineered cells expressing a transmembrane immunomodulatory protein of the present 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 protein or engineered cells expressing an immunomodulatory protein of the present 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.

[0154] The term "tumor specific antigen" or "TSA" as used herein refers to a an antigen that is present primarily on tumor cells of a mammalian subject but generally not found on normal cells of the mammalian subject. In some cases, a tumor specific antigen is a counter structure or cognate binding partner of an IgSF member. 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 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.

[0155] The term "wild-type" or "natural" or "native" as used herein is used in connection with biological materials such as nucleic acid molecules, proteins, IgSF members, host cells, and the like, refers to those which are found in nature and not modified by human intervention.

II. IMMUNOMODULATORY PROTEINS CONTAINING AFFINITY-MODIFIED DOMAINS

[0156] In some embodiments, the immunomodulatory protein, including secretable immunomodulatory proteins (SIPs) or transmembrane immunomodulatory proteins (TIPs), includes at least one affinity-modified IgSF domain compared to an IgSF domain of a wild-type mammalian IgSF member. The wild-type mammalian IgSF member excludes antibodies (i.e., immunoglobulins) such as those that are mammalian or may be of mammalian origin. Thus, the present invention relates to IgSF domains that are non-immunoglobulin (i.e., non-antibody) IgSF domains. Wild-type mammalian IgSF family members that are not immunoglobulins (i.e. antibodies) are known in the art as are their nucleic and amino acid sequences. Affinity-

modified IgSF domains of a wild-type IgSF domain of all non-immunoglobulin mammalian IgSF family members are included within the scope of the invention.

[0157] In some embodiments, immunomodulatory proteins as provided in their various embodiments comprise at least one affinity-modified mammalian IgSF domain, such as at least one affinity modified non-immunoglobulin mammalian IgSF domain. In some embodiments, the non-immunoglobulin IgSF family members, and the corresponding IgSF domains present therein, are of mouse, rat, cynomolgus monkey, or human origin. In some embodiments, the IgSF family members are members from at least or exactly one, two, three, four, five, or more IgSF subfamilies such as: 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, or Killer-cell immunoglobulin-like receptors (KIR) family. In some embodiments, the at least one IgSF domain is derived from an IgSF protein that is any 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), NC R3 (NKp30), VISTA, VSIG3, and VSIG8.

[0158] In some embodiments, the immunomodulatory protein contains at least one affinity-modified IgSF domain. In some embodiments, the at least one affinity-modified IgSF domain is affinity-modified compared to a corresponding IgSF domain of a non-immunoglobulin IgSF family member that is a mammalian IgSF member. In some embodiments, the mammalian IgSF member is one of the IgSF members or comprises an IgSF domain from one of the IgSF members as indicated in Table 1 including any mammalian orthologs thereof. Orthologs are genes in different species that evolved from a common ancestral gene by speciation. Normally, orthologs retain the same function in the course of evolution. In some embodiments, the affinity

modified IgSF domain is an affinity modified IgV or IgC domain, including IgC1 or IgC2 domain.

[0159] In some embodiments, the immunomodulatory protein of the present invention comprises the sequence of the extracellular domain of a wild-type mammalian non-immunoglobulin (i.e., non-antibody) IgSF family member but wherein at least one IgSF domain therein is affinity modified. Solely by way of example, in some embodiments, a wild-type mammalian non-immunoglobulin IgSF family member comprises a first IgSF domain and a second IgSF domain, and an immunomodulatory protein comprises the first IgSF domain and the second IgSF domain of the wild-type IgSF family member, except at least the first IgSF domain or the second IgSF domain is affinity-modified. Immunomodulatory proteins comprising the sequence of the extracellular domain of a wild-type mammalian immunoglobulin (i.e., non-antibody) IgSF family member, but wherein at least one IgSF domain is affinity modified can be referred to as "Type I" immunomodulatory proteins. Additional domains present within the IgSF family can be affinity modified, such as at least two, three, four, or five IgSF domains and, in some embodiments, exactly two, three, four, or five IgSF domains. In some embodiments of an immunomodulatory protein of the invention, the mammalian IgSF member will be one of the IgSF members as indicated in Table 1 including any mammalian orthologs thereof

[0160] The first column of Table 1 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. 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). 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). Column 5 indicates for some of the listed IgSF members, some of its cognate cell surface binding partners.

[0161] Typically, the affinity-modified IgSF domain of the immunomodulatory protein of the provided embodiments is a human or murine affinity modified IgSF domain.

TABLE 1. 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, 35-141 or 37-138 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: 381	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: 382	SEQ ID NO: 29
CD274 (PD-L1, B7-H1)	Q9NZQ7.1	24-130 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: 383	SEQ ID NO: 30
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: 384	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: 385	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: 386	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: 387	SEQ ID NO: 34

TABLE 1. 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
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: 388	SEQ ID NO: 35
CTLA4	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: 389	SEQ ID NO: 36
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: 390	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: 391	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: 392	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: 393	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: 394	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: 395	SEQ ID NO: 42
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: 396	SEQ ID NO: 43

TABLE 1. 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
HAVCR2 (TIM-3)	Q8TDQ0.3	22-124 IgV	S: 1-21, E: 22-202, T: 203-223, C: 224-301	CEACAM-1, phosphatidyl serine, Galectin-9, HMGB1	SEQ ID NO: 17 (22-301)	SEQ ID NO: 397	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: 398	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: 399	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: 400	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: 401	SEQ ID NO: 48
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: 402	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: 403	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: 404	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: 405	SEQ ID NO: 52

TABLE 1. 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
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: 406	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: 407	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: 408 (22-414)	SEQ ID NO: 409	SEQ ID NO: 410

[0162] In some embodiments, the immunomodulatory protein contains at least one affinity-modified domain and at least one non-affinity modified IgSF domain (e.g. unmodified or wild-type IgSF domain). In some embodiments, the immunomodulatory protein contains at least two affinity modified domains. In some embodiments, the immunomodulatory protein contains a plurality of non-affinity modified IgSF domains and/or affinity-modified IgSF domains, such as 1, 2, 3, 4, 5, or 6 non-affinity modified IgSF and/or affinity modified IgSF domains.

[0163] In some embodiments, the immunomodulatory protein comprises a combination (a "non-wild-type combination") and/or arrangement (a "non-wild type arrangement" or "non-wild-type permutation") of an affinity-modified and/or non-affinity modified IgSF domain sequences that are not found in wild-type IgSF family members ("Type II" immunomodulatory proteins). The sequences of the IgSF domains which are non-affinity modified (e.g., wild-type) or have been affinity modified can be mammalian, such as from mouse, rat, cynomolgus monkey, or human origin, or combinations thereof. In some embodiments, the sequence of the non-affinity modified domain is any IgSF domain set forth in Table 1. The number of such non-affinity modified or affinity modified IgSF domains present in these embodiments of a Type II immunomodulatory protein (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.

[0164] In some embodiments, at least two of the affinity modified IgSF domains are identical affinity modified IgSF domains. In some embodiments, the 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 IgSF domains from which they are designed was the same. Thus, for example, a combination of at least two non-identical IgSF domains in the immunomodulatory protein of the present invention can comprise at least one IgSF domain sequence whose origin is from and unique to one IgSF family member and at least one of a second IgSF domain sequence whose origin is from and unique to another IgSF family member wherein the IgSF domains of the immunomodulatory protein are in affinity modified form. However, in alternative embodiments, the two non-identical IgSF domains originate from the same IgSF domain sequence but are affinity modified differently such that they specifically bind to different cognate binding partners. In some embodiments, the number of non-identical affinity modified IgSF domains present in the immunomodulatory protein of the invention is at least 2, 3, 4, or 5 and in some embodiments exactly 2, 3, 4, or 5 non-identical affinity modified IgSF domains. In some embodiments, the non-identical IgSF domains are combinations from at least two IgSF members indicated in Table 1, and in some embodiments at least three or four IgSF members of Table 1.

[0165] In other embodiments an immunomodulatory protein provided herein comprises at least two IgSF domains from a single IgSF member but in a non-wild-type arrangement. One illustrative example of a non-wild type arrangement or permutation is an immunomodulatory protein of the present invention comprising a non-wild type order of affinity modified IgSF domain sequences relative to those found in the wild-type mammalian IgSF family member whose IgSF domain sequences served as the source of the affinity modified IgSF domains. The mammalian wild-type IgSF member in the preceding embodiment specifically includes those listed in Table 1. Thus, in one example, if the wild-type family member comprises an IgC1 domain proximal to the N-terminus of the protein and an IgV domain distal to the N-terminus, then the immunomodulatory protein provided herein can comprise an IgV proximal and an IgC1 distal to the N-terminus, albeit in affinity modified form. The presence, in an immunomodulatory protein, of both non-wild type combinations and non-wild type arrangements of affinity modified IgSF domains is also within the scope of the present invention. A plurality of affinity-modified IgSF domains in an immunomodulatory protein's

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 affinity-modified IgSF domains to each other. Such "peptide linkers" can be a single amino acid residue or greater in length.

[0166] In some embodiments, the affinity modified IgSF domain can be affinity modified to specifically bind to a single (e.g., 1) or multiple (e.g., 2, 3, 4, or more) counter-structures (also called a "cognate binding partner") expressed on a mammalian cell. Typically, the cognate binding partner is a native cognate binding partner of the wild-type IgSF domain that has been affinity modified. In some embodiments, the cognate binding partner is an IgSF member. In some embodiments the cognate binding partner e is a non-IgSF family member. For example, in some embodiments the cognate binding partner of an affinity-modified IgSF domain such as BTLA (B- and T-lymphocyte attenuation) is the non-IgSF member cognate binding partner HVEM (herpes virus entry mediator). BTLA-HVEM complexes negatively regulate T-cell immune responses. Each IgSF domain present in an immunomodulatory protein can be affinity modified to independently increase or attenuate specific binding affinity or avidity to each of the single or multiple cognate binding partners to which it binds. By this method, specific binding to each of multiple cognate binding partners is independently tuned to a particular affinity or avidity.

[0167] In some embodiments, the cognate binding partner of an IgSF domain is at least one, and sometimes at least two or three of the counter-structures (cognate binding partners) of the wild-type IgSF domain, such as those listed in Table 1.

[0168] The sequence of the IgSF domain, such as mammalian IgSF domain, is affinity-modified by altering its sequence with at least one substitution, addition, or deletion. Alteration of the sequence can occur at the binding site for the cognate binding partner or at an allosteric site. In some embodiments, a nucleic acid encoding an IgSF domain, such as a mammalian IgSF domain, is affinity modified by substitution, addition, deletion, or combinations thereof, of specific and pre-determined nucleotide sites to yield a nucleic acid encoding an immunomodulatory protein of the invention. In some contrasting embodiments, a nucleic acid encoding an IgSF domain, such as a mammalian IgSF domain, is affinity modified by substitution, addition, deletion, or combinations thereof, at random sites within the nucleic acid. In some embodiments, a combination of the two approaches (pre-determined and random) is

utilized. In some embodiments, design of the affinity modified IgSF domains is performed in silico.

[0169] In some embodiments, the affinity-modified IgSF domain of the immunomodulatory protein contains one or more amino acid substitutions (alternatively, "mutations" or "replacements") relative to a wild-type or unmodified polypeptide or a portion thereof containing an immunoglobulin superfamily (IgSF) domain. In some embodiments, the IgSF domain is an IgV domain or an IgC domain or specific binding fragment of the IgV domain or the IgC domain. In some embodiments, the immunomodulatory protein comprises an affinity modified IgSF domain that contains an IgV domain or an IgC domain or specific binding fragments thereof in which the at least one of the amino acid substitutions is in the IgV domain or IgC domain or a specific binding fragment thereof. In some embodiments, by virtue of the altered binding activity or affinity, the IgV domain or IgC domain is an affinity-modified IgSF domain.

[0170] In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with no more than a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions, additions, deletions, or combinations thereof. In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions, additions, deletions, or combinations thereof. In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with between 1 (or 2, 3, 4, 5, 6, 7, 8, or 9) and 10 (or 9, 8, 7, 6, 5, 4, 3, or 2) amino acid substitutions, additions, deletions, or combinations thereof. In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with no more than a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions. In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions. In some embodiments, the IgSF domain, such as a mammalian IgSF domain, is affinity-modified in sequence with between 1 (or 2, 3, 4, 5, 6, 7, 8, or 9) and 10 (or 9, 8, 7, 6, 5, 4, 3, or 2) amino acid substitutions. In some embodiments, the substitutions are conservative substitutions. In some embodiments, the substitutions are non-conservative. In some embodiments, the substitutions are a combination of conservative and non-conservative substitutions. In some embodiments, the modification in sequence is made at the binding site of the IgSF domain for its cognate binding partner.

[0171] In some embodiments, the wild-type or unmodified IgSF domain is a mammalian IgSF domain. In some embodiments, the wild-type or unmodified IgSF domain can be an IgSF domain that includes, but is not limited to, human, mouse, cynomolgus monkey, or rat. In some embodiments, the wild-type or unmodified IgSF domain is human.

[0172] In some embodiments, the wild-type or unmodified IgSF domain is or comprises an extracellular domain of an IgSF family member or a portion thereof containing an IgSF domain (e.g. IgV domain or IgC domain). In some cases, the extracellular domain of an unmodified or wild-type IgSF domain can comprise more than one IgSF domain, for example, an IgV domain and an IgC domain. However, the affinity modified IgSF domain need not comprise both the IgV domain and the IgC domain. In some embodiments, the affinity modified IgSF domain comprises or consists essentially of the IgV domain or a specific binding fragment thereof. In some embodiments, the affinity modified IgSF domain comprises or consists essentially of the IgC domain or a specific binding fragment thereof. In some embodiments, the affinity modified IgSF domain comprises the IgV domain or a specific binding fragment thereof, and the IgC domain or a specific binding fragment thereof.

[0173] In some embodiments, the one or more amino acid substitutions of the affinity modified IgSF domain can be located in any one or more of the IgSF polypeptide domains. For example, in some embodiments, one or more amino acid substitutions are located in the extracellular domain of the IgSF polypeptide. In some embodiments, one or more amino acid substitutions are located in the IgV domain or specific binding fragment of the IgV domain. In some embodiments, one or more amino acid substitutions are located in the IgC domain or specific binding fragment of the IgC domain.

[0174] In some embodiments, the wild-type or unmodified IgSF domain is an IgSF domain or specific binding fragment thereof contained in the sequence of amino acids set forth in any of SEQ ID NOS:1-27 and 408 or contained in 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:1-27 and 408. In some embodiments, the IgSF domain is an IgV domain or IgC domain contained therein or specific binding fragments thereof. Table 1 identifies the IgSF domains contained in each of SEQ ID NOS: 1-27 and 408.

[0175] In some embodiments, the unmodified or wild-type IgSF domain comprises the extracellular domain (ECD) or a portion comprising an IgSF domain (e.g. IgV domain or IgC domain) of an IgSF member, such as a mammalian IgSF member. In some embodiments, the

unmodified or wild-type IgSF domain comprises (i) the sequence of amino acids set forth in any of SEQ ID NOS:28-54 and 410, (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 any of SEQ ID NOS: 28-54 and 410, or (iii) is a specific binding fragment of (i) or (ii) comprising an IgV domain or an IgC domain.

[0176] In some embodiments, at least one IgSF domain, such as at least one mammalian IgSF domain, of an immunomodulatory protein of the present invention is independently affinity modified in sequence to have at least 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86% 85%, or 80% sequence identity with the corresponding wild-type IgSF domain or specific binding fragment thereof contained in a wild-type or unmodified IgSF protein, such as, but not limited to, those disclosed in Table 1 as SEQ ID NOS: 1-27 and 408.

[0177] In some embodiments, the affinity-modified IgSF domain of an immunomodulatory protein provided herein is a specific binding fragment of a wild-type or unmodified IgSF domain contained in a wild-type or unmodified IgSF protein, such as but not limited to, those disclosed in Table 1 in SEQ ID NOS: 1-27 and 408. In some embodiments, 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, the 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 wild-type or unmodified IgV domain. In some embodiments, the specific binding fragment of the IgC 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 wild-type or unmodified IgC domain. In some embodiments, the specific binding fragment modulates immunological activity. In more specific embodiments, the specific binding fragment of an IgSF domain increases immunological activity. In alternative embodiments, the specific binding fragment decreases immunological activity.

[0178] In some embodiments, to determine the percent identity of two nucleic acid sequences or of two amino acids, the sequences are aligned for optimal comparison purposes (e.g., gaps may be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide

as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions (e.g., overlapping positions) x 100). In one embodiment the two sequences are the same length. One may manually align the sequences and count the number of identical nucleic acids or amino acids. Alternatively, alignment of two sequences for the determination of percent identity may be accomplished using a mathematical algorithm. Such an algorithm is incorporated into the NBLAST and XBLAST programs. BLAST nucleotide searches may be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches may be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecule of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST may be utilized. Alternatively, PSI-Blast may be used to perform an iterated search which detects distant relationships between molecules. When utilizing the NBLAST, XBLAST, and Gapped BLAST programs, the default parameters of the respective programs may be used such as those available on the NCBI website. Alternatively, sequence identity may be calculated after the sequences have been aligned e.g. by the BLAST program in the NCBI database. Generally, the default settings with respect to e.g. "scoring matrix" and "gap penalty" may be used for alignment. In the context of the present invention, the BLASTN and PSI BLAST NCBI default settings may be employed.

[0179] The means by which the affinity-modified IgSF domains of the immunomodulatory proteins are designed or created is not limited to any particular method. In some embodiments, however, wild-type IgSF domains are mutagenized (site specific, random, or combinations thereof) from wild-type IgSF genetic material and screened for altered binding according to the methods disclosed in the Examples. Methods or mutagenizing nucleic acids is known to those of skill in the art. In some embodiments, the affinity modified IgSF domains are 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.

[0180] In some embodiments, at least one non-affinity modified IgSF domain and/or one affinity modified IgSF domain present in the immunomodulatory protein provided herein

specifically binds to at least one cell surface molecular species expressed on mammalian cells forming the immunological synapse (IS). In some embodiments, an immunomodulatory protein provided herein can comprise a plurality of non-affinity modified IgSF domains and/or affinity modified IgSF domains such as 1, 2, 3, 4, 5, or 6 non-affinity modified IgSF and/or affinity modified IgSF domains. One or more of these non-affinity modified IgSF domains and/or affinity modified IgSF domains can independently specifically bind to either one or both of the mammalian cells forming the IS.

[0181] Often, the cell surface molecular species to which the affinity- modified IgSF domain of the immunomodulatory protein specifically binds will be the cognate binding partner of the wild type IgSF family member or wild type IgSF domain that has been affinity modified. In some embodiments, the cell surface molecular species is a mammalian IgSF member. In some embodiments, the cell surface molecular species is a human IgSF member. In some embodiments, the cell surface molecular species will be the cell surface cognate binding partners as indicated in Table 1. In some embodiments, the cell surface molecular species will be a viral protein, such as a poliovirus protein, on the cell surface of a mammalian cell such as a human cell.

[0182] In some embodiments, at least one non-affinity modified and/or affinity modified IgSF domain of the immunomodulatory protein provided herein binds to at least two or three cell surface molecular species present on mammalian cells forming the IS. The cell surface molecular species to which the non-affinity modified IgSF domains and/or the affinity modified IgSF domains of the immunomodulatory protein specifically bind to can exclusively be on one or the other of the two mammalian cells (i.e. in cis configuration) forming the IS or, alternatively, the cell surface molecular species can be present on both.

[0183] In some embodiments, the affinity modified IgSF domain specifically binds to at least two cell surface molecular species wherein one of the molecular species is present on one of the two mammalian cells forming the IS and the other molecular species is present on the second of the two mammalian cells forming the IS. In such embodiments, the cell surface molecular species is not necessarily present solely on one or the other of the two mammalian cells forming the IS (i.e., in a trans configuration) although in some embodiments it is. Thus, embodiments provided herein include those wherein each cell surface molecular species is exclusively on one or the other of the mammalian cells forming the IS (cis configuration) as well

as those where the cell surface molecular species to which each affinity modified IgSF binds is present on both of the mammalian cells forming the IS (i.e., cis and trans configuration).

[0184] Those of skill will recognize that antigen presenting cells (APCs) and tumor cells form an immunological synapse with lymphocytes. Thus, in some embodiments at least one non-affinity modified IgSF domain and/or at least one affinity modified IgSF domain of the immunomodulatory protein specifically binds to only cell surface molecular species present on a cancer cell, wherein the cancer cell in conjunction with a lymphocyte forms the IS. In other embodiments, at least one non-affinity modified IgSF domain and/or at least one affinity modified IgSF domain of the immunomodulatory protein specifically binds to only cell surface molecular species present on a lymphocyte, wherein the lymphocyte in conjunction with an APC or tumor cell forms the IS. In some embodiments, the non-affinity modified IgSF domain and/or affinity modified IgSF domain bind to cell surface molecular species present on both the target cell (or APC) and the lymphocyte forming the IS.

[0185] Embodiments of the invention include those in which an immunomodulatory protein provided herein comprises at least one affinity modified IgSF domain with an amino acid sequence that differs from a wild-type or unmodified IgSF domain (e.g. a mammalian IgSF domain) such that the binding affinity (or avidity if in a multimeric or other relevant structure) of the affinity-modified IgSF domain, under specific binding conditions, to at least one of its cognate binding partners is either increased or decreased relative to the unaltered wild-type or unmodified IgSF domain control. In some embodiments, an affinity modified IgSF domain has a binding affinity for a cognate binding partner that differs from that of a wild-type or unmodified IgSF control sequence as determined by, for example, solid-phase ELISA immunoassays, flow cytometry or Biacore assays. In some embodiments, the affinity modified IgSF domain has an increased binding affinity for one or more cognate binding partners, relative to a wild-type or unmodified IgSF domain. In some embodiments, the affinity modified IgSF domain has a decreased binding affinity for one or more cognate binding partners, relative to a wild-type or unmodified IgSF domain. In some embodiments, the cognate binding partner can be a mammalian protein, such as a human protein or a murine protein.

[0186] Binding affinities for each of the cognate binding partners are independent; that is, in some embodiments, an affinity modified IgSF domain has an increased binding affinity for one, two or three different cognate binding partners, and a decreased binding affinity for one, two or three of different cognate binding partners, relative to a wild-type or unmodified polypeptide.

[0187] In some embodiments, the immunomodulatory protein provided herein comprises at least one affinity modified domain in which the binding affinity or avidity of the affinity modified IgSF domain is increased at least 10%, 20%, 30%, 40%, 50%, 100%, 200%, 300%, 400%, 500%, 1000%, 5000%, or 10,000% relative to the wild type or unmodified control IgSF domain. In some embodiments, the increase in binding affinity relative to the wild-type or unmodified IgSF domain 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.

[0188] In some embodiments, the immunomodulatory protein provided herein comprises at least one affinity modified domain in which the binding affinity or avidity of the affinity modified IgSF domain is decreased at least 10%, and up to 20%, 30%, 40%, 50%, 60%, 70%, 80% or up to 90% relative to the wild-type or unmodified control IgSF domain. In some embodiments, the decrease in binding affinity relative to the wild-type or unmodified IgSF domain 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.

[0189] In some embodiments, the immunomodulatory protein provided herein comprises at least one affinity modified domain in which the selectivity of the affinity modified IgSF domain for a particular cognate binding partner is increased compared to the wild-type or unmodified control IgSF domain. In some embodiments, the selectivity is represented as a ratio for binding of the particular cognate binding partner compared to one or more other cognate binding partner. In some embodiments, the selectivity ratio for binding a particular cognate binding partner is greater than or greater than 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. In some embodiments, the selectivity of the affinity modified IgSF domain is increased at least 10%, 20%, 30%, 40%, 50%, 100%, 200%, 300%, 400%, 500%, 1000%, 5000%, or 10,000% relative to the wild type or unmodified control IgSF domain.

[0190] In some embodiments, the immunomodulatory protein provided herein comprises at least one affinity modified domain in which its specific binding affinity to a cognate binding partner can be less than or less than about $1x10^{-5}$ M, $1x10^{-6}$ M, $1x10^{-7}$ M, $1x10^{-8}$ M, $1x10^{-9}$ M, $1x10^{-10}$ M or $1x10^{-11}$ M, or $1x10^{-12}$ M.

[0191] In some embodiments, the immunomodulatory protein provided comprises at least two IgSF domains in which at least one of the IgSF domain is affinity modified while in some embodiments both are affinity modified, and wherein at least one of the affinity modified IgSF

domains has increased affinity (or avidity) to its cognate binding partner and at least one affinity modified IgSF domain has a decreased affinity (or avidity) to its cognate binding partner. Functionally, and irrespective of whether specific binding to its cognate binding partner is increased or decreased, the immunomodulatory protein comprising one or more affinity-modified IgSF domains acts to enhance or suppress immunological activity of engineered immune cells, such as lymphocytes or antigen presenting cells, relative to engineered immune cells expressing the wild-type, parental molecule under the appropriate assay controls. In some embodiments, an immunomodulatory protein comprising an at least two affinity modified IgSF domains is one in which at least one of the affinity-modified IgSF domains agonizes an activating receptor and at least one affinity modified IgSF domain acts to antagonize an inhibitory receptor. In some embodiments, an enhancement of immunological activity 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 such as in a cytotoxic activity assay, an assay for assessing cellular cytokines or a cell proliferation assay. In some embodiments, suppression of immunological activity can be a decrease of at least 10%, and up to 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90%.

[0192] The affinity modified IgSF domains of the immunomodulatory proteins of the invention can in some embodiments specifically bind competitively to its cognate binding partner. In other embodiments the affinity modified IgSF domains of the present invention specifically bind non-competitively to its cognate binding partner.

[0193] In some embodiments, the immunomodulatory protein provided herein contains an IgSF domain that otherwise binds to multiple cell surface molecular species but is affinity modified such that it substantially no longer specifically binds to one of its cognate cell surface molecular species. Thus, in these embodiments the specific binding to one of its cognate cell surface molecular species is reduced to specific binding of no more than 90% of the wild type level, such as no more than 80%, 70%, 60%, 50%, 40%, 30%, 20% or less. In some embodiments, the specific binding to one of its cognate cell surface molecular species is reduced to specific binding of no more than 10% of the wild type level and often no more than 7%, 5%, 3%, 1%, or no detectable or statistically significant specific binding.

[0194] In some embodiments, a specific binding site on a mammalian IgSF domain is inactivated or substantially inactivated with respect to at least one of the cell surface molecular species. Thus, for example, if a wild type IgSF domain specifically binds to exactly two cell

surface molecular species then in some embodiments it is affinity modified to specifically bind to exactly one cell surface molecular species. And, if a wild type IgSF domain specifically binds to exactly three cell surface molecular species then in some embodiments it is affinity modified to specifically bind to exactly two cell surface molecular species. The IgSF domain that is affinity modified to substantially no longer specifically bind to one of its cognate cell surface molecular species can be an IgSF domain that otherwise specifically binds competitively or non-competitively to its cell surface molecular species. An illustrative example concerns native CD80 (B7-1) which specifically binds cognate binding partners: CD28, PD-L1, and CTLA4. In some embodiments, CD80 can be IgSF affinity modified to increase or attenuate its specific binding to CD28 and/or PD-L1 but not to specifically bind to any physiologically significant extent to CTLA4. The IgSF domain that is affinity modified to substantially no longer specifically bind to one of its cell surface cognate binding partners can be an IgSF domain that otherwise specifically binds competitively or non-competitively to its cognate binding partner. Those of skill will appreciate that a wild-type IgSF domain that competitively binds to two cognate binding partners can nonetheless be inactivated with respect to exactly one of them if, for example, their binding sites are not precisely coextensive but merely overlap such that specific binding of one inhibits binding of the other cognate binding partner and yet both competitive binding sites are distinct.

[0195] The non-affinity modified IgSF domains and/or affinity modified IgSF domains of the immunomodulatory proteins provided herein can, in some embodiments, specifically bind competitively to its cognate cell surface molecular species. In other embodiments the non-affinity-modified IgSF domain(s) and/or affinity-modified IgSF domain(s) of the immunomodulatory protein provided herein specifically bind non-competitively to its cognate cell surface molecular species. Any number of the non-affinity modified IgSF domains and/or affinity modified IgSF domains present in the immunomodulatory protein provided herein can specifically bind competitively or non-competitively.

[0196] In some embodiments, the immunomodulatory protein provided herein comprises at least two non-affinity modified IgSF domains, or at least one non-affinity modified IgSF domain and at least one affinity modified IgSF domain, or at least two affinity modified IgSF domains wherein one IgSF domain specifically binds competitively and a second IgSF domain binds non-competitively to its cognate cell surface molecular species. More generally, the immunomodulatory protein provided herein can comprise 1, 2, 3, 4, 5, or 6 competitive or 1, 2,

3, 4, 5, or 6 non-competitive binding non-affinity modified IgSF and/or affinity modified IgSF domains or any combination thereof. Thus, the immunomodulatory protein provided herein can have the number of non-competitive and competitive binding IgSF domains, respectively, of: 0 and 1, 0 and 2, 0 and 3, 0 and 4, 1 and 0, 1 and 1, 1 and 2, 1 and 3, 2 and 0, 2 and 1, 2 and 2, 2 and 3, 3 and 0, 3 and 1, 3 and 2, 3 and 3, 4 and 0, 4 and 1, and, 4 and 2.

[0197] In some embodiments in which the immunomodulatory protein contains a plurality of IgSF domains, the plurality of non-affinity modified and/or affinity modified IgSF domains of the immunomodulatory protein provided herein 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.

[0198] 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 non-affinity modified or affinity-modified IgSF domain. Thus, linkages can be made via terminal or internal amino acid residues or combinations thereof.

[0199] The "peptide linkers" that link the non-affinity modified and/or affinity modified IgSF domains 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 (in one-letter amino acid code): GGGGS ("4GS"; SEQ ID NO: 1870) 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: 229 (2xGGGGS) or SEQ ID NO: 228 (3xGGGGS). In some embodiments, the linker (in one-letter amino acid code) is GSGGGGS (SEQ ID NO:1869).

III. EXEMPLARY AFFINITY-MODIFIED DOMAINS AND IMMUNOMODULATORY PROTEINS

[0200] In some embodiments, the immunomodulatory protein contains an affinity-modified IgSF domain that has one or more amino acid substitutions in an IgSF domain of a wild-type or unmodified IgSF protein, such as set forth in Table 1 above. In some embodiments, the one or more amino acid substitutions are in the IgV domain or specific binding fragment thereof. In some embodiments, the one or more amino acid substitutions are in the IgC domain or specific

binding fragment thereof. In some embodiments, one or more amino acid substitutions are in the IgV domain or a specific binding fragment thereof, and some of the one or more amino acid substitutions are in the IgC domain or a specific binding fragment thereof.

[0201] The wild-type or unmodified IgSF domain sequence does not necessarily have to be used as a starting composition to generate variant IgSF domain 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 IgSF protein. Variant IgSF 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 IgSF polypeptides are designed or created is not limited to any particular method. In some embodiments, however, a wild-type or unmodified IgSF polypeptide encoding nucleic acid is mutagenized from wild-type or unmodified 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 IgSF 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.

[0202] Unless stated otherwise, as indicated throughout the present disclosure, the amino acid substitution(s) are designated by amino acid position number corresponding to the numbering of positions of the unmodified ECD sequences set forth in Table 1.

[0203] It is within the level of a skilled artisan to identify the corresponding position of a modification, e.g. amino acid substitution, in an affinity-modified IgSF domain, including portion thereof containing an IgSF domain (e.g. IgV) thereof, such as by alignment of a reference sequence. 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.

[0204] In some embodiments, the affinity-modified IgSF domain 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 substitutions. The substitutions can be in the IgV domain or the IgC domain. In some embodiments, the affinity modified IgSF domain 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 substitutions in the IgV domain or specific binding fragment thereof. In some embodiments, the affinity modified IgSF domain 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 substitutions in the IgC domain or specific binding fragment thereof. In some embodiments, the affinity modified IgSF domain 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 IgSF domain or specific binding fragment thereof, such as an IgSF domain contained in the IgSF protein set forth in any of SEQ ID NOS: 1-27 and 408.

[0205] In some embodiments, the immunomodulatory protein contains at least one affinity-modified IgSF domain containing one or more amino acid substitutions in a wild-type or unmodified IgSF domain of a B7 IgSF family member. In some embodiments, the B7 IgSF family member is CD80, CD86 or ICOS Ligand (ICOSL). In some embodiments, the affinity modified IgSF domain of the immunomodulatory protein 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 IgSF domain or specific binding fragment thereof of CD80, CD86 or ICOS Ligand (ICOSL), such as the IgSF domain (e.g. IgV or IgC) contained in the IgSF protein set forth in any of SEQ ID NOS: 1, 2 or 5. Exemplary affinity modified IgSF domains of CD80 are set forth in Table 2 and Table 3. In some embodiments, the affinity modified IgSF domain of CD80 exhibits increased binding affinity or increased binding selectivity to CD28. In some embodiments, the affinity modified IgSF domain of CD80 exhibits increased binding affinity or increased binding selectivity to CTLA-4. Exemplary affinity modified IgSF domains of ICOSL are set forth in Table 4. In some embodiments, the affinity modified IgSF domain of ICOSL exhibits increased binding affinity or increased binding selectivity to CD28 or ICOS. Exemplary affinity modified IgSF domains of CD86 are set forth in Table 5.

TABLE 2: Exemplary variant CD80 polypeptides

Mutation(s)	ECD SEQ ID NO	IgV SEQ ID NO
Wild-type	28	152, 504, 578
L70Q/A91G	55	153
L70Q/A91G/T130A	56	
L70Q/A91G/I118A/T120S/T130A	57	
V4M/L70Q/A91G/T120S/T130A	58	154
L70Q/A91G/T120S/T130A	59	
V20L/L70Q/A91S/T120S/T130A	60	155
S44P/L70Q/A91G/T130A	61	156
L70Q/A91G/E117G/T120S/T130A	62	
A91G/T120S/T130A	63	157
L70R/A91G/T120S/T130A	64	158
L70Q/E81A/A91G/T120S/I127T/T130A	65	159
L70Q/Y87N/A91G/T130A	66	160
T28S/L70Q/A91G/E95K/T120S/T130A	67	161
N63S/L70Q/A91G/T120S/T130A	68	162
K36E/I67T/L70Q/A91G/T120S/T130A/N152T	69	163
E52G/L70Q/A91G/T120S/T130A	70	164
K37E/F59S/L70Q/A91G/T120S/T130A	71	165
A91G/S103P	72	
K89E/T130A	73	166
A91G	74	
D60V/A91G/T120S/T130A	75	167
K54M/A91G/T120S	76	168
M38T/L70Q/E77G/A91G/T120S/T130A/N152T	77	169
R29H/E52G/L70R/E88G/A91G/T130A	78	170
Y31H/T41G/L70Q/A91G/T120S/T130A	79	171
V68A/T110A	80	172
S66H/D90G/T110A/F116L	81	173
R29H/E52G/T120S/T130A	82	174
A91G/L102S	83	
I67T/L70Q/A91G/T120S	84	175
L70Q/A91G/T110A/T120S/T130A	85	
M38V/T41D/M43I/W50G/D76G/V83A/K89E/T120S/T130A	86	176
V22A/L70Q/S121P	87	177
A12V/S15F/Y31H/T41G/T130A/P137L/N152T	88	178
I67F/L70R/E88G/A91G/T120S/T130A	89	179
E24G/L25P/L70Q/T120S	90	180
A91G/F92L/F108L/T120S	91	181
R29D/Y31L/Q33H/K36G/M38I/T41A/M43R/M47T/E81V/L85R/K89N/A91T/F92P/K93V/R94L/I118T/N149S	92	182
R29D/Y31L/Q33H/K36G/M38I/T41A/M43R/M47T/E81V/L85R/K89N/A91T/F92P/K93V/R94L/N144S/N149S	93	
R29D/Y31L/Q33H/K36G/M38I/T41A/M42T/M43R/M47T/E81V/L85	94	183

TABLE 2: Exemplary variant CD80 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
R/K89N/A91T/F92P/K93V/R94L/L148S/N149S		
E24G/R29D/Y31L/Q33H/K36G/M38I/T41A/M43R/M47T/F59L/E81V/L85R/K89N/A91T/F92P/K93V/R94L/H96R/N149S/C182S	95	184
R29D/Y31L/Q33H/K36G/M38I/T41A/M43R/M47T/E81V/L85R/K89N/A91T/F92P/K93V/R94L/N149S	96	
R29V/M43Q/E81R/L85I/K89R/D90L/A91E/F92N/K93Q/R94G	97	185
T41I/A91G	98	186
K89R/D90K/A91G/F92Y/K93R/N122S/N177S	99	187
K89R/D90K/A91G/F92Y/K93R	100	
K36G/K37Q/M38I/F59L/E81V/L85R/K89N/A91T/F92P/K93V/R94L/E99G/T130A/N149S	101	188
E88D/K89R/D90K/A91G/F92Y/K93R	102	189
K36G/K37Q/M38I/L40M	103	190
K36G	104	191
R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	105	192
A12T/H18L/M43V/F59L/E77K/P109S/I118T	106	193
R29V/Y31F/K36G/M38L/M43Q/E81R/V83I/L85I/K89R/D90L/A91E/F92N/K93Q/R94G	107	194
V68M/L70P/L72P/K86E	108	195

TABLE 3: Exemplary variant CD80 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	28	152, 504, 578
L70P	431	505, 579
I30F/L70P	432	506, 580
Q27H/T41S/A71D	433	507, 581
I30T/L70R	434	508, 582
T13R/C16R/L70Q/A71D	435	509, 583
T57I	436	510, 584
M43I/C82R	437	511, 585
V22L/M38V/M47T/A71D/L85M	438	512, 586
I30V/T57I/L70P/A71D/A91T	439	513, 587
V22I/L70M/A71D	440	514, 588
N55D/L70P/E77G	441	515, 589
T57A/I69T	442	516, 590
N55D/K86M	443	517, 591
L72P/T79I	444	518, 592
L70P/F92S	445	519, 593
T79P	446	520, 594

TABLE 3: Exemplary variant CD80 polypeptides		
E35D/M47I/L65P/D90N	447	521, 595
L25S/E35D/M47I/D90N	448	522, 596
A71D	450	524, 598
E81K/A91S	452	526, 600
A12V/M47V/L70M	453	527, 601
K34E/T41A/L72V	454	528, 602
T41S/A71D/V84A	455	529, 603
E35D/A71D	456	530, 604
E35D/M47I	457	531, 605
K36R/G78A	458	532, 606
Q33E/T41A	459	533, 607
M47V/N48H	460	534, 608
M47L/V68A	461	535, 609
S44P/A71D	462	536, 610
Q27H/M43I/A71D/R73S	463	537, 611
E35D/T57I/L70Q/A71D	465	539, 613
M47I/E88D	466	540, 614
M42I/I61V/A71D	467	541, 615
P51A/A71D	468	542, 616
H18Y/M47I/T57I/A71G	469	543, 617
V20I/M47V/T57I/V84I	470	544, 618
V20I/M47V/A71D	471	545, 619
A71D/L72V/E95K	472	546, 620
V22L/E35G/A71D/L72P	473	547, 621
E35D/A71D	474	548, 622
E35D/I67L/A71D	475	549, 623
Q27H/E35G/A71D/L72P/T79I	476	550, 624
T13R/M42V/M47I/A71D	477	551, 625
E35D	478	552, 626
E35D/M47I/L70M	479	553, 627
E35D/A71D/L72V	480	554, 628
E35D/M43L/L70M	481	555, 629
A26P/E35D/M43I/L85Q/E88D	482	556, 630
E35D/D46V/L85Q	483	557, 631
Q27L/E35D/M47I/T57I/L70Q/E88D	484	558, 632
M47V/I69F/A71D/V83I	485	559, 633
E35D/T57A/A71D/L85Q	486	560, 634
H18Y/A26T/E35D/A71D/L85Q	487	561, 635
E35D/M47L	488	562, 636
E23D/M42V/M43I/I58V/L70R	489	563, 637
V68M/L70M/A71D/E95K	490	564, 638
N55I/T57I/I69F	491	565, 639
E35D/M43I/A71D	492	566, 640
T41S/T57I/L70R	493	567, 641
H18Y/A71D/L72P/E88V	494	568, 642
V20I/A71D	495	569, 643

TABLE 3: Exemplary variant CD80 polypeptides		
E23G/A26S/E35D/T62N/A71D/L72V/L85M	496	570, 644
A12T/E24D/E35D/D46V/I61V/L72P/E95V	497	571, 645
V22L/E35D/M43L/A71G/D76H	498	572, 646
E35G/K54E/A71D/L72P	499	573, 647
L70Q/A71D	500	574, 648
A26E/E35D/M47L/L85Q	501	575, 649
D46E/A71D	502	576, 650
Y31H/E35D/T41S/V68L/K93R/R94W	503	577, 651

TABLE 4: Exemplary variant ICOSL polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	32	196
N52S	109	197
N52H	110	198
N52D	111	199
N52Y/N57Y/F138L/L203P	112	200
N52H/N57Y/Q100P	113	201
N52S/Y146C/Y152C	114	
N52H/C198R	115	
N52H/C140D/T225A	116	
N52H/C198R/T225A	117	
N52H/K92R	118	202
N52H/S99G	119	203
N52Y	120	204
N57Y	121	205
N57Y/Q100P	122	206
N52S/S130G/Y152C	123	
N52S/Y152C	124	
N52S/C198R	125	
N52Y/N57Y/Y152C	126	
N52Y/N57Y/129P/C198R	127	
N52H/L161P/C198R	128	
N52S/T113E	129	
S54A	130	207
N52D/S54P	131	208
N52K/L208P	132	209
N52S/Y152H	133	
N52D/V151A	134	
N52H/I143T	135	
N52S/L80P	136	210
F120S/Y152H/N201S	137	
N52S/R75Q/L203P	138	211
N52S/D158G	139	

N52D/Q133H	140	
N52S/N57Y/H94D/L96F/L98F/Q100R	141	212
N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S	142	213
N52S/G103E	239	240
N52H/C140delta/T225A	1563	
N52S/S54P	1564	1565

TABLE 5: Exemplary variant CD86 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	29	220
Q35H/H90L/Q102H	148	221
Q35H	149	222
H90L	150	223
Q102H	151	224

[0206] In some embodiments, the affinity-modified IgSF domain binds, in some cases with higher binding affinity or selectivity, to an inhibitory receptor. In some embodiments, the affinity-modified IgSF domain contains one or more amino acid modifications (e.g. substitutions, deletions or additions) in a wild-type or unmodified IgSF domain (e.g. IgV) of an IgSF family member that binds to an inhibitory receptor. Exemplary of such inhibitory receptors are PD-1, CTLA-4, LAG3, TIGIT, TIM-3, or BTLA.

[0207] In some embodiments, the immunomodulatory protein contains at least one affinity modified IgSF domain containing one or more amino acid substitutions in a wild-type or unmodified IgSF domain of a poliovirus receptor IgSF family member. In some embodiments, the poliovirus IgSF family member is CD155 (PVR) or CD122 (PRR-2). In some embodiments, the affinity modified IgSF domain of the immunomodulatory protein 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 IgSF domain or specific binding fragment thereof of CD155 or CD112, such as an IgSF domain (e.g. IgV or IgC) contained in the IgSF protein set forth in any of SEQ ID NO:20 or 21. Exemplary affinity modified IgSF domains of CD155 are set forth in Table 6. Exemplary affinity modified IgSF domains of CD112 are set forth in Table 7. In some embodiments, the affinity modified IgSF domain of CD155 or CD122 exhibits increased binding affinity or increased binding selectivity to TIGIT.

TABLE 6: Exemplary variant CD155 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	47	241, 652
P18S, P64S, F91S	242	264, 653
P18S, F91S, L104P	243	265, 654
L44P	244	266, 655
A56V	245	267, 656
P18L, L79V, F91S	246	268, 657
P18S, F91S	247	269, 658
P18T, F91S	248	270, 659
P18T, S42P, F91S	249	271, 660
G7E, P18T, Y30C, F91S	250	272, 661
P18T, F91S, G111D	251	273, 662
P18S, F91P	252	274, 663
P18T, F91S, F108L	253	275, 664
P18T, T45A, F91S	255	277, 665
P18T, F91S, R94H	256	278, 666
P18S, Y30C, F91S	257	279, 667
A81V, L83P	258	280, 668
L88P	259	281, 669
R94H	260	282, 670
A13E, P18S, A56V, F91S	261	283, 671
P18T, F91S, V115A	262	284, 672
P18T, Q60K	263	285, 673
S52M	674	771, 868
T45Q, S52L, L104E, G111R	675	772, 869
S42G	676	773, 870
Q62F	677	774, 871
S52Q	678	775, 872
S42A, L104Q, G111R	679	776, 873
S42A, S52Q, L104Q, G111R	680	777, 874
S52W, L104E	681	778, 875
S42C	682	779, 876
S52W	683	780, 877
S52M, L104Q	684	781, 878
S42L, S52L, Q62F, L104Q	685	782, 879
S42W	686	783, 880
S42Q	687	784, 881
S52L	688	785, 882
S52R	689	786, 883
L104E	690	787, 884
G111R	691	788, 885
S52E	692	789, 886

Q62Y	693	790, 887
T45Q, S52M, L104E	694	791, 888
S42N, L104Q, G111R	695	792, 889
S52M, V57L	696	793, 890
S42N, S52Q, Q62F	697	794, 891
S42A, S52L, L104E, G111R	698	795, 892
S42W, S52Q, V57L, Q62Y	699	796, 893
L104Q	700	797, 894
S42L, S52Q, L104E	701	798, 895
S42C, S52L	702	799, 896
S42W, S52R, Q62Y, L104Q	703	800, 897
T45Q, S52R, L104E	704	801, 898
S52R, Q62F, L104Q, G111R	705	802, 899
T45Q, S52L, V57L, L104E	706	803, 900
S52M, Q62Y	707	804, 901
Q62F, L104E, G111R	708	805, 902
T45Q, S52Q	709	806, 903
S52L, L104E	710	807, 904
S42V, S52E	711	808, 905
T45Q, S52R, G111R	712	809, 906
S42G, S52Q, L104E, G111R	713	810, 907
S42N, S52E, V57L, L104E	714	811, 908
S42C, S52M, Q62F	715	812, 909
S42L	716	813, 910
S42A	717	814, 911
S42G, S52L, Q62F, L104Q	718	815, 912
S42N	719	816, 913
P18T, S65A, S67V, F91S	720	817, 914
P18F, T39A, T45Q, T61R, S65N, S67L, E73G, R78G	721	818, 915
P18T, T45Q, T61R, S65N, S67L	722	819, 916
P18F, S65A, S67V, F91S	723	820, 917
P18F, T45Q, T61R, S65N, S67L, F91S, L104P	724	821, 918
P18S, L79P, L104M	725	822, 919
P18S, L104M	726	823, 920
L79P, L104M	727	824, 921
P18T, T45Q, L79P	728	825, 922
P18T, T45Q, T61R, S65H, S67H	729	826, 923
P18T, A81E	730	827, 924
P18S, D23Y, E37P, S52G, Q62M, G80S, A81P, G99Y, S112N	731	828, 925
A13R, D23Y, E37P, S42P, Q62Y, A81E	732	829, 926
A13R, D23Y, E37P, G99Y, S112N	733	830, 927
A13R, D23Y, E37P, Q62M, A77V, G80S, A81P, G99Y	734	831, 928
P18L, E37S, Q62M, G80S, A81P, G99Y, S112N	735	832, 929
P18S, L104T	736	833, 930
P18S, Q62H, L79Q, F91S	737	834, 931
T45Q, S52K, Q62F, L104Q, G111R	738	835, 932

T45Q, S52Q, Q62Y, L104Q, G111R	739	836, 933
T45Q, S52Q, Q62Y, L104E, G111R	740	837, 934
V57A, T61M, S65W, S67A, E96D, L104T	741	838, 935
P18L, V57T, T61S, S65Y, S67A, L104T	742	839, 936
P18T, T45Q	743	840, 937
P18L, V57A, T61M, S65W, S67A, L104T	744	841, 938
T61M, S65W, S67A, L104T	745	842, 939
P18S, V41A, S42G, T45G, L104N	746	843, 940
P18H, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104N	747	844, 941
P18S, S42G, T45V, F58L, S67W, L104N	748	845, 942
P18S, T45I, L104N	749	846, 943
P18S, S42G, T45G, L104N, V106A	750	847, 944
P18H, H40R, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104Y, V106L, F108H	751	848, 945
E37V, S42G, T45G, L104N	752	849, 946
P18S, T45Q, L79P, L104T	753	850, 947
P18L, Q62R	754	851, 948
A13R, D23Y, E37P, S42L, S52G, Q62Y, A81E	755	852, 949
P18L, H49R, L104T, D116N	756	853, 950
A13R, D23Y, E37P, Q62M, G80S, A81P, L104T	757	854, 951
S65T, L104T	758	855, 952
A13R, D23Y, E37P, S52G, V57A, Q62M, K70E, L104T	759	856, 953
P18L, A47V, Q62Y, E73D, L104T	760	857, 954
H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, D97G, E98S, L104T, D116N	761	858, 955
P18L, S42P, T45Q, T61G, S65H, S67E, L104T, D116N	762	859, 956
P18S, H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, L104M, V106A	763	860, 957
H40T, V41M, A47V, S52Q, Q62L, S65T, E68G, E73R, D97G, E98S, L104T	764	861, 958
T45Q, S52E, L104E	765	862, 959
T45Q, S52E, Q62F, L104E	766	863, 960
P18F, T26M, L44V, Q62K, L79P, F91S, L104M, G111D	767	864, 961
P18S, T45S, T61K, S65W, S67A, F91S, G111R	768	865, 962
P18S, L79P, L104M, T107M	769	866, 963
P18S, S65W, S67A, M90V, V95A, L104Q, G111R	770	867, 964
P18S, A47G, L79P, F91S, L104M, T107A, R113W	1701	1655, 1678
P18T, D23G, S24A, N35D, H49L, L79P, F91S, L104M, G111R	1702	1656, 1679
V9L, P18S, Q60R, V75L, L79P, R89K, F91S, L104E, G111R	1703	1657, 1680
P18S, H49R, E73D, L79P, N85D, F91S, V95A, L104M, G111R	1704	1658, 1681
V11A, P18S, L79P, F91S, L104M, G111R	1705	1659, 1682
V11A, P18S, S54R, Q60P, Q62K, L79P, N85D, F91S, T107M	1706	1660, 1683
P18T, S52P, S65A, S67V, L79P, F91S, L104M, G111R	1707	1661, 1684
P18T, M36T, L79P, F91S, G111R	1708	1662, 1685
D8G, P18S, M36I, V38A, H49Q, A76E, F91S, L104M, T107A, R113W	1709	1663, 1686

P18S, S52P, S65A, S67V, L79P, F91S, L104M, T107S, R113W	1710	1664, 1687
T15I, P18T, L79P, F91S, L104M, G111R	1711	1665, 1688
P18F, T26M, L44V, Q62K, L79P, E82D, F91S, L104M, G111D	1712	1666, 1689
P18T, E37G, G53R, Q62K, L79P, F91S, E98D, L104M, T107M	1713	1667, 1690
P18L, K70E, L79P, F91S, V95A, G111R	1714	1668, 1691
V9I, Q12K, P18F, S65A, S67V, L79P, L104T, G111R, S112I	1715	1669, 1692
P18F, S65A, S67V, F91S, L104M, G111R	1716	1670, 1693
V9I, V10I, P18S, F20S, T45A, L79P, F91S, L104M, F108Y, G111R, S112V	1717	1671, 1694
V9L, P18L, L79P, M90I, F91S, T102S, L104M, G111R	1718	1672, 1695
P18C, T26M, L44V, M55I, Q62K, L79P, F91S, L104M, T107M	1719	1673, 1696
V9I, P18T, D23G, L79P, F91S, G111R	1720	1674, 1697
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1721	1675, 1698
P18T, M36T, S65A, S67E, L79Q, A81T, F91S, G111R	1722	1676, 1699
V9L, P18T, Q62R, L79P, F91S, L104M, G111R	1723	1677, 1700
P18S, S65W, S67A, L104Q, G111R	1724	1725,1726
P18T, G19D, M36T, S54N, L79P, L83Q, F91S, T107M, F108Y	1727	1773, 1819
V9L, P18L, M55V, S69L, L79P, A81E, F91S, T107M	1728	1774, 1820
P18F, H40Q, T61K, Q62K, L79P, F91S, L104M, T107V	1729	1775, 1821
P18S, Q32R, Q62K, R78G, L79P, F91S, T107A, R113W	1730	1776, 1822
Q12H, P18T, L21S, G22S, V57A, Q62R, L79P, F91S, T107M	1731	1777, 1823
V9I, P18S, S24P, H49Q, F58Y, Q60R, Q62K, L79P, F91S, T107M	1732	1778, 1824
P18T, W46C, H49R, S65A, S67V, A76T, L79P, S87T, L104M	1733	1779, 1825
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1734	1780, 1826
V10F, T15S, P18L, R48Q, L79P, F91S, T107M, V115M	1735	1781, 1827
P18S, L21M, Y30F, N35D, R84W, F91S, T107M, D116G	1736	1782, 1828
P18F, E51V, S54G, Q60R, L79Q, E82G, S87T, M90I, F91S, G92R, T107M	1737	1783, 1829
Q16H, P18F, F91S, T107M	1738	1784, 1830
P18T, D23G, Q60R, S67L, L79P, F91S, T107M, V115A	1739	1785, 1831
D8G, V9I, V11A, P18T, T26M, S52P, L79P, F91S, G92A, T107L, V115A	1740	1786, 1832
V9I, P18F, A47E, G50S, E68G, L79P, F91S, T107M	1741	1787, 1833
P18S, M55I, Q62K, S69P, L79P, F91S, T107M	1742	1788, 1834
P18T, T39S, S52P, S54R, L79P, F91S, T107M	1743	1789, 1835
P18S, D23N, L79P, F91S, T107M, S114N	1744	1790, 1836
P18S, P34S, E51V, L79P, F91S, G111R	1745	1791, 1837
P18S, H59N, V75A, L79P, A81T, F91S, L104M, T107M	1746	1792, 1838
P18S, W46R, E68D, L79P, F91S, T107M, R113G	1747	1793, 1839
V9L, P18F, T45A, S65A, S67V, R78K, L79V, F91S, T107M, S114T	1748	1794, 1840
P18T, M55L, T61R, L79P, F91S, V106I, T107M	1749	1795, 1841
T15I, P18S, V33M, N35F, T39S, M55L, R78S, L79P, F91S, T107M	1750	1796, 1842
P18S, Q62K, K70E, L79P, F91S, G92E, R113W	1751	1797, 1843
P18F, F20I, T26M, A47V, E51K, L79P, F91S	1752	1798, 1844
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1753	1799, 1845

P18S, D23G, C29R, N35D, E37G, M55I, Q62K, S65A, S67G, R78G, L79P, F91S, L104M, T107M, Q110R	1754	1800, 1846
A13E, P18S, M36R, Q62K, S67T, L79P, N85D, F91S, T107M	1755	1801, 1847
V9I, P18T, H49R, L79P, N85D, F91S, L104T, T107M	1756	1802, 1848
V9A, P18F, T61S, Q62L, L79P, F91S, G111R	1757	1803, 1849
D8E, P18T, T61A, L79P, F91S, T107M	1758	1804, 1850
P18S, V41A, H49R, S54C, L79S, N85Y, L88P, F91S, L104M, T107M	1759	1805, 1851
V11E, P18H, F20Y, V25E, N35S, H49R, L79P, F91S, T107M, G111R	1760	1806, 1852
V11A, P18F, D23A, L79P, G80D, V95A, T107M	1761	1807, 1853
P18S, K70R, L79P, F91S, G111R	1762	1808, 1854
V9L, V11M, P18S, N35S, S54G, Q62K, L79P, L104M, T107M, V115M	1763	1809, 1855
V9L, P18Y, V25A, V38G, M55V, A77T, L79P, M90I, F91S, L104M	1764	1810, 1856
V10G, P18T, L72Q, L79P, F91S, T107M	1765	1811, 1857
P18S, H59R, A76G, R78S, L79P	1766	1812, 1858
V9A, P18S, M36T, S65G, L79P, F91S, L104T, G111R, S112I	1767	1813, 1859
P18T, S52A, V57A, Q60R, Q62K, S65C, L79P, F91T, N100Y, T107M	1768	1814, 1860
V11A, P18F, N35D, A47E, Q62K, L79P, F91S, G99D, T107M, S114N	1769	1815, 1861
V11A, P18T, N35S, L79P, S87T, F91S	1770	1816, 1862
V9D, V11M, Q12L, P18S, E37V, M55I, Q60R, K70Q, L79P, F91S, L104M, T107M	1771	1817, 1863
T15S, P18S, Y30H, Q32L, Q62R, L79P, F91S, T107M	1772	1818, 1864

TABLE 7: Exemplary variant CD112 polypeptides

Mutation(s)	ECD SEQ ID NO	IgV SEQ ID NO
Wild-type	48	286, 965
Y33H, A112V, G117D	287	334, 966
V19A, Y33H, S64G, S80G, G98S, N106Y, A112V	288	335, 967
L32P, A112V	289	336, 968
A95V, A112I	290	337, 969
P28S, A112V	291	338, 970
P27A, T38N, V101A, A112V	292	339, 971
S118F	293	340, 972
R12W, H48Y, F54S, S118F	294	341, 973
R12W, Q79R, S118F	295	342, 974
T113S, S118Y	296	343, 975
S118Y	297	344, 976
N106I, S118Y	298	345, 977
N106I, S118F	299	346, 978
A95T, L96P, S118Y	300	347, 979
Y33H, P67S, N106Y, A112V	301	348, 980
N106Y, A112V	302	349, 981

TABLE 7: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
T18S, Y33H, A112V	303	350, 982
P9S, Y33H, N47S, A112V	304	351, 983
P42S, P67H, A112V	305	352, 984
P27L, L32P, P42S, A112V	306	353, 985
G98D, A112V	307	354, 986
Y33H, S35P, N106Y, A112V	308	355, 987
L32P, P42S, T100A, A112V	309	356, 988
P27S, P45S, N106I, A112V	310	357, 989
Y33H, N47K, A112V	311	358, 990
Y33H, N106Y, A112V	312	359, 991
K78R, D84G, A112V, F114S	313	360, 992
Y33H, N47K, F54L, A112V	314	361, 993
Y33H, A112V	315	362, 994
A95V, A112V	316	363, 995
R12W, A112V	317	364, 996
R12W, P27S, A112V	318	365, 997
Y33H, V51M, A112V	319	366, 998
Y33H, A112V, S118T	320	367, 999
Y33H, V101A, A112V, P115S	321	368, 1000
H24R, T38N, D43G, A112V	322	369, 1001
A112V	323	370, 1002
P27A, A112V	324	371, 1003
A112V, S118T	325	372, 1004
R12W, A112V, M122I	326	373, 1005
Q83K, N106Y, A112V	327	374, 1006
R12W, P27S, A112V, S118T	328	375, 1007
P28S, Y33H, A112V	329	376, 1008
P27S, Q90R, A112V	330	377, 1009
L15V, P27A, A112V, S118T	331	378, 1010
Y33H, N106Y, T108I, A112V	332	379, 1011
Y33H, P56L, V75M, V101M, A112V	333	380, 1012
N47K, Q79R, S118F	1013	1054, 1095
Q40R, P60T, A112V, S118T	1014	1055, 1096
F114Y, S118F	1015	1056, 1097
Y33H, K78R, S118Y	1016	1057, 1098
R12W, A46T, K66M, Q79R, N106I, T113A, S118F	1017	1058, 1099
Y33H, A112V, S118F	1018	1059, 1100
R12W, Y33H, N106I, S118F	1019	1060, 1101
L15V, Q90R, S118F	1020	1061, 1102
N47K, D84G, N106I, S118Y	1021	1062, 1103
L32P, S118F	1022	1063, 1104

TABLE 7: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Y33H, Q79R, A112V, S118Y	1023	1064, 1105
T18A, N106I, S118T	1024	1065, 1106
L15V, Y33H, N106Y, A112V, S118F	1025	1066, 1107
V37M, S118F	1026	1067, 1108
N47K, A112V, S118Y	1027	1068, 1109
A46T, A112V	1028	1069, 1110
P28S, Y33H, N106I, S118Y	1029	1070, 1111
P30S, Y33H, N47K, V75M, Q79R, N106I, S118Y	1030	1071, 1112
V19A, N47K, N106Y, K116E, S118Y	1031	1072, 1113
Q79R, T85A, A112V, S118Y	1032	1073, 1114
V101M, N106I, S118Y	1033	1074, 1115
Y33H, Q79R, N106I, A112V, S118T	1034	1075, 1116
Q79R, A112V	1035	1076, 1117
Y33H, A46T, Q79R, N106I, S118F	1036	1077, 1118
A112V, G121S	1037	1078, 1119
Y33H, Q79R, N106I, S118Y	1038	1079, 1120
Y33H, N106I, A112V	1039	1080, 1121
Y33H, A46T, V101M, A112V, S118T	1040	1081, 1122
L32P, L99M, N106I, S118F	1041	1082, 1123
L32P, T108A, S118F	1042	1083, 1124
R12W, Q79R, A112V	1043	1084, 1125
Y33H, N106Y, E110G, A112V	1044	1085, 1126
Y33H, N106I, S118Y	1045	1086, 1127
Q79R, S118F	1046	1087, 1128
Y33H, Q79R, G98D, V101M, A112V	1047	1088, 1129
N47K, T81S, V101M, A112V, S118F	1048	1089, 1130
G82S, S118Y	1049	1090, 1131
Y33H, A112V, S118Y	1050	1091, 1132
Y33H, N47K, Q79R, N106Y, A112V	1051	1092, 1133
Y33H, S118T	1052	1093, 1134
R12W, Y33H, Q79R, V101M, A112V	1053	1094, 1135
Y33H, Q83K, A112V, S118T	1583	1607, 1631
V29M, Y33H, N106I, S118F	1584	1608, 1632
Y33H, A46T, A112V	1585	1609, 1633
Y33H, Q79R, S118F	1586	1610, 1634
Y33H, N47K, F74L, S118F	1587	1611, 1635
R12W, V101M, N106I, S118Y	1588	1612, 1636
A46T, V101A, N106I, S118Y	1589	1613, 1637
N106Y, A112V, S118T	1590	1614, 1638
S76P, T81I, V101M, N106Y, A112V, S118F	1591	1615, 1639
P9R, L21V, P22L, I34M, S69F, F74L, A87V, A112V, L125A	1592	1616, 1640

TABLE 7: Exemplary variant CD112 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Y33H, V101M, A112V	1593	1617, 1641
V29A, L32P, S118F	1594	1618, 1642
Y33H, V101M, N106I, A112V	1595	1619, 1643
R12W, Y33H, N47K, Q79R, S118Y	1596	1620, 1644
Y33H, A46T, A112V, S118T	1597	1621, 1645
Y33H, A112V, F114L, S118T	1598	1622, 1646
Y33H, T38A, A46T, V101M, A112V	1599	1623, 1647
P28S, Y33H, S69P, N106I, A112V, S118Y	1600	1624, 1648
Y33H, P42L, N47K, V101M, A112V	1601	1625, 1649
Y33H, N47K, F74S, Q83K, N106I, F111L, A112V, S118T	1602	1626, 1650
Y33H, A112V, S118T, V119A	1603	1627, 1651
Y33H, N106I, A112V, S118F	1604	1628, 1652
Y33H, K66M, S118F, W124L	1605	1629, 1653
N106I, A112V	1606	1630, 1654

[0209] In some embodiments, the immunomodulatory protein contains at least one affinity modified IgSF domain containing one or more amino acid substitutions in a wild-type or unmodified IgSF domain of PD-L1 or PD-L2. In some embodiments, the affinity modified IgSF domain of the immunomodulatory protein 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 IgSF domain or specific binding fragment thereof of PD-L1 or PD-L2, such as an IgSF domain (e.g. IgV or IgC) contained in the IgSF protein set forth in SEQ ID NO:3 or 4. Exemplary affinity modified IgSF domains of PD-L1 are set forth in Table 8. Exemplary affinity modified IgSF domains of PD-L2 are set forth in Table 9. In some embodiments, the affinity modified IgSF domain of PD-L1 or PD-L2 exhibits increased binding affinity or increased binding selectivity to PD-1.

TABLE 8: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	30, 1874	1136, 1332
K28N/M41V/N45T/H51N/K57E	1137, 2087	1202, 1267
I20L/I36T/N45D/I47T	1138, 2088	1203, 1268
I20L/M41K/K44E	1139, 2089	1204, 1269
P6S/N45T/N78I/I83T	1140, 2090	1205, 1270

TABLE 8: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
N78I	1141, 2091	1206, 1271
M41K/N78I	1142, 2092	1207, 1272
N45T/N78I	1143, 2093	1208, 1273
I20L/N45T	1144, 2094	1209, 1274
N45T	1145, 2095	1210, 1275
M41K	1146, 2096	1211, 1276
I20L/I36T/N45D	1147, 2097	1212, 1277
N17D/N45T/V50A/D72G	1148, 2098	1213, 1278
I20L/F49S	1149, 2099	1214, 1279
N45T/V50A	1150, 2100	1215, 1280
I20L/N45T/N78I	1151, 2101	1216, 1281
I20L/N45T/V50A	1152, 2102	1217, 1282
M41V/N45T	1153, 2103	1218, 1283
M41K/N45T	1154, 2104	1219, 1284
A33D/S75P/D85E	1155, 2105	1220, 1285
M18I/M41K/D43G/H51R/N78I	1156, 2106	1221, 1286
V11E/I20L/I36T/N45D/H60R/S75P	1157, 2107	1222, 1287
A33D/V50A	1158, 2108	1223, 1288
S16G/A33D/K71E/S75P	1159, 2109	1224, 1289
E27G/N45T/M97I	1160, 2110	1225, 1290
E27G/N45T/K57R	1161, 2111	1226, 1291
A33D/E53V	1162, 2112	1227, 1292
D43G/N45D/V58A	1163, 2113	1228, 1293
E40G/D43V/N45T/V50A	1164, 2114	1229, 1294
Y14S/K28E/N45T	1165, 2115	1230, 1295
A33D/N78S	1166, 2116	1231, 1296
A33D/N78I	1167, 2117	1232, 1297
A33D/N45T	1168, 2118	1233, 1298
A33D/N45T/N78I	1169, 2119	1234, 1299
E27G/N45T/V50A	1170, 2120	1235, 1300
N45T/V50A/N78S	1171, 2121	1236, 1301
I20L/N45T/V110M	1172, 2122	1237, 1302
I20L/I36T/N45T/V50A	1173, 2123	1238, 1303
N45T/L74P/S75P	1174, 2124	1239, 1304
N45T/S75P	1175, 2125	1240, 1305
S75P/K106R	1176, 2126	1241, 1306
S75P	1177, 2127	1242, 1307
A33D/S75P	1178, 2128	1243, 1308
A33D/S75P/D104G	1179, 2129	1244, 1309
A33D/S75P	1180, 2130	1245, 1310
I20L/E27G/N45T/V50A	1181, 2131	1246, 1311
I20L/E27G/D43G/N45D/V58A/N78I	1182, 2132	1247, 1312

TABLE 8: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
I20L/D43G/N45D/V58A/N78I	1183, 2133	1248, 1313
I20L/A33D/D43G/N45D/V58A/N78I	1184, 2134	1249, 1314
I20L/D43G/N45D/N78I	1185, 2135	1250, 1315
E27G/N45T/V50A/N78I	1186, 2136	1251, 1316
N45T/V50A/N78I	1187, 2137	1252, 1317
V11A/I20L/E27G/D43G/N45D/H51Y/S99G	1188, 2138	1253, 1318
I20L/E27G/D43G/N45T/V50A	1189, 2139	1254, 1319
I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG)	1190, 2140	1255, 1320
I20L/I36T/N45D	1191, 2141	1256, 1321
I20L/K28E/D43G/N45D/E53G/V58A/N78I	1192, 2142	1257, 1322
A33D/D43G/N45D/V58A/S75P	1193, 2143	1258, 1323
K23R/D43G/N45D	1194, 2144	1259, 1324
I20L/D43G/N45D/V58A/N78I/D90G/G101D	1195, 2145	1260, 1325
D43G/N45D/L56Q/V58A/G101G-ins(G101GG)	1196, 2146	1261, 1326
I20L/K23E/D43G/N45D/V58A/N78I	1197, 2147	1262, 1327
I20L/K23E/D43G/N45D/V50A/N78I	1198, 2148	1263, 1328
T19I/E27G/N45I/V50A/N78I/M97K	1199, 2149	1264, 1329
I20L/M41K/D43G/N45D	1200, 2150	1265, 1330
K23R/N45T/N78I	1201, 2151	1266, 1331
I20L/K28E/D43G/N45D/V58A/Q89R/G101G-ins (G101GG)	1871, 2152	1754, 1755
K57R/S99G	1875, 1965	2054, 2069
K57R/S99G/F189L	1876, 1966	
M18V/M97L/F193S/R195G/E200K/H202Q	1877, 1967	
I36S/M41K/M97L/K144Q/R195G/E200K/H202Q/L206F	1878, 1968	
C22R/Q65L/L124S/K144Q/R195G/E200N/H202Q/T221L	1879	
M18V/I98L/L124S/P198T/L206F	1880, 1969	
S99G/N117S/I148V/K171R/R180S	1881, 1970	
I36T/M97L/A103V/Q155H	1882, 1971	
K28I/S99G	1883, 1972	2055, 2070
R195S	1884, 1973	
A79T/S99G/T185A/R195G/E200K/H202Q/L206F	1885, 1974	
K57R/S99G/L124S/K144Q	1886, 1975	
K57R/S99G/R195G	1887, 1976	
D55V/M97L/S99G	1888, 1977	2056, 2071
E27G/I36T/D55N/M97L/K111E	1889, 1978	2057, 2072
E54G/M97L/S99G	1890, 1979	2058, 2073
G15A/I36T/M97L/K111E/H202Q	1891, 1980	
G15A/I36T/V129D	1892, 1981	
G15A/I36T/V129D/R195G	1893, 1982	
G15A/V129D	1894, 1983	
I36S/M97L	1895, 1984	2059, 2074
I36T/D55N/M97L/K111E/A204T	1896, 1985	

TABLE 8: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
I36T/D55N/M97L/K111E/V129A/F173L	1897, 1986	
I36T/D55S/M97L/K111E/I148V/R180S	1898, 1987	
I36T/G52R/M97L/V112A/K144E/V175A/P198T	1899, 1988	
I36T/I46V/D55G/M97L/K106E/K144E/T185A/R195G	1900, 1989	
I36T/I83T/M97L/K144E/P198T	1901, 1990	
I36T/M97L/K111E	1902, 1991	2060, 2075
I36T/M97L/K144E/P198T	1903, 1992	
I36T/M97L/Q155H/F193S/N201Y	1904, 1993	
I36T/M97L/V129D	1905, 1994	
L35P/I36S/M97L/K111E	1906, 1995	2061, 2076
M18I/I36T/E53G/M97L/K144E/E199G/V207A	1907, 1996	
M18T/I36T/D55N/M97L/K111E	1908, 1997	2062, 2077
M18V/M97L/T176N/R195G	1909, 1998	
M97L/S99G	1910, 1999	2063, 2078
N17D/M97L/S99G	1911, 2000	2064, 2079
S99G/T185A/R195G/P198T	1912, 2001	
V129D/H202Q	1913, 2002	
V129D/P198T	1914, 2003	
V129D/T150A	1915, 2004	
V93E/V129D	1916, 2005	
Y10F/M18V/S99G/Q138R/T203A	1917, 2006	
N45D	1918, 2007	2065, 2080
K160M/R195G	1919, 2008	
N45D/K144E	1920, 2009	
N45D/P198S	1921, 2010	
N45D/P198T	1922, 2011	
N45D/R195G	1923, 2012	
N45D/R195S	1924, 2013	
N45D/S131F	1925, 2014	
N45D/V58D	1926, 2015	2066, 2081
V129D/R195S	1927, 2016	
I98T/F173Y/L196S	1928, 2017	
N45D/E134G/L213P	1929, 2018	
N45D/F173I/S177C	1930, 2019	
N45D/I148V/R195G	1931, 2020	
N45D/K111T/R195G	1932, 2021	
N45D/N113Y/R195S	1933, 2022	
N45D/N165Y/E170G	1934, 2023	
N45D/Q89R/I98V	1935, 2024	2067, 2082
N45D/S131F/P198S	1936, 2025	
N45D/S75P/P198S	1937, 2026	
N45D/V50A/R195T	1938, 2027	

TABLE 8: Exemplary variant PD-L1 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
E27D/N45D/T183A/I188V	1939, 2028	
F173Y/T183I/L196S/T203A	1940, 2029	
K23N/N45D/S75P/N120S	1941, 2030	
N45D/G102D/R194W/R195G	1942, 2031	
N45D/G52V/Q121L/P198S	1943, 2032	
N45D/I148V/R195G/N201D	1944, 2033	
N45D/K111T/T183A/I188V	1945, 2034	
N45D/Q89R/F189S/P198S	1946, 2035	
N45D/S99G/C137R/V207A	1947, 2036	
N45D/T163I/K167R/R195G	1948, 2037	
N45D/T183A/T192S/R194G	1949, 2038	
N45D/V50A/I119T/K144E	1950, 2039	
T19A/N45D/K144E/R195G	1951, 2040	
V11E/N45D/T130A/P198T	1952, 2041	
V26A/N45D/T163I/T185A	1953, 2042	
K23N/N45D/L124S/K167T/R195G	1954, 2043	
K23N/N45D/Q73R/T163I	1955, 2044	
K28E/N45D/W149R/S158G/P198T	1956, 2045	
K28R/N45D/K57E/I98V/R195S	1957, 2046	
K28R/N45D/V129D/T163N/R195T	1958, 2047	
M41K/D43G/N45D/R64S/R195G	1959, 2048	
M41K/D43G/N45D/R64S/S99G	1960, 2049	2068, 2083
N45D/R68L/F173L/D197G/P198S	1961, 2050	
N45D/V50A/I148V/R195G/N201D	1962, 2051	
M41K/D43G/K44E/N45D/R195G/N201D	1963, 2052	
N45D/V50A/L124S/K144E/L179P/R195G	1964, 2053	

TABLE 9: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
Wild-type	31	1333, 1393
H15Q	1334	1411, 1487
N24D	1335	1412, 1488
E44D	1336	1413, 1489
V89D	1337	1414, 1490
Q82R/V89D	1338	1415, 1491
E59G/Q82R	1339	1416, 1492
S39I/V89D	1340	1417, 1493
S67L/V89D	1341	1418, 1494
S67L/I85F	1342	1419, 1495
S67L/I86T	1343	1420, 1496

TABLE 9: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
H15Q/K65R	1344	1421, 1497
H15Q/Q72H/V89D	1345	1422, 1498
H15Q/S67L/R76G	1346	1423, 1499
H15Q/R76G/I85F	1347	1424, 1500
H15Q/T47A/Q82R	1348	1425, 1501
H15Q/Q82R/V89D	1349	1426, 1502
H15Q/C23S/I86T	1350	1427, 1503
H15Q/S39I/I86T	1351	1428, 1504
H15Q/R76G/I85F	1352	1429, 1505
E44D/V89D/W91R	1353	1430, 1506
I13V/S67L/V89D	1354	1431, 1507
H15Q/S67L/I86T	1355	1432, 1508
I13V/H15Q/S67L/I86T	1356	1433, 1509
I13V/H15Q/E44D/V89D	1357	1434, 1510
I13V/S39I/E44D/Q82R/V89D	1358	1435, 1511
I13V/E44D/Q82R/V89D	1359	1436, 1512
I13V/Q72H/R76G/I86T	1360	1437, 1513
I13V/H15Q/R76G/I85F	1361	1438, 1514
H15Q/S39I/R76G/V89D	1362	1439, 1515
H15Q/S67L/R76G/I85F	1363	1440, 1516
H15Q/T47A/Q72H/R76G/I86T	1364	1441, 1517
H15Q/T47A/Q72H/R76G	1365	1442, 1518
I13V/H15Q/T47A/Q72H/R76G	1366	1443, 1519
H15Q/E44D/R76G/I85F	1367	1444, 1520
H15Q/S39I/S67L/V89D	1368	1445, 1521
H15Q/N32D/S67L/V89D	1369	1446, 1522
N32D/S67L/V89D	1370	1447, 1523
H15Q/S67L/Q72H/R76G/V89D	1371	1448, 1524
H15Q/Q72H/Q74R/R76G/I86T	1372	1449, 1525
G28V/Q72H/R76G/I86T	1373	1450, 1526
I13V/H15Q/S39I/E44D/S67L	1374	1451, 1527
E44D/S67L/Q72H/Q82R/V89D	1375	1452, 1528
H15Q/V89D	1376	1453, 1529
H15Q/T47A	1377	1454, 1530
I13V/H15Q/Q82R	1378	1455, 1531
I13V/H15Q/V89D	1379	1456, 1532
I13V/S67L/Q82R/V89D	1380	1457, 1533
I13V/H15Q/Q82R/V89D	1381	1458, 1534
H15Q/V31M/S67L/Q82R/V89D	1382	1459, 1535
I13V/H15Q/T47A/Q82R	1383	1460, 1536
I13V/H15Q/V31A/N45S/Q82R/V89D	1384	1461, 1537
I13V/T20A/T47A/K65X/Q82R/V89D	1385	1462, 1538

TABLE 9: Exemplary variant PD-L2 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgV SEQ ID NO**
H15Q/T47A/H69L/Q82R/V89D	1386	1463, 1539
I13V/H15Q/T47A/H69L/R76G/V89D	1387	1464, 1540
I12V/I13V/H15Q/T47A/Q82R/V89D	1388	1465, 1541
I13V/H15Q/R76G/D77N/Q82R/V89D	1389	1466, 1542
I13V/H15Q/T47A/R76G/V89D	1390	1467, 1543
I13V/H15Q/T47A/Q82R/V89D	1391	1468, 1544
I13V/H15Q/N24D/Q82R/V89D	1392	1469, 1545
I13V/H15Q/I36V/T47A/S67L/V89D	1394	1470, 1546
H15Q/T47A/K65R/S67L/Q82R/V89D	1395	1471, 1547
H15Q/L33P/T47A/S67L/P71S/V89D	1396	1472, 1548
I13V/H15Q/Q72H/R76G/I86T	1397	1473, 1549
H15Q/T47A/S67L/Q82R/V89D	1398	1474, 1550
F2L/H15Q/D46E/T47A/Q72H/R76G/Q82R/V89D	1399	1475, 1551
I13V/H15Q/L33F/T47A/Q82R/V89D	1400	1476, 1552
I13V/H15Q/T47A/E58G/S67L/Q82R/V89D	1401	1477, 1553
H15Q/N24S/T47A/Q72H/R76G/V89D	1402	1478, 1554
I13V/H15Q/E44V/T47A/Q82R/V89D	1403	1479, 1555
H15Q/N18D/T47A/Q72H/V73A/R76G/I86T/V89D	1404	1480, 1556
I13V/H15Q/T37A/E44D/S48C/S67L/Q82R/V89D	1405	1481, 1557
H15Q/L33H/S67L/R76G/Q82R/V89D	1406	1482, 1558
I13V/H15Q/T47A/Q72H/R76G/I86T	1407	1483, 1559
H15Q/S39I/E44D/Q72H/V75G/R76G/Q82R/V89D	1408	1484, 1560
H15Q/T47A/S67L/R76G/Q82R/V89D	1409	1485, 1561
I13V/H15Q/T47A/S67L/Q72H/R76G/Q82R/V89D	1410	1486, 1562

[0210] In some embodiments, the immunomodulatory protein contains an affinity modified IgSF domain containing one or more amino acid substitutions in a wild-type or unmodified IgSF domain of an NKp30 family member. In some embodiments, the affinity modified IgSF domain 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 IgSF domain or specific binding fragment thereof of an NKp30 family member, such as the IgSF domain (e.g. IgC) contained in the IgSF protein set forth in SEQ ID NO: 27. Table 10 provides exemplary affinity modified NKp30 IgSF domains.

TABLE 10: Exemplary variant NKp30 polypeptides		
Mutation(s)	**ECD SEQ ID NO**	**IgC-like domain SEQ ID NO**
Wild-type	54	214
L30V/A60V/S64P/S86G	143	215
L30V	144	216
A60V	145	217
S64P	146	218
S86G	147	219

IV. SECRETABLE IMMUNOMODULATORY PROTEINS AND ENGINEERED CELLS

[0211] Provided herein are immunomodulatory proteins, such as any described above, which can be expressed and secreted by engineered cells. Secretable immunomodulatory proteins (SIPs), and engineered cells expressing and secreting such secretable immunomodulatory proteins, can have therapeutic utility by modulating immunological activity in a mammal with a disease or disorder in which modulation of the immune system response is beneficial.

[0212] In some embodiments, the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain. In some embodiments, the affinity-modified IgSF domain can include an affinity-modified IgSF domain of an Ig super family member, such as any described herein. In some embodiments, the affinity-modified IgSF domain is in an IgSF family member of the B7 family of proteins. In some embodiments, the affinity-modified IgSF domain is in an IgSF family member that binds an inhibitory receptor. In some embodiments, the affinity-modified IgSF domain comprises any one or more amino acid substitution in an IgSF domain, such as any one or more amino acid substitution(s) set forth in any of Tables 2-10.

[0213] In some embodiments, the immunomodulatory protein does not comprise a transmembrane domain. In some embodiments, the immunomodulatory protein is not conjugated to a half-life extending moiety (such as an Fc domain or a multimerization domain). In some embodiments, the 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).

A. Signal Peptide

[0214] In some embodiments, the immunomodulatory proteins provided herein further comprises a signal peptide. In some embodiments, provided herein is a nucleic acid molecule encoding the immunomodulatory protein operably connected to a secretion sequence encoding the signal peptide.

[0215] 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).

[0216] In some embodiments, the signal peptide is a native signal peptide from the corresponding wild-type IgSF family member. For example, in some embodiments, the immunomodulatory protein comprises at least one non-immunoglobulin affinity modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain from a wild-type IgSF family member, and a signal peptide from the wild-type IgSF family member. Exemplary signal peptides from IgSF family members are identified in Table 1.

[0217] 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 IgSF family member, 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 11.

TABLE 11. Exemplary Signal Peptides

SEQ ID NO	Signal Peptide	Peptide Sequence
SEQ ID NO: 413	HSA signal peptide	MKWVTFISLLFLFSSAYS
SEQ ID NO: 414	Ig kappa light chain	MDMRAPAGIFGFLLVLFPGYRS
SEQ ID NO: 415	human azurocidin preprotein signal sequence	MTRLTVLALLAGLLASSRA
SEQ ID NO: 416	IgG heavy chain signal peptide	MELGLSWIFLLAILKGVQC
SEQ ID NO: 417	IgG heavy chain signal peptide	MELGLRWVFLVAILEGVQC
SEQ ID NO: 418	IgG heavy chain signal peptide	MKHLWFFLLLVAAPRWVLS
SEQ ID NO: 419	IgG heavy chain signal peptide	MDWTWRILFLVAAATGAHS
SEQ ID NO: 420	IgG heavy chain signal peptide	MDWTWRFLFVVAAATGVQS
SEQ ID NO: 421	IgG heavy chain signal peptide	MEFGLSWLFLVAILKGVQC
SEQ ID NO: 422	IgG heavy chain signal peptide	MEFGLSWVFLVALFRGVQC
SEQ ID NO: 423	IgG heavy chain signal peptide	MDLLHKNMKHLWFFLLLVAA PRWVLS
SEQ ID NO: 424	IgG Kappa light chain signal sequences:	MDMRVPAQLLGLLLLWLSGA RC
SEQ ID NO: 425	IgG Kappa light chain signal sequences:	MKYLLPTAAAGLLLLAAQPAM A
SEQ ID NO: 426	Gaussia luciferase	MGVKVLFALICIAVAEA
SEQ ID NO: 427	Human albumin	MKWVTFISLLFLFSSAYS
SEQ ID NO: 428	Human chymotrypsinogen	MAFLWLLSCWALLGTTFG
SEQ ID NO: 429	Human interleukin-2	MQLLSCIALILALV
SEQ ID NO: 430	Human trypsinogen-2	MNLLLILTFVAAAVA

[0218] In some embodiments, 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.

B. Nucleic Acid Molecules and Expression Vectors

[0219] Provided herein are isolated or recombinant nucleic acids collectively referred to as "nucleic acids" which encode any of the various provided embodiments of the immunomodulatory polypeptides of the invention. In one aspect, there is provided a nucleic acid encoding an immunomodulatory protein comprising at least one non-immunoglobulin affinity-

modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain. 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 the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein.

[0220] Nucleic acids provided herein, including all described below, are useful in recombinant expression of the immunomodulatory proteins, including for engineering 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 of the invention 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.

[0221] Also provided herein are expression vectors useful in engineering cells to express the immunomodulatory proteins of the present invention. In one aspect, there is provided a recombinant expression vector comprising a nucleic acid encoding an immunomodulatory protein under the operable control of a signal sequence for secretion, wherein the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain. 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.

[0222] 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 a 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).

[0223] In some embodiments, a DNA insert can be generated encoding one or more affinity-modified IgSF domains and, in some embodiments, a signal peptide. 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.

[0224] 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 affecting 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. 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.

[0225] In some embodiments, expression of the immunomodulatory protein is controlled by a promoter to enhance to control or regulate expression. The promoter is operably linked to the portion of the nucleic acid molecule encoding the 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).

[0226] In some embodiments, a constitutive promoter is operatively linked to the nucleic acid molecule encoding the 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.

[0227] In some embodiments, an inducible promoter is operatively linked to the nucleic acid molecule encoding the 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).

[0228] 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.

[0229] 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 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.

[0230] 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.

[0231] 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.

C. Exemplary Immunomodulatory Proteins and Encoding Nucleic Acid Molecules

[0232] Provided herein is a immunomodulatory protein, e.g. secretable immunomodulatory protein, in accord with the above description that 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 any of SEQ ID NOS: 28-54 and 410 or to a specific binding fragment thereof containing an IgSF domain (e.g. IgV domain or IgC domain), and that contains at least one affinity-modified IgSF domain as described containing one or more amino acid modifications, e.g. amino acid substitutions, in an IgSF domain. In some embodiments, the immunomodulatory protein e.g. secretable immunomodulatory protein, comprises a sequence of amino acids that comprises the IgV domain or a specific fragment thereof contained within the sequence of amino acids set forth in any of SEQ ID NOS: 28-54 and 410 (see e.g. Table 1) but in which is contained therein one or more amino acid modifications, e.g. amino acid substitutions, such that the IgV domain exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to the corresponding IgV domain contained in any of SEQ ID NOS: 28-54 and 410. In some embodiments, the immunomodulatory protein contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more amino acid modifications, e.g. amino acid substitutions. In some embodiments, the immunomodulatory protein further comprises a signal peptide as described. In some embodiments, the signal peptide is the native signal peptide of the corresponding wild-type IgSF member (see e.g. Table 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

[0233] Also provided herein is a nucleic acid molecule encoding an immunomodulatory protein comprising 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 any of SEQ ID NOS: 28-54 and 410 or to a specific binding fragment thereof containing an IgSF domain (e.g. IgV domain or IgC domain) and that contains at least one affinity-modified IgSF domain as described containing one or more amino acid modifications, e.g. amino acid substitutions. In some embodiments, the immunomodulatory protein e.g. secretable immunomodulatory protein, comprises a nucleotide sequence that

encodes a sequence of amino acids that comprises the IgV domain or a specific fragment thereof contained within the sequence of amino acids set forth in any of SEQ ID NOS: 28-54 and 410 (see e.g. Table 1) but in which is contained therein one or more amino acid modifications, e.g. amino acid substitutions, such that the IgV domain exhibits at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to the corresponding IgV domain contained in any of SEQ ID NOS: 28-54 and 410. In some embodiments, the nucleic acid molecule further comprises 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 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

[0234] In some embodiments, the immunomodulatory protein has the sequence of amino acids set forth in any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10, 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 any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10 and that contains the recited amino acid modifications (e.g. amino acid substitutions). In some embodiments, the immunomodulatory protein further comprises a signal peptide as described. In some embodiments, the signal peptide is the native signal peptide of the corresponding wild-type IgSF member (see e.g. Table 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

[0235] In some embodiments, the nucleic acid molecule encodes an immunomodulatory protein that has the sequence of amino acids set forth in any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10, 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 any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10 and that contains the recited amino acid modifications (e.g. amino acid substitutions). In some embodiments, the nucleic acid molecule further comprises 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 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

V. TRANSMEMBRANE IMMUNOMODULATORY PROTEIN

[0236] Provided herein are immunomodulatory proteins that are transmembrane proteins ("transmembrane immunomodulatory proteins"). Transmembrane immunomodulatory proteins, and engineered cells expressing such transmembrane immunomodulatory proteins, generally have therapeutic utility by modulating immunological activity in a mammal with a disease or disorder in which modulation of the immune system response is beneficial. A transmembrane immunomodulatory protein of the present invention comprises an ectodomain, a transmembrane, and in some embodiments, an endodomain, such as a cytoplasmic signaling domain.

A. Ectodomain

[0237] In some embodiments, the provided transmembrane immunomodulatory proteins include an ectodomain comprising at least one affinity modified IgSF domain compared to an IgSF domain of a wild-type mammalian IgSF member. In some embodiments, the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain. In some embodiments, the affinity-modified IgSF domain can include an affinity-modified IgSF domain of an Ig super family member, such as any described herein In some embodiments, the affinity-modified IgSF domain is in an IgSF family member of the B7 family of proteins. In some embodiments, the affinity-modified IgSF domain is in an IgSF family member that binds an inhibitory receptor. In some embodiments, the affinity-modified IgSF domain comprises any one or more amino acid substitution in an IgSF domain described herein, such as any one or more amino acid substitution(s) set forth in any of Tables 2-10.

B. Transmembrane Domain

[0238] 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.

[0239] 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. CD80 or ICOSL 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. CD80 or ICOSL). 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 any of SEQ ID NOs:1-27 and 408 (see Table 1).

[0240] In some embodiments, the transmembrane domain is a non-native transmembrane domain that is not the transmembrane domain of the wild-type IgSF member. In some embodiments, the transmembrane domain is derived from a transmembrane domain from another non-IgSF 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: 1574 or a portion thereof containing the CD8 transmembrane domain. In some embodiments, the transmembrane domain is a synthetic transmembrane domain.

C. Endodomain

[0241] 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 any of SEQ ID NOS:1-27 and 408 (see Table 1).

[0242] 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: 1575 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:1575 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 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.

[0243] In some embodiments, a CAR-related transmembrane immunomodulatory protein comprises an antigen binding region that is engineered to specifically bind to a desired counter-structure. In some embodiments, an affinity modified IgSF domain specifically binds its native counter-structure. In some embodiments the counter-structure is an IgSF family member. In some embodiments, provided is a CAR-related transmembrane immunomodulatory protein that specifically binds to a tumor specific IgSF counter-structure. In some embodiments, the antigen binding region (ectodomain) is an affinity modified IgSF domain NKp30. In some embodiments, the affinity modified IgSF domain specifically binds the tumor specific antigen NKp30 ligand B7-H6 (see, Levin et al., The Journal of Immunology, 2009, 182, 134.20). In examples of such embodiments, the endodomain comprises at least one ITAM (immunoreceptor tyrosine-based activation motif) containing signaling domain, such as a CD3-zeta signaling domain. In some embodiments, the endodomain can further comprises at least one of: a CD28 costimulatory domain, an OX40 signaling domain, and a 41BB signaling domain.

[0244] 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 any of SEQ ID NOS:1-27 and 408 (see Table 1). 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.

D. Nucleic Acid Molecules and Vectors

[0245] Provided herein are isolated or recombinant nucleic acids collectively referred to as "nucleic acids" which encode any of the various provided embodiments of the transmembrane immunomodulatory polypeptides of the invention. Nucleic acids provided herein, including all described below, are useful in recombinant expression of the transmembrane immunomodulatory proteins, including for engineering 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 of the invention 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.

[0246] In some embodiments, expression of the transmembrane immunomodulatory protein is controlled by a promoter to enhancer to control or regulate expression, such as described herein for the alternative secretable immunomodulatory proteins. The promoter is operably linked to the portion of the nucleic acid molecule encoding the 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). Any promoter or element for enhancing, controlling or regulating expression, either constitutively or inducibly, can be employed, include any described herein. In particular aspects, the promoter is a promoter that is responsive to an element responsive to T-cell activation signaling, for example, by signaling through an engineered T cell receptor (TCR) or a chimeric antigen receptor (CAR). Exemplary of such promoters are those containing a

binding site for NFAT or NF-κB as described. For example, in some embodiments, the promoter is an NFAT or NF-κB promoter or a functional variant thereof.

[0247] Also provided herein are expression vectors useful in engineering cells to express the transmembrane immunomodulatory proteins of the present invention. The immunomodulatory polypeptides provided herein can be introduced into cells using recombinant DNA techniques. To do so, a recombinant DNA molecule encoding a transmembrane 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).

[0248] In some embodiments, a full length DNA insert can be generated comprising an optional endodomain (i.e., cytoplasmic domain), a transmembrane anchor domain, an optional spacer domain, an optional epitope tag, and finally one or more extracellular affinity modified IgSF domains. This DNA insert can be cloned into an appropriate T cell transduction/transfection vector as is known to those of skill in the art. Also provided are vectors containing the nucleic acid molecules.

[0249] In some embodiments, the expression vectors are capable of expressing the transmembrane immunomodulatory proteins in an appropriate cell under conditions suited to expression of the protein. In some aspects, an expression vector comprises the DNA molecule that codes for the transmembrane immunomodulatory protein operatively linked to appropriate expression control sequences. Methods of affecting 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. 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 transmembrane immunomodulatory protein.

[0250] 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.

E. Exemplary Transmembrane Immunomodulatory Proteins and Encoding Nucleic Acid Molecules

[0251] Provided herein is a transmembrane immunomodulatory protein in accord with the above description that 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 any of SEQ ID NOS: 381-407 and 409 or to a portion thereof that contains an ectodomain comprising at least one affinity-modified IgSF domain as described and a transmembrane domain. In some embodiments, the transmembrane immunomodulatory protein has an ecotodomain containing the sequence of amino acids set forth in any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10, 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 any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10 and that contains the recited amino acid modifications (e.g. amino acid substitutions). In some embodiments, the encoded immunomodulatory protein contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more amino acid modifications, e.g. amino acid substitutions. In some embodiments, the transmembrane immunomodulatory protein can further comprise a cytoplasmic domain as described, such as a cytoplasmic domain of any of SEQ ID NOS: 381-407 and 409 as set forth in Table 1. 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 the corresponding wild-type IgSF member (see e.g. Table 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

[0252] Also provided herein is a nucleic acid molecule encoding a transmembrane immunomodulatory protein comprising 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 any of SEQ ID NOS: 381-407 and 409 or to a portion thereof that 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 encodes an immunomodulatory protein that has the sequence of amino acids set forth in any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10, 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 any of the SEQ ID NOS of an ECD or an IgV set forth in any of Tables 2-10 and that contains the recited amino acid modifications (e.g. amino acid substitutions). In some embodiments, the encoded immunomodulatory protein contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more amino acid modifications, e.g. amino acid substitutions. 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 1). In some embodiments, the signal peptide is a non-native signal peptide, such as any as described, e.g. Table 11.

VI. ENGINEERED CELLS

[0253] Provided herein are engineered cells that comprise an immunomodulatory protein or a nucleic acid (such as an expression vector) that encodes an immunomodulatory protein as described herein.

[0254] In some embodiments, the engineered cells contain a secretable immunomodulatory protein or a nucleic acid molecule encoding a secretable immunomodulatory protein, such as any as described. In some embodiments, the engineered cell expresses and secretes the immunomodulatory protein. 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.

[0255] In one aspect, there is provided an engineered immune cell comprising a nucleic acid molecule that encodes an immunomodulatory protein, wherein the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid modifications (e.g., substitutions) in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and the engineered cell is configured to express and secrete the immunomodulatory protein. In some embodiments, the immunomodulatory protein does not comprise a transmembrane domain. In some embodiments, the immunomodulatory protein is not conjugated to half-life extending moiety

(such as a multimerization domain or an Fc domain). In some embodiments, the nucleic acid molecule comprises a sequence encoding a secretory signal peptide operably linked to the sequence encoding the immunomodulatory protein.

[0256] In some embodiments, the engineered cells contain a transmembrane immunomodulatory protein or a nucleic acid molecule encoding a transmembrane immunomodulatory protein, such as any as described. In some embodiments, the engineered cells express the immunomodulatory protein on its surface.

[0257] In some embodiments, the engineered cell is an immune cell, such as a lymphocyte (for example, a tumor infiltrating lymphocyte (TIL), T-cell or NK cell) or on a myeloid cell. In some embodiments, the engineered cell is an antigen presenting cell (APC). In some embodiments, the engineered cells are engineered mammalian T cells or engineered mammalian antigen presenting cells (APCs). In some embodiments, the engineered immune cells or APCs are human or murine cells.

[0258] 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+. In addition to the signal of the MHC, engineered T-cells also require a co-stimulatory signal which in some embodiments is provided by the immunomodulatory proteins as discussed herein.

[0259] 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 aspects, 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 one or more cognate binding partners or other molecule recognized by the affinity modified IgSF domain of the immunomodulatory proteins provided herein.

[0260] In some embodiments a cellular aAPC can be engineered to contain a SIP or TIP and TCR agonist which is used in adoptive cellular therapy. In some embodiments, a cellular aAPC

can be engineered to contain a SIP or 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 SIP or TIP can include any variant or affinity-modified IgSF domain that exhibits binding affinity for a cognate binding partner on a T cell.

[0261] In some embodiments, a 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. 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. Thus, in some embodiments, the immunomodulatory protein is expressed and secreted in an engineered T-cell receptor cell or and engineered chimeric antigen receptor cell. In such embodiments, the engineered cell co-expresses the immunomodulatory protein 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.

[0262] 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 examples, 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.

[0263] 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:1576 or SEQ ID NO:1577.

[0264] 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.

[0265] In some embodiments, the CAR further includes a costimulatory signaling domain. 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: 1574, 1578, 2158 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:1574, 1578, 2158. 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: 1575 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:1575 and retains the activity of T cell signaling. In some embodiments, the endodomain of a CAR can further comprise a costimulatory signaling domain

or region to further modulate immunomodulatory responses of the T-cell. In some embodiments, the costimulatory signaling domain is CD28, ICOSL, 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:1579-1582 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:1579-1582 and retains the activity of T cell costimulatory signaling.

[0266] 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: 2165, 2169, 2177 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: 2165, 2169, 2177. In some embodiments, the T2A is encoded by the sequence of nucleotides set forth in SEQ ID NO:2176 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: 2176. An exemplary sequence of a P2A self-cleaving peptide is set in SEQ ID NO: 2178 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: 2178.

[0267] 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: 2164, 2170, 2179, 2180, 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: 2164 or 2170.

[0268] In some embodiments, the CAR has the sequence of amino acids set forth in any of SEQ ID NOS: 2166, 2171, 2172, 2173, 2159, 2160, 2162, or 2163 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: 2166, 2171, 2172, 2173, 2159, 2160, 2162 or 2163. In some embodiments, the CAR is encoded by a sequence of nucleotides set forth in SEQ ID NO: 2175 or 2161 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: 2175 or 2161.

[0269] 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.

[0270] In some embodiments, nucleic acids encoding the immunomodulatory protein, such as transmembrane immunomodulatory polypeptides or secretable immunomodulatory polypeptides, are 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 causes the expressed immunomodulatory proteins to be secreted from the cell. In some embodiments, a nucleic acid encoding an immunomodulatory protein 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 and secreted.

[0271] 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, the DNA vector encoding the immunomodulatory protein of the present invention 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 protein expression and secretion by, for example, using anti-epitope tag or antibodies that cross-react with native parental molecule and affinity modified variant.

[0272] Upon immunomodulatory protein expression and secretion, the engineered T cell can be assayed for improved 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 and secretion of the immunomodulatory construct. Once validated, standard in vitro cytotoxicity, proliferation, or cytokine assays can be used to assess the function of the engineered 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 cells, 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 protein construct expressed and secreted by 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 and secreted by the engineered T cells.

[0273] 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 expressing and secreting an immunomodulatory protein. 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 cell 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 cognate binding partner on the xenograft and is co-expressed with the immunomodulatory protein containing an affinity-modified IgSF domain (which is also secreted) 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 that express and secrete an 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.

A. Exemplary Functional Activities and Features

[0274] In some aspects, engineered cells, such as engineered lymphocytes (e.g. tumor infiltrating lymphocytes, T cells or NK cells) or myeloid cells (e.g. antigen presenting cells), exhibit one or more desirable features or activities.

[0275] In some embodiments, when expressed on or from cells, the affinity-modified IgSF domain of the immunomodulatory protein specifically binds to at least one cognate binding partner expressed on a mammalian cell. In some embodiments, the mammalian cell is an autologous or allogeneic mouse, rat, cynomolgus monkey, or human cell. In some aspects, the mammalian cell can include such embodiments as an antigen presenting cell (APC), a tumor cell, or a T-cell. In some embodiments, the tumor cell is a mouse, rat, cynomolgus monkey, or human tumor cell.

[0276] An immunomodulatory protein can comprise one or multiple (e.g., 2, 3, or 4) affinity modified IgSF domains. Thus, in some embodiments the immunomodulatory protein binds to no more than one cognate binding partner on the mammalian cell. In some embodiments, an affinity-modified IgSF domain of an immunomodulatory protein specifically binds to no more than one cognate binding partner on the mammalian cell. Alternatively, in some embodiments, an immunomodulatory protein specifically binds to at least two, three or four, or exactly two, three, or four, cognate binding partners expressed on a mammalian cell. In some embodiments, the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partners. Specific binding of the immunomodulatory protein containing one or more affinity-modified IgSF domains to the cognate binding partner on a mammalian cell modulates immunological activity of the mammalian cell. Specific binding by and between an affinity-modified IgSF domain and a mammalian cell cognate binding partner can be specific binding in cis arrangement (i.e., specific binding on the same cell) or in trans arrangement (i.e., specific binding on different cells) or in both cis and trans arrangement. Immunological activity of the cell can be increased as evidenced by increased, e.g., cell survival, cell proliferation, cytokine

production, or T-cell cytotoxicity. In alternative embodiments, the immunological activity of the cell is attenuated as evidenced by a decrease of cell survival, cell proliferation, cytokine production, or T-cell cytotoxicity.

[0277] In some embodiments, at least one affinity-modified IgSF domain present in an immunomodulatory protein specifically binds to at least one cell surface cognate binding partner expressed on a mammalian cell and in which modulation of immunological activity is desired. In some embodiments, the cognate binding partner to which the affinity modified IgSF domain specifically binds is the native cognate binding partner of the wild-type IgSF family member or wild-type IgSF domain that has been affinity modified. In some embodiments, the specific binding increases and/or attenuates activity a mammalian cell expressing a cognate binding partner to which the affinity modified IgSF domain exhibits improved binding . Thus, by increasing specific binding affinity, the provided immunomodulatory proteins can either increase or attenuate immunological activity of a mammalian cell. In some embodiments, the specific binding modulates, such as increases, immunological activity of the engineered cell with the immunomodulatory protein.

[0278] In some embodiments, the cognate binding partner expressed on the mammalian cell is a mammalian IgSF member. The mammalian cell is, in some embodiments, an antigen presenting cell (APC), a lymphocyte, or a tumor cell. In some embodiments, the lymphocyte is a tumor infiltrating lymphocyte (TIL), an engineered or native T-cell, or an engineered or native NK cell. In some embodiments, the cognate binding partner of the affinity modified IgSF domain is a native human IgSF member. In some embodiments, the cognate binding partner is a "cell surface cognate binding partner" as indicated in Table 1.

[0279] In some embodiments, an immunomodulatory protein comprising an affinity-modified IgSF when expressed and secreted by an immune cell (e.g. a lymphocyte such as a T-cell) can specifically bind at least one cognate binding partner expressed on a second immune cells, e.g. a lymphocyte such as a T-cell. The cognate binding partner on the second immune cells, e.g. second T-cell, can be an inhibitory cognate binding partner or a stimulatory cognate binding partner. Exemplary cognate binding partners include cell surface receptors or ligands. Examples of inhibitory receptors/ligands include PD-1/PD-L1, PD-L2, CTLA-4/B7-1/B7-2, BTLA/HVEM, LAG3/MHC class II, TIGIT/PVR, TIM-3/CEACAM-1/GAL9 and VSIG8/VISTA. Examples of stimulatory receptors/ligands include CD28/B7-1/B7-2, ICOS/ICOSL, and CD226/PVR.

[0280] In a particular embodiment, the immunomodulatory protein is expressed and secreted by a T cell and comprises an affinity modified IgSF domain that specifically binds to a cognate binding partner expressed on a T-cell. In some embodiments the first and second T-cells are separate T-cells and in this embodiment the immunomodulatory protein and cognate binding partner are in trans to each other. In some embodiments, the immunomodulatory protein and cognate binding partner are expressed on the same T-cell (wherein the immunomodulatory protein is secreted) and are cis to each other. In some embodiments, at least one of the T-cells is a native T-cell or an engineered T-cell. In some embodiments, the engineered T-cell is a chimeric antigen receptor (CAR) T-cell or a T-cell receptor (TCR) engineered T-cell.

[0281] In some embodiments, a immunomodulatory protein comprises an affinity modified IgSF domain with increased affinity to a cell surface receptor to stimulate an increase in receptor signal transduction. Stimulating an increase in receptor signaling can in some embodiments increase immunological activity of that cell if, for example, the receptor is a stimulatory receptor that works to mediate those effects. In some cases, the inflammatory activity of the cell in which receptor signaling is stimulated is increased. In some embodiments, the immunomodulatory protein increases the activity of a stimulatory receptor. In such examples, an IgSF domain of an immunomodulatory protein can be affinity modified to increase the specific binding affinity to the native cognate binding partner on a mammalian cell, which, in some cases, is a stimulatory receptor. In some embodiments, the stimulatory receptor is expressed on T cells. In certain embodiments, the affinity modified IgSF domain of the immunomodulatory protein, such as is expressed and secreted by an engineered cell (e.g. a first T cell), specifically binds to a stimulatory cognate binding partner expressed on a T cell (e.g. a second T cell) with increased affinity (relative to the non-affinity modified IgSF domain as a control). In certain embodiments, the affinity modified IgSF domain of the immunomodulatory protein specifically binds to a stimulatory cognate binding partner expressed on a T cell (e.g. second T cell) and increases immunomodulatory activity of the T-cell. In some embodiments, the affinity modified IgSF domain of an immunomodulatory protein binds to a stimulatory cognate binding partner on the T cell (e.g. second T-cell) with increased affinity and increases immunomodulatory activity of the T-cell.

[0282] In some embodiments, the stimulatory receptor is CD28, ICOS or CD226 and the immunomodulatory protein containing an affinity-modified IgSF domain that exhibits increased binding affinity to one of CD28, ICOS or CD226 compared to a protein containing a wild-type

IgSF domain. In some embodiments, the affinity modified IgSF domain is an affinity modified domain of CD80 (B7-1). In some embodiments, an affinity modified CD80 (B7-1) IgSF domain of an immunomodulatory protein of the present invention is expressed on a first T-cell and is affinity modified to bind with increased affinity to the stimulatory cognate binding partner CD28 on the second T-cell. In some embodiments, the affinity modified IgSF domain is an affinity modified domain of ICOSL. In specific embodiments, the affinity modified IgSF domain is an affinity modified ICOSL (inducible costimulator ligand) domain and the stimulatory cognate binding partner is at least one of: ICOS (inducible costimulator) or CD28. In some embodiments, the ICOSL domain is affinity-modified to specifically bind to both ICOS and CD28. In some embodiments, ICOSL is affinity modified to specifically bind to either ICOS or to CD28 but not both. In some embodiments, binding affinity to one of ICOS or CD28 is increased while binding affinity to the other is attenuated. In some embodiments, the affinity modified IgSF domain is an affinity modified CD155 and the activating cognate ligand is CD226. In some embodiment, the affinity modified IgSF domain is an affinity modified CD112 and the activating cognate ligand is CD226.

[0283] In some methods of the present invention, the immunomodulatory protein attenuates the activity of an inhibitory receptor. In some cases, the increased binding affinity of the immunomodulatory protein to a cognate cell surface molecule results in inhibition of specific binding between native cognate binding partners on mammalian cells. The greater affinity for that native cognate binding partner (relative to the competing affinity of the native IgSF member) attenuates specific binding affinity of native molecule to its cognate binding partner. Those of skill in the art will appreciate that antagonizing an inhibitory receptor signaling can in some embodiments attenuate immunological activity of that cell if, for example, the receptor is an inhibitory receptor that serves to cause those cellular effects. In some embodiments, one or more activities between the inhibitory receptor and its ligand from among CD155/TIGIT, CD112/TIGIT, CD80/CTLA-4, ICOSL/CTLA-4. PD-L1/PD-1 or PD-:2/PD-1is blocked by the immunomodulatory protein.

[0284] Thus, in some embodiments, an immunomodulatory protein can be used to stimulate a cell for which the immunomodulatory protein is not expressed and secreted (i.e., the trans cell) while attenuating inhibition of the cell by which the immunomodulatory protein is expressed and secreted (the cis cell). For example, in some embodiments, the immunomodulatory protein comprises at least one affinity-modified IgSF domain, and in some cases at least two affinity

modified domains, that results in increased binding affinity to at least two cell surface cognate binding partners. In some embodiments, a first cognate binding partner is a stimulatory receptor and the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor. In some embodiments, binding of the affinity-modified domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor. In some embodiments, the stimulatory receptor and inhibitory receptor can independently be expressed on immune cells, such as T cells or antigen presenting cells. In some embodiments the stimulatory receptor is expressed on lymphocytes, such as T cells. In some embodiments, the stimulatory receptor is CD28, ICOS, or CD226 and/or the ligand of the stimulatory receptor is ICOSL. In some embodiments, the inhibitory receptor is expressed on the engineered cells, such as an engineered T-cell. In some embodiments, the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, VSIG3, or VSIG8 and/or the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, CD112, CD155, HVEM, MHC class II, PVR, CEACAM-1,GAL9 or VISTA (see e.g. Table 1). In some embodiments, the inhibitory cognate binding partner is PD-L1 or PD-L2.

[0285] In some embodiments, an immunomodulatory protein can be used to attenuate inhibition of the cell that expresses and secretes the immunomodulatory protein, such as a T cell that expresses and secretes the immunomodulatory protein. For example, an immunomodulatory protein expressed and secreted by a T cell (e.g. first T cell) can comprise an affinity-modified IgSF domain that inhibits specific binding between a cognate binding partner on a second T cell. In some embodiments, a ligand of an inhibitory receptor is affinity-modified and, when secreted from an engineered cell, antagonizes or inhibits its inhibitory receptor. In some embodiments, the affinity-modified ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR (e.g. CD112 or CD155), CEACAM-1, GAL9 or VISTA (see e.g. Table 1). In some embodiments, the affinity-modified domain that is a ligand of the inhibitory receptor retains or exhibits increased binding for another receptor, such as a stimulatory receptor. For example, the affinity-modified domain can be CD155 or CD112 that is affinity-modified to exhibit reduced binding to CD226 but that retains or exhibits increased binding to TIGIT, and, in some cases, CD112R. In such embodiments, the affinity-modified CD155 or CD112 can antagonize TIGIT when expressed and secreted from a cell.

[0286] In some cases, this embodiment can be used independently or in conjunction with embodiments wherein an affinity-modified IgSF domain of the invention is expressed and

secreted by a first T cell and specifically binds at least one stimulatory cognate binding partner expressed on a second T cell and increases immunological activity in the second T cell. By this mechanism, an increased immunomodulatory response is generated in the second T cell by specific binding of the immunomodulatory protein expressed on the first T cell to a stimulatory cognate binding partner on the second cell; and the second T cell is inhibited from attenuating the immunomodulatory activity of the first T cell by specific binding of an affinity modified IgSF domain expressed on the first T cell that inhibits specific binding by and between a cognate binding partner on the second T cell and an inhibitory cognate binding partner expressed on the first T cell. The T cells used in this and the preceding embodiments are generally murine or human T-cells although other mammalian T-cells can be employed. Often, cytotoxic T-cells (CTL) are used.

[0287] As previously noted, in some embodiments an immunomodulatory protein of the present invention is expressed on a first T-cell and comprises an affinity-modified IgSF domain that specifically binds to a stimulatory cognate binding partner (e.g. stimulatory receptor) on a second T cell while also inhibiting specific binding between a native cognate binding partner (e.g. inhibitory ligand) on the second T-cell to its inhibitory native cognate binding partner (e.g. inhibitory receptor) on the first T-cell. Inhibition of specific binding between the cognate binding partner on the second T-cell to the cognate binding partner on the first T-cell can be achieved by competitive binding of an affinity-modified IgSF domain with at least one of the two native cognate binding partners such that their mutual binding is interfered with. Typically, the IgSF domain is affinity modified to have a higher binding affinity to its cognate binding partner than the native cognate binding partners have to each other. In some embodiments of this design, an immunomodulatory protein can comprise an affinity-modified IgSF domain that binds to both the inhibitory and stimulatory cognate binding partners. Thus, in this embodiment the affinity-modified IgSF has dual binding capability. In some embodiments, an immunomodulatory protein comprises a first affinity-modified IgSF domain that binds a cognate binding partner on the first T-cell and a second affinity-modified IgSF domain that inhibits specific binding by and between the cognate binding partners on the first and second T-cells.

[0288] In yet another embodiment, the affinity-modified IgSF domain that binds to the stimulatory cognate binding partner on the first T-cell is on a first immunomodulatory protein and the affinity-modified IgSF domain that inhibits specific binding by and between the cognate binding partners on the first and second T cells is on a second immunomodulatory protein. In

this embodiment, the first and second immunomodulatory proteins are different polypeptide chains. In some embodiments, the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are the identical affinity-modified IgSF domain. For example, in a specific embodiment the ICOSL (inducible costimulator ligand) IgSF domain (e.g. affinity modified IgV domain) is affinity modified to specifically bind with increased affinity to both ICOS and CD28. In some embodiments, the affinity modified IgSF domain is an affinity modified ICOSL IgSF domain (e.g. affinity modified IgV domain) with increased affinity to both ICOS and CD28, or decreased affinity to one of or both of: ICOS and CD28.

[0289] In some embodiments, the immunomodulatory protein results in inhibition of specific binding by and between native cognate binding partners. In some embodiments, this can be achieved by an affinity-modified IgSF domain having greater affinity for one or both native cognate binding partners thereby competitively inhibiting the specific binding by and between these cognate binding partners.

[0290] In some embodiments, the immunomodulatory protein comprises an affinity-modified IgSF domain that is an affinity-modified CD155 IgSF domain with increased affinity to CD226 and attenuated affinity to TIGIT (T-cell immunoreceptor with Ig and ITIM domains).

[0291] In some embodiments, the immunomodulatory protein (e.g. expressed on a first T cell) comprises an affinity-modified CD80 (B7-1) IgSF domain that is affinity modified to bind with increased affinity to the stimulatory cognate binding partner CD28 (e.g. on a second T-cell). Additionally, in this embodiment, the affinity-modified CD80 (B7-1) IgSF domain can bind with increased affinity to PD-L1 (e.g. expressed on the second T-cell) and inhibit specific binding to its cognate binding partner PD-1 (e.g. expressed on the first T-cell). In yet a further addition either of the preceding embodiments, the affinity-modified CD80 (B7-1) IgSF domain can be affinity modified such that it does not substantially specifically bind to CTLA-4 or binds with attenuated affinity and therefore is not significantly inhibited in its specific binding to the stimulatory cognate binding partner CD28 by CTLA-4.

[0292] In some embodiments, an immunomodulatory protein is used as a decoy cognate binding partner to inhibit specific binding by and between native cognate binding partners, at least one of which comprises an IgSF family member. In some cases, specific binding of an immunomodulatory protein comprising an affinity-modified IgSF domain with one of the native cognate binding partners inhibits mutual specific binding by and between the native cognate

binding partners (e.g. native receptor and ligand pairs). Thus, in some embodiments, immunomodulatory proteins can attenuate specific binding by means of competitive or non-competitive binding. In some embodiments, the native cognate binding partner is a cell surface receptor, which can be a stimulatory receptor or an inhibitory receptor. Embodiments wherein specific binding of the affinity modified IgSF domain of a cognate binding partner increases or attenuates immunological activity of the T-cell are included within the scope of the invention.

[0293] In some embodiments, a native cognate binding partner is an inhibitory cognate binding partner that acts to attenuate immunological activity when specifically bound by its native cognate binding partner. For example, a native cell surface cognate binding partner expressed on an antigen presenting cell (APC) or a mammalian tumor cell can specifically bind a native inhibitory cognate binding partner on an NK cell or a lymphocyte such as a T-cell. Specific binding to the inhibitory cognate binding partner acts to attenuate immunomodulatory activity of the NK cell or lymphocyte on which the inhibitory cognate binding partner is expressed.

[0294] In some embodiments, an inhibitory cognate binding partner is an inhibitory receptor. In some embodiments, the inhibitory cognate binding partner is an ITIM (immunoreceptor tyrosine-based inhibition motif) containing inhibitory cognate binding partner. The ITIM motif is found in the endodomain of many inhibitory receptors of the immune system (Cell Signal, 16 (4): 435-456, 2004). In some embodiments, the affinity-modified IgSF domain is an affinity-modified form of a wild-type inhibitory receptor IgSF domain that results in greater affinity of the affinity-modified IgSF domain of the immunomodulatory protein for its native cognate binding partner than the wild-type inhibitory receptor for the native cognate binding partner. Thus, in these embodiments a immunomodulatory protein can attenuate the inhibitory response of ITIM motif receptors by specific binding of the immunomodulatory protein affinity-modified IgSF domain to its native IgSF domain cognate binding partner, such as specific binding of the immunomodulatory protein affinity-modified IgSF domain to the ITIM containing inhibitory receptor. As an example, an ITIM containing cognate binding partner is PD-1. Typically, PD-1 is the inhibitory receptor that is specifically bound to the inhibitory ligand PD-1. Upon specific binding of PD-L1 to PD-1, PD-1 is involved in inhibiting T-cell activation via signal transduction from the ITIM domain.

[0295] In some embodiments, the inhibitory receptor cognate binding partner is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8. In some embodiments, the

immunomodulatory protein contains an affinity-modified IgSF domain that is an affinity-modified IgSF domain of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, or BTLA that binds with greater affinity to the native inhibitory ligand of the inhibitory receptor than the wild-type inhibitory receptor (see Table 1 for ligand binding partners of exemplary inhibitory receptors). In some embodiments, an immunomodulatory protein can comprise an affinity-modified PD-1 IgSF domain that binds with greater affinity to PD-L1 than wild-type PD-1. Specific binding can be achieved by competitive or non-competitive binding and are specific embodiments of the invention. Competitive binding by and between the affinity-modified IgSF domain and the cognate binding partner (i.e. inhibitory receptor, e.g. PD-1) inhibits its binding to its native ligand cognate binding partner (e.g., PD-L1). In some embodiments, the immunomodulatory protein of this embodiment substantially lacks the signal transduction mechanism of the wild-type inhibitory receptor and therefore does not itself induce an inhibitory response.

VII. INFECTIOUS AGENTS

[0296] Also provided are infectious agents that contain nucleic acids encoding any of the immunomodulatory proteins containing an affinity-modified IgSF domain, including secretable or transmembrane immunomodulatory proteins described herein. In some embodiments, such infectious agents can deliver the nucleic acids encoding the immunomodulatory polypeptides described herein 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.

[0297] 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 immunomodulatory proteins, 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 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.

[0298] In some embodiments, the infectious agent, e.g., virus or bacteria, contains nucleic acid sequences that encode any of the immunomodulatory proteins, 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 immunomodulatory proteins, 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*.

[0299] In some embodiments, the immunomodulatory protein is a transmembrane immunomodulatory proteins that is expressed by the cell infected by the infectious agent and is surface expressed. In some embodiments, the immunomodulatory protein is a secretable immunomodulatory protein that is expressed by the cell infected by the infectious agent and is expressed and secreted from the cell. The transmembrane immunomodulatory protein or secreted immunomodulatory protein can be any described herein.

[0300] 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 immunomodulatory protein, 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.

[0301] 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 and 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).

A. Viruses

[0302] 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).

[0303] 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 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 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.

[0304] 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 immunomodulatory polypeptides described herein to such solid tumors.

[0305] Oncolytic viruses for use in delivering the nucleic acids encoding variant ICOSL 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.

[0306] 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®.

[0307] 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 immunomodulatory polypeptides 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.

[0308] 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 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 immunomodulatory polypeptides described herein) to a DC. In some embodiments, the virus includes those described in WO 2008/011636, 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™.

B. Bacteria

[0309] In some embodiments, the infectious agent is a bacterium. For example, in some embodiments, the bacteria can deliver nucleic acids encoding any of the 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 immunomodulatory polypeptides and/or to target specific cells in the environment for expression of the variant immunomodulatory polypeptides.

[0310] 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.

[0311] 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.

[0312] 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 immunomodulatory polypeptides, conjugates and/or fusions provided herein, and/or to express such immunomodulatory polypeptides in the subject.

VIII. COMPOSITIONS, METHODS, AND THERAPEUTIC APPLICATIONS

[0313] Provided herein are compositions and methods relating to the provided immunomodulatory proteins, engineered cells and infectious agents described herein for use in modulating immunological activity of a mammalian cell. The compositions 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. In some embodiments, the method comprises contacting an immunomodulatory protein (which may be secreted by an engineered cell) 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. The methods can be employed ex vivo or in vivo.

[0314] In some embodiments, the method of modulating immunological activity is achieved by expression and secretion of an immunomodulatory protein of the present invention by an immune cell, such as a lymphocyte (e.g., a T-cell or TIL) or NK cell engineered or infected to express and secrete the immunomodulatory protein. In some embodiments, the method of modulating immunological activity is achieved by expression and surface expression of an

immunomodulatory protein of the present invention by an immune cell, such as a lymphocyte (e.g., a T-cell or TIL) or NK cell engineered or infected to express on their surface a transmembrane immunomodulatory protein. In some embodiments, a tumor cell can be infected, e.g. with an oncolytic virus, to express a secretable immunomodulatory protein or transmembrane immunomodulatory protein modulation of immune cells in the tumor environment. In some embodiments, the cell expressing and secreting the immunomodulatory protein is contacted with a mammalian cell such as an APC, a second lymphocyte or tumor cell under conditions that are permissive of specific binding of the affinity modified IgSF domain to a cognate binding partner on the mammalian cell such that immunological activity can be modulated in the mammalian cell.

[0315] In some embodiments, the method is conducted by adoptive cell transfer of engineered cells expressing and secreting the immunomodulatory protein (e.g., a T-cell) are infused back into the patient. In some embodiments, the method is conducted by adoptive cell transfer of engineered cells (e.g. T cells) expressing on their surface a transmembrane immunomodulatory protein.

[0316] Provided herein are methods of administering an effective amount of engineered cells configured to express and secrete or surface express an immunomodulatory proteins to a subject in need (for example a subject having a disease or disorder). The pharmaceutical compositions 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 an immune response to treat the disease. For example, in some embodiments, the pharmaceutical composition stimulates the immune response, which can be useful, for example, in the treatment of cancer, viral infections, or bacterial infections. 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.

[0317] The provided methods are believed to have utility in a variety of applications, including, but not limited to, e.g., in prophylactic or therapeutic methods for treating a variety of immune system diseases or conditions in a mammal in which modulation or regulation of the immune system and immune system responses is beneficial. For example, suppressing an immune response can be beneficial in prophylactic and/or therapeutic methods for inhibiting

rejection of a tissue, cell, or organ transplant from a donor by a recipient. In a therapeutic context, the mammalian subject is typically one with an immune system disease or condition, and administration is conducted to prevent further progression of the disease or condition.

[0318] Cell compositions engineered to express and secrete immunomodulatory proteins of the present invention and associated methods can be used in immunotherapy applications. In some embodiments, cells isolated from a mammal, such as a mouse or human, and can be engineered to express and secrete or surface express an immunomodulatory protein. In some embodiments, the mammalian cell serving as a host cell for expression and secretion or surface expression of an immunomodulatory protein is a lymphocyte such as a tumor infiltrating lymphocyte (TIL), a natural killer (NK) cell, or a T-cell such as a CD8+ cytotoxic T lymphocyte or a CD4+ helper T lymphocyte. In some embodiments, the cells are autologous cells. In aspects of the provided method, the engineered cells are contacted, generally under physiological conditions, with a mammalian cell in which modulation of immunological activity is desired. For example, the mammalian cell can be a murine or human cell such as an antigen presenting cell or tumor cell. In some embodiments, the engineered cells are autologous cells. In other embodiments, the cells are allogeneic. Cells can be contacted in vivo or ex vivo. In some embodiments, the engineered cells are administered to the subject, such as by infusion. Thus, composition and methods can be used in adoptive cell transfer immunotherapy.

[0319] In some embodiments, the method is conducted by administration of a pharmaceutical compositions containing infectious agent containing a nucleic acid molecule encoding the immunomodulatory protein, either secretable immunomodulatory protein or transmembrane immunomodulatory protein. 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

[0320] In some embodiments, an effective amount of a pharmaceutical composition is administered to inhibit, halt, or reverse progression of cancers that are sensitive to modulation of immunological activity by immunomodulatory proteins of the present invention. In some embodiments, the 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. Other cancers which can be treated by the methods of the invention 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, gastric carcinoma, or Ewing's sarcoma.

[0321] 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.

[0322] In some embodiments, a pharmaceutical composition of the invention can also be used to inhibit growth of mammalian, particularly human, cancer cells as a monotherapy (i.e., as a single agent), in combination with at least one chemotherapeutic agent (i.e., a combination therapy), in combination with a cancer vaccine, in combination with an immune checkpoint

inhibitor and/or in combination with radiation therapy. In some aspects of the present disclosure, the immune checkpoint inhibitor is nivolumab, tremelimumab, pembrolizumab, ipilimumab, or the like.

[0323] In some embodiments, the provided compositions can attenuate an immune response, such as, for example, where the immunomodulatory protein comprises an affinity modified IgSF domain of an inhibitory ligand. In some embodiments, the compositions can be used to treat an autoimmune disease. In some embodiments, the administration of a therapeutic composition of the invention to a subject suffering from an immune system disease (e.g., autoimmune disease) can result in suppression or inhibition of such immune system attack or biological responses associated therewith. By suppressing this immune system attack on healthy body tissues, the resulting physical symptoms (e.g., pain, joint inflammation, joint swelling or tenderness) resulting from or associated with such attack on healthy tissues can be decreased or alleviated, and the biological and physical damage resulting from or associated with the immune system attack can be decreased, retarded, or stopped. In a prophylactic context, the subject may be one with, susceptible to, or believed to present an immune system disease, disorder or condition, and administration is typically conducted to prevent progression of the disease, disorder or condition, inhibit or alleviate symptoms, signs, or biological responses associated therewith, prevent bodily damage potentially resulting therefrom, and/or maintain or improve the subject's physical functioning.

[0324] 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.

[0325] In some embodiments, the pharmaceutical compositions comprising cells engineered to express and secrete immunomodulatory proteins can be used to treat one or more other immune disease or disorder in the subject. The immune system disease or disorder of the patient may be or involve, e.g., but is not limited to, Addison's Disease, Allergy, Alopecia Areata, Alzheimer's, Antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis, Ankylosing Spondylitis, Antiphospholipid Syndrome (Hughes Syndrome), arthritis, Asthma, Atherosclerosis, Atherosclerotic plaque, autoimmune disease (e.g., lupus, RA, MS, Graves' disease, etc.), 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 (CIPD), Chronic relapsing polyneuropathy (Guillain-Barré syndrome), Churg-Strauss Syndrome (CSS), Cicatricial Pemphigoid, Cold Agglutinin Disease (CAD), COPD, 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, graft-related disease or disorder, Graves'Disease, GVHD, Hashimoto's Thyroiditis, Idiopathic Pulmonary Fibrosis, Idiopathic Thrombocytopenia Purpura (ITP), IgA Nephropathy, immunoproliferative disease or disorder (e.g., psoriasis), Inflammatory bowel disease (IBD), Insulin Dependent Diabetes Mellitus (IDDM), Interstitial lung disease, juvenile diabetes, Juvenile Arthritis, juvenile idiopathic arthritis (JIA), Kawasaki's Disease, Lambert-Eaton Myasthenic Syndrome, Lichen Planus, lupus, Lupus Nephritis, Lymphoscytic Lypophisitis, 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, Rheumatoid Arthritis, Sarcoidosis, Schmidt's syndrome, Scleroderma, Sjörgen's Syndrome, Solid-organ transplant rejection (kidney, heart, liver, lung, etc.), Stiff-Man Syndrome, Systemic Lupus Erythematosus (SLE), systemic scleroderma, Takayasu Arteritis, Temporal Arteritis/Giant Cell Arteritis, Thyroiditis, Type 1 diabetes, Type 2 diabetes, Ulcerative colitis, Uveitis, Vasculitis, Vitiligo, Wegener's Granulomatosis, and preventing or suppressing an immune response associated with rejection of a donor tissue, cell, graft, or organ transplant by a recipient subject. Graft-related diseases or disorders include graft versus host disease (GVDH), such as associated with bone marrow transplantation, and immune disorders resulting from or associated with rejection of organ, tissue, or cell graft transplantation (e.g., tissue or cell

allografts or xenografts), including, e.g., grafts of skin, muscle, neurons, islets, organs, parenchymal cells of the liver, etc. With regard to a donor tissue, cell, graft or solid organ transplant in a recipient subject, it is believed that a therapeutic composition of the invention disclosed herein may be effective in preventing acute rejection of such transplant in the recipient and/or for long-term maintenance therapy to prevent rejection of such transplant in the recipient (e.g., inhibiting rejection of insulin-producing islet cell transplant from a donor in the subject recipient suffering from diabetes).

[0326] In some embodiments, a therapeutic amount of the pharmaceutical 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.

[0327] The administration of the subject compositions may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, or intraperitoneally. In one embodiment, the therapeutic composition is administered to a patient by intradermal or subcutaneous injection. In another embodiment, the therapeutic composition is administered by i.v. injection. In some cases, the cell compositions may be injected directly into a tumor, lymph node, or site of infection.

A. Pharmaceutical Compositions

[0328] Provided are pharmaceutical compositions containing the immunomodulatory protein, engineered cells configured to express and secrete or surface express such

immunomodulatory proteins or infectious agents. In some embodiments, the pharmaceutical compositions and formulations include one or more optional pharmaceutically acceptable carrier or excipient.

[0329] 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.

[0330] Pharmaceutical compositions of the present invention may be administered in a manner appropriate to the disease to be treated (or prevented). The quantity and frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

[0331] 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 is "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.

[0332] In some embodiments, the pharmaceutical composition is sterile. In some embodiments, the pharmaceutical composition is free or essentially free of bacteria or viruses. In some embodiments, the pharmaceutical composition is free or essentially free of cells other than the engineered cells described herein.

[0333] An effective amount of a pharmaceutical composition to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will thus vary depending, in part, upon the molecule delivered, the indication for which the binding agent molecule is being used, the route of administration, and the size (body weight, body surface or

organ size) and condition (the age and general health) of the patient. Accordingly, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. The pharmaceutical composition of the invention can be administered parentally, subcutaneously, or intravenously, or as described elsewhere herein. The pharmaceutical composition of the invention may be administered in a therapeutically effective amount one, two, three or four times per month, two times per week, biweekly (every two weeks), or bimonthly (every two months). Administration may last for a period of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months or longer (e.g., one, two, three, four or more years, including for the life of the subject).

[0334] For any composition, 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 cell composition 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. 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).

[0335] 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, 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.

IX. EXEMPLARY EMBODIMENTS

[0336] By way of example, among the provided embodiments are:

1. An immunomodulatory protein comprising at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein:

the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain;

the immunomodulatory protein does not comprise a transmembrane domain; and

the immunomodulatory protein is not conjugated to a half-life extending moiety.

2. The immunomodulatory protein of embodiment 1, wherein the half-life extending moiety is a multimerization domain.

3. The immunomodulatory protein of embodiment 1 or 2, wherein the half-life extending moiety is an Fc domain.

4. The immunomodulatory protein of any one of embodiments 1-3, wherein the immunomodulatory protein further comprises a signal peptide.

5. The immunomodulatory protein of embodiment 4, wherein the signal peptide is a native signal peptide from the corresponding wild-type IgSF member.

6. The immunomodulatory protein of embodiment 4, wherein the signal peptide is a non-native signal peptide.

7. The immunomodulatory protein of embodiment 4 or 6, wherein the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide.

8. The immunomodulatory protein of any one of embodiments 1-7, wherein the at least one cell surface cognate binding partner is expressed on a mammalian cell.

9. The immunomodulatory protein of embodiment 8, wherein the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte.

10. The immunomodulatory protein of embodiment 8 or 9, wherein the mammalian cell is a T-cell.

11. The immunomodulatory protein of any of embodiments 8-10, wherein the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

12. The immunomodulatory protein of any of embodiments 1-11, wherein the at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain.

13. The immunomodulatory protein of any of embodiments 8-12, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

14. The immunomodulatory protein of any of embodiments 8-13, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain.

15. The immunomodulatory protein of any of embodiments 8-13, wherein specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

16. The immunomodulatory protein of any of embodiments 1-15, wherein the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family.

17. The immunomodulatory protein of any of embodiments 1-16, wherein the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8.

18. The immunomodulatory protein of any of embodiments 1-17, wherein the wild-type IgSF domain is a human IgSF domain.

19. The immunomodulatory protein of any of embodiments 1-18, wherein the at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408.

20. The immunomodulatory protein of any of embodiments 1-19, wherein the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence

selected from any of SEQ ID NOS:28-54 and 410 or to a specific binding fragment thereof containing an IgSF domain.

21. The immunomodulatory protein of any of embodiments 1-20, wherein the wild-type IgSF domain is a member of the B7 family.

22. The immunomodulatory protein of any of embodiments 1-21, wherein the wild-type IgSF domain is a domain of CD80, CD86 or ICOSL.

23. The immunomodulatory protein of any of embodiments 1-22, wherein the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell, and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor.

24. The immunomodulatory protein of embodiment 23, wherein binding of the affinity-modified IgSF domain to the stimulatory receptor increases immunological activity of the T-cell.

25. The immunomodulatory protein of embodiment 23 or 24, wherein the stimulatory receptor is CD28, ICOS, or CD226.

26. The immunomodulatory protein of any one of embodiments 23-25, wherein the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28.

27. The immunomodulatory protein of any one of embodiments 23-26, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS.

28. The immunomodulatory protein of any one of embodiments 23-26, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28.

29. The immunomodulatory protein of any one of embodiments 23-25, wherein the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28.

30. The immunomodulatory protein of any one of embodiments 23-29, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

31. The immunomodulatory protein of any of embodiments 1-30, wherein the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner.

32. The immunomodulatory protein of any of embodiments 1-31, wherein the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

33. The immunomodulatory protein of any of embodiments 1-30, wherein the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners.

34. The immunomodulatory protein of embodiment 33, wherein:

the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and

the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell.

35. The immunomodulatory protein of embodiment 34, wherein binding of the affinity-modified domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor.

36. The immunomodulatory protein of embodiment 34 or embodiment 35, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, VSIG3, or VSIG8; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9, or VISTA.

37. The immunomodulatory protein of any one of embodiments 34-36, wherein the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28.

38. The immunomodulatory protein of embodiment 37, wherein the inhibitory ligand is PD-L1 and the inhibitory receptor is PD-1.

39. The immunomodulatory protein of embodiment 37 or embodiment 38, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CTLA-4 compared to the wild-type IgSF domain.

40. The immunomodulatory protein of any one of embodiments 37-39, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4.

41. The immunomodulatory protein of any of embodiments 1-20, wherein the affinity modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R.

42. The immunomodulatory protein of embodiment 41, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226 and, optionally, retains or exhibits increased binding to TIGIT (T-cell immunoreceptor with Ig and ITIM domains) or CD112R compared to the binding affinity of the wild-type IgSF domain.

43. The immunomodulatory protein of any of embodiments 1-20, wherein the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen.

44. The immunomodulatory protein of embodiment 43, wherein the tumor specific antigen is B7-H6.

45. The immunomodulatory protein of embodiment 43 or 44, wherein the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

46. The immunomodulatory protein of any one of embodiments 1-45, wherein the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain.

47. The immunomodulatory protein of embodiment 46, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different.

48. The immunomodulatory protein of embodiment 46 or 47, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more different amino acid substitutions in the same wild-type IgSF domain.

49. The immunomodulatory protein of embodiment 46 or 47, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

50. The immunomodulatory protein of any of embodiments 1-20, wherein the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor, the inhibitory receptor comprising an ITIM signaling domain.

51. The immunomodulatory protein of embodiment 50, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, or BTLA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively.

52. The immunomodulatory protein of embodiment 50 or 51, wherein the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-1.

53. The immunomodulatory protein of any of embodiments 50-52, wherein the affinity-modified IgSF domain has increased binding affinity for a trans surface cognate binding partner compared to the wildtype IgSF domain, whereby the increased binding affinity competitively inhibits binding of the trans surface cognate binding partner to the inhibitory receptor.

54. The immunomodulatory protein of any of embodiments 1-53, wherein the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain.

55. The immunomodulatory protein of any of embodiments 1-54, wherein the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

56. The immunomodulatory protein of any of embodiments 1-55, wherein the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

57. The immunomodulatory protein of any of embodiments 1-56, wherein the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

58. The immunomodulatory protein of any one of embodiments 1-56, wherein the immunomodulatory protein has been secreted from an engineered cell.

59. The immunomodulatory protein of embodiment 58, wherein the engineered cell is an immune cell.

60. The immunomodulatory protein of embodiment 58 or 59, wherein the engineered cell is a primary cell.

61. A recombinant nucleic acid encoding the immunomodulatory protein of any of embodiments 1-60.

62. The recombinant nucleic acid of embodiment 61, wherein the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein.

63. The recombinant nucleic acid of embodiment 62, wherein the promoter is a constitutively active promoter.

64. The recombinant nucleic acid of embodiment 62, wherein the promoter is an inducible promoter.

65. The recombinant nucleic acid of embodiment 64, wherein the promoter is responsive to an element responsive to T-cell activation signaling.

66. The recombinant nucleic acid of embodiment 64, or 65, wherein the promoter comprises a binding site for NFAT or a binding site for NF-κB.

67. A recombinant expression vector comprising the nucleic acid of any of embodiments 61-66.

68. A recombinant expression vector comprising a nucleic acid encoding an immunomodulatory protein under the operable control of a signal sequence for secretion, wherein:

the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

the encoded immunomodulatory protein is secreted when expressed from a cell.

69. The expression vector of embodiment 68, wherein the immunomodulatory protein does not comprise a transmembrane domain.

70. The expression vector of embodiment 68 or 69, wherein the immunomodulatory protein is not conjugated to a half-life extending moiety.

71. The expression vector of any one of embodiments 68-70, wherein the half-life extending moiety is a multimerization domain.

72. The expression vector of any one of embodiments 68-71, wherein the half-life extending moiety is an Fc domain.

73. The expression vector of any one of embodiments 68-72, wherein the signal sequence for secretion encodes a secretory signal peptide.

74. The expression vector of embodiment 73, wherein the signal peptide is a native signal peptide from the corresponding wild-type IgSF member.

75. The expression vector of embodiment 73, wherein the signal peptide is a non-native signal peptide.

76. The expression vector of embodiment 73 or 75, wherein the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide.

77. The expression vector of any of embodiments 68-76, wherein the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein.

78. The expression vector of embodiment 77, wherein the promoter is a constitutively active promoter.

79. The expression vector of embodiment 77, wherein the promoter is an inducible promoter.

80. The expression vector of embodiment 79 wherein the promoter is responsive to an element responsive to T-cell activation signaling.

81. The expression vector of embodiment 79 or 80, wherein the promoter comprises a binding site for NFAT or a binding site for NF-κB.

82. The expression vector of any of embodiments 68-81, wherein the vector is a viral vector.

83. The expression vector of embodiment 82, wherein the viral vector is a retroviral vector.

84. The expression vector of embodiment 82 or 83, wherein the viral vector is a lentiviral vector or a gammaretroviral vector.

85. The expression vector of any one of embodiments 68-84, wherein the at least one affinity-modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain.

86. The expression vector of any one of embodiments 68-85, wherein the at least one cell surface cognate binding partner is expressed on a mammalian cell.

87. The expression vector of embodiment 86, wherein the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte.

88. The expression vector of embodiment 86 or 87, wherein the mammalian cell is a T-cell.

89. The expression vector of any one of embodiments 86-88, wherein the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

90. The expression vector of any one of embodiments 86-89, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

91. The expression vector of any one of embodiments 86-90, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain.

92. The expression vector of any one of embodiments 86-910, wherein specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

93. The expression vector of any one of embodiments 68-92, wherein the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family.

94. The expression vector of any one of embodiments 68-93, wherein the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-

alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8.

95. The expression vector of any one of embodiments 68-94, wherein the wild-type IgSF domain is a human IgSF domain.

96. The expression vector of any one of embodiments 68-95, wherein the at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408.

97. The expression vector of any one of embodiments 68-96, wherein the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 28-54 and 410.

98. The expression vector of any of embodiments 68-97, wherein the wild-type IgSF domain is a member of the B7 family.

99. The expression vector of any of embodiments 68-98, wherein the wild-type IgSF domain is a domain of CD80, CD86 or ICOSL.

100. The expression vector of any one of embodiments 68-99, wherein the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor.

101. The expression vector of embodiment 100, wherein binding of the affinity-modified IgSF domain to the stimulatory receptor increases immunological activity of the T-cell.

102. The expression vector of embodiment 100 or 101, wherein the stimulatory receptor is CD28, ICOS, or CD226.

103. The expression vector of any one of embodiments 100-102, wherein the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28.

104. The expression vector of any one of embodiments 100-103, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS.

105. The expression vector of any one of embodiments 100-103, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28.

106. The expression vector of any one of embodiments 100-102, wherein the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28.

107. The expression vector of any one of embodiments 100-106, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

108. The expression vector of any one of embodiments 68-107, wherein the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner.

109. The expression vector of any one of embodiments 68-108, wherein the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

110. The expression vector of any one of embodiments 68-107, wherein the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners.

111. The expression vector of embodiment 110, wherein:

the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and

the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell.

112. The expression vector of embodiment 111, wherein binding of the affinity-modified IgSF domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor.

113. The expression vector of embodiment 111 or 112, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160, TIM-3, VSIG3, or VSIG8; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9 or VISTA.

114. The expression vector of any one of embodiments 111-113, wherein the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28.

115. The expression vector of embodiment 114, wherein the inhibitory ligand is PD-L1 and the inhibitory receptor is PD-1.

116. The expression vector of embodiment 114 or 115, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CTLA-4 compared to the wild-type IgSF domain.

117. The expression vector of any one of embodiments 114-116, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4.

118. The expression vector of any of embodiments 68-97, wherein the affinity-modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R.

119. The expression vector of embodiment 118, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226 and, optionally, retains or exhibits increased binding to TIGIT (T-cell immunoreceptor with Ig and ITIM domains) or CD112R compared to the binding affinity of the wild-type IgSF domain.

120. The expression vector of any of embodiments 68-97, wherein the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen.

121. The expression vector of embodiment 120, wherein the tumor specific antigen is B7-H6.

122. The expression vector of embodiment 120 or 121, wherein the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

123. The expression vector of any one of embodiments 68-122, wherein the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain.

124. The expression vector of embodiment 123, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different.

125. The expression vector of embodiment 123 or 124, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more different amino acid substitutions in the same wild-type IgSF domain.

126. The expression vector of embodiment 123 or 124, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

127. The expression vector of any of embodiments 68-97, wherein the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor, the inhibitory receptor comprising an ITIM signaling domain.

128. The expression vector of embodiment 127, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, or BTLA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively.

129. The expression vector of embodiment 127 or 128, wherein the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-1.

130. The expression vector of any of embodiments 127-129, wherein the affinity-modified IgSF domain has increased binding affinity for a trans surface cognate binding partner compared to the wildtype IgSF domain, whereby the increased binding affinity competitively inhibits binding of the trans surface cognate binding partner to the inhibitory receptor.

131. The expression vector of any of embodiments 68-130, wherein the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain.

132. The expression vector of any of embodiments 68-131, wherein the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

133. The expression vector of any of embodiments 68-132, wherein the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity

modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

134. The expression vector of any of embodiments 68-133, wherein the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

135. An engineered cell comprising the nucleic acid of any one of embodiments 61-66 or the expression vector of any one of embodiments 67-134.

136. An engineered cell comprising the immunomodulatory protein of any one of embodiments 1-60.

137. An engineered cell that secretes the immunomodulatory protein of any one of embodiments 1-60.

138. The engineered cell of any of embodiments 135-137, wherein the cell is an immune cell.

139. An engineered immune cell comprising a nucleic acid molecule that encodes an immunomodulatory protein, wherein:

the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

the engineered cell expresses and secretes the immunomodulatory protein.

140. The engineered immune cell of embodiment 139, wherein the immunomodulatory protein does not comprise a transmembrane domain.

141. The engineered immune cell of embodiment 139 or 140, wherein the immunomodulatory protein is not conjugated to a half-life extending moiety.

142. The engineered immune cell of embodiment 141, wherein the half-life extending moiety is a multimerization domain.

143. The engineered immune cell of embodiment 141 or 142, wherein the half-life extending moiety is an Fc domain.

144. The engineered immune cell of any one of embodiments 139-143, wherein the nucleic acid molecule comprises a sequence encoding a secretory signal peptide operably linked to the sequence encoding the immunomodulatory protein.

145. The engineered immune cell of embodiment 144, wherein the signal peptide is the native signal peptide from the corresponding wild-type IgSF member.

146. The engineered immune cell of embodiment 144, wherein the signal peptide is a non-native signal sequence.

147. The engineered immune cell of embodiment 144 or 146, wherein the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide.

148. The engineered immune cell of any one of embodiments 139-148, wherein the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein.

149. The engineered immune cell of embodiment 148, wherein the promoter is a constitutively active promoter.

150. The engineered immune cell of embodiment 148, wherein the promoter is an inducible promoter.

151. The engineered immune cell of embodiment 148 or 150, wherein the promoter is responsive to an element responsive to T-cell activation signaling.

152. The engineered immune cell of any one of embodiments 148, 150, and 151, wherein the promoter comprises a binding site for NFAT or a binding site for NF-κB.

153. The engineered cell of embodiments 135-152, wherein the immunomodulatory protein is expressed and secreted by the engineered cell after the engineered cell is contacted with an inducing agent or after induction of T cell activation signaling, which optionally is induced upon binding of an antigen to a chimeric antigen receptor (CAR) or engineered T-cell receptor (TCR) expressed by the engineered cell.

154. The engineered cell of any one of embodiments 135-153, wherein the cell is a lymphocyte.

155. The engineered cell of embodiment 154, wherein the lymphocyte is a T cell, a B cell or an NK cell.

156. The engineered cell of any one of embodiments 135-155, wherein the cell is a T cell.

157. The engineered cell of embodiment 156, wherein the T cells is CD4+ or CD8+.

158. The engineered cell of any one of embodiments 135-154, wherein the cell is an antigen presenting cell.

159. The engineered cell of any one of embodiments 135-158, wherein the cell is a primary cell obtained from a subject.

160. The engineered cell of embodiment 159, wherein the subject is a human subject.

161. The engineered cell of any one of embodiments 135-160, wherein the at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the wild-type IgSF domain.

162. The engineered cell of any one of embodiments 135-161, wherein the at least one cell surface cognate binding partner is expressed on a mammalian cell.

163. The engineered cell of embodiment 162, wherein the mammalian cell is an antigen presenting cell (APC), a tumor cell, or a lymphocyte.

164. The engineered cell of embodiment 162 or 163, wherein the mammalian cell is a T-cell.

165. The engineered cell of any one of embodiments 162-164, wherein the mammalian cell is a mouse, rat, cynomolgus monkey, or human cell.

166. The engineered cell of any one of embodiments 162-165, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain modulates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

167. The engineered cell of any one of embodiments 162-166, wherein specific binding of the immunomodulatory protein comprising the at least one affinity-modified IgSF domain increases immunological activity of the mammalian cell compared to the wild-type IgSF domain.

168. The engineered cell of any one of embodiments 162-166, wherein specific binding of the immunomodulatory protein attenuates immunological activity of the mammalian cell compared to the wild-type IgSF domain.

169. The engineered cell of any one of embodiments 135-168, wherein the wild-type IgSF domain is from an IgSF family member of a family selected from the group consisting of 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, and Killer-cell immunoglobulin-like receptors (KIR) family.

170. The engineered cell of any one of embodiments 135-169, wherein the wild-type IgSF domain is from an IgSF member selected from the group consisting of CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8.

171. The engineered cell of any one of embodiments 135-170, wherein the wild-type IgSF domain is a human IgSF domain.

172. The engineered cell of any one of embodiments 135-171, wherein the at least one affinity modified IgSF domain has at least 90% sequence identity to a wild-type 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 408.

173. The engineered cell of any one of embodiments 135-172, wherein the immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 28-54 and 410.

174. The engineered cell of any one of embodiments 135-173, wherein the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell and the at least one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor.

175. The engineered cell of embodiment 174, wherein binding of the affinity-modified IgSF domain to the stimulatory receptor increases immunological activity of the T-cell.

176. The engineered cell of embodiment 174 or 175, wherein the stimulatory receptor is CD28, ICOS, or CD226.

177. The engineered cell of any one of embodiments 174-176, wherein the at least one affinity-modified IgSF domain is an affinity-modified ICOSL IgSF domain that has increased binding affinity to at least one of: ICOS and CD28.

178. The engineered cell of any one of embodiments 174-177, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is ICOS.

179. The engineered cell of any one of embodiments 174-177, wherein the at least one affinity-modified IgSF domain is an affinity modified ICOSL IgSF domain and the stimulatory receptor is CD28.

180. The engineered cell of any one of embodiments 174-176, wherein the at least one affinity-modified IgSF domain is an affinity modified CD80 IgSF domain and the stimulatory receptor is CD28.

181. The engineered cell of any one of embodiments 174-180, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4 or exhibits decreased binding affinity to CTLA-4 compared to the binding affinity of wild-type IgSF domain to CTLA-4.

182. The engineered cell of any one of embodiments 135-181, wherein the at least one affinity-modified IgSF domain specifically binds to no more than one cell surface cognate binding partner.

183. The engineered cell of any one of embodiments 135-182, wherein the immunomodulatory protein specifically binds to no more than one cell surface cognate binding partner.

184. The engineered cell of any one of embodiments 135-181, wherein the at least one affinity-modified domain specifically binds to at least two cell surface cognate binding partners.

185. The engineered cell of embodiment 184, wherein:

the first cell surface cognate binding partner is a stimulatory receptor expressed on a T cell; and

the second cell surface cognate binding partner is an inhibitory ligand of an inhibitory receptor, wherein the inhibitory receptor is expressed on a T-cell.

186. The engineered cell of embodiment 185, wherein binding of the affinity-modified domain to the inhibitory ligand competitively inhibits binding of the inhibitory ligand to the inhibitory receptor.

187. The engineered cell of embodiment 185 or 186, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG-3, TIGIT, CD96, CD112R, BTLA, CD160,TIM-3, VSIG3, or VSIG8; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, HVEM, MHC class II, PVR, CEACAM-1, GAL9 or VISTA.

188. The engineered cell of any one of embodiments 185-187, wherein the affinity modified IgSF domain is an affinity modified CD80 domain and the stimulatory receptor is CD28.

189. The engineered cell of embodiment 188, wherein the inhibitory ligand is PD-L1 and the inhibitory receptor is PD-1.

190. The engineered cell of embodiment 188 or 189, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CTLA-4 compared to the wild-type IgSF domain.

191. The engineered cell of any one of embodiments 188-190, wherein the affinity-modified IgSF domain does not substantially specifically bind to CTLA-4.

192. The engineered cell of any of embodiments 135-173, wherein the affinity modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R.

193. The engineered cell of embodiment 192, wherein the affinity-modified IgSF domain exhibits decreased binding affinity to CD226 compared to the binding affinity of the wild-type IgSF domain to CD226 and, optionally, retains or exhibits increased binding to TIGIT (T-cell immunoreceptor with Ig and ITIM domains) or CD112R compared to the binding affinity of the wild-type IgSF domain.

194. The engineered cell of any of embodiments 135-173, wherein the at least one affinity-modified IgSF domain specifically binds to a cell surface cognate binding partner that is a tumor specific antigen.

195. The engineered cell of embodiment 194, wherein the tumor specific antigen is B7-H6.

196. The engineered cell of embodiment 194 or 195, wherein the affinity-modified IgSF domain is an affinity modified NKp30 IgSF domain.

197. The engineered cell of any one of embodiments 135-173, wherein the at least one affinity-modified IgSF domain comprises a first affinity-modified IgSF domain and a second affinity-modified IgSF domain.

198. The engineered cell of embodiment 197, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain are different.

199. The engineered cell of embodiment 197 or 198, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprises one or more different amino acid substitutions in the same wild-type IgSF domain.

200. The engineered cell of embodiment 197 or 198, wherein the first affinity-modified IgSF domain and the second affinity-modified IgSF domain each comprise one or more amino acid substitutions in a different wild-type IgSF domain.

201. The engineered cell of any of embodiments 135-173, wherein the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor, the inhibitory receptor comprising an ITIM signaling domain.

202. The engineered cell of embodiment 201, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, or BTLA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-L1, PD-L2, B7-1, B7-2, MHC class II, PVR, CEACAM-1, GAL9 or VISTA, respectively.

203. The engineered cell of embodiment 201 or 202, wherein the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-1.

204. The engineered cell of any of embodiments 201-203, wherein the affinity-modified IgSF domain has increased binding affinity for a trans surface cognate binding partner compared to the wildtype IgSF domain, whereby the increased binding affinity competitively inhibits binding of the trans surface cognate binding partner to the inhibitory receptor.

205. The engineered cell of any of embodiments 135-204, wherein the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain.

206. The engineered cell of any of embodiments 135-205, wherein the affinity modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

207. The engineered cell of any of embodiments 135-206, wherein the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

208. The engineered cell of any of embodiments 135-207, wherein the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

209. The engineered cell of any of embodiments 135-208, further comprising a chimeric antigen receptor (CAR) or an engineered T-cell receptor (TCR).

210. A pharmaceutical composition comprising the cell of any of embodiments 135-209 or the infectious agent of any of embodiments 230-252 and a pharmaceutically acceptable carrier.

211. The pharmaceutical composition of embodiment 210 that is sterile.

212. A method of introducing an immunomodulatory protein into a subject, comprising administering an engineered cell of any one of embodiments 135-209, the infectious agent of any of embodiments 230-252 or a pharmaceutical composition of embodiment 210 or 211 to the subject.

213. A method of modulating an immune response in a subject, comprising administering the cell of any one of embodiments 135-209, an infectious agent of any of embodiments 230-252 or a pharmaceutical composition of embodiment 210 or 211 to the subject.

214. The method of embodiment 213, wherein modulating the immune response treats a disease or disorder in the subject.

215. The method of embodiment 213 or 214, wherein the modulated immune response is increased.

216. The method of embodiment 214 or 215, wherein the disease or disorder is a tumor.

217. The method of any one of embodiments 214-216, wherein the disease or disorder is a cancer.

218. The method of any one of embodiments 214-217, wherein the disease or disorder is melanoma, lung cancer, bladder cancer, or a hematological malignancy.

219. The method of embodiment 213 or 214, wherein the modulated immune response is decreased.

220. The method of embodiment 214 or 219, wherein the disease or disorder is an inflammatory disease or condition.

221. The method of any one of embodiments 214, 219, and 220, wherein the disease or condition is Crohn's disease, ulcerative colitis, multiple sclerosis, asthma, rheumatoid arthritis, or psoriasis.

222. The method of any one of embodiments 212-221, wherein the subject is human.

223. The method of any of embodiments 212-222, wherein the cell is autologous to the subject.

224. The method of any of embodiments 212-222, wherein the cell is allogenic to the subject.

225. The method of any one of embodiments 212-224 wherein the engineered cell expresses and secretes the immunomodulatory protein.

226. The method of any one of embodiments 212-225, wherein the immunomodulatory protein is constitutively expressed by the engineered cell.

227. The method of any one of embodiments 212-225, wherein the immunomodulatory protein is expressed and secreted by the engineered cell after the engineered cell is contacted with an inducing agent.

228. The method of any one of embodiments 212-227, wherein the immunomodulatory protein is expressed and secreted by the engineered cell upon T cell activation signaling.

229. The method of embodiment 228, wherein the engineered cell expresses a chimeric antigen receptor (CAR) or an engineered T-cell receptor (TCR) and T cell activation signaling is induced upon binding of an antigen by the CAR or TCR.

230. An infectious agent, comprising a nucleic acid molecule encoding the immunomodulatory protein of any one of embodiments 1-60, a nucleic acid molecule of any of embodiments 61-66 or the expression vector of any one of embodiments 67-134.

231. An infectious agent, comprising a nucleic acid molecule encoding a transmembrane immunomodulatory protein (TIP) comprising:

(i) an ectodomain comprising at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitution(s) in a wild-type IgSF domain, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

(ii) a transmembrane domain.

232. The infectious agent of embodiment 231, wherein the at least one affinity modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the reference wild-type IgSF domain.

233. The infectious agent of embodiment 231 or embodiment 232, wherein the wild-type IgSF domain is from 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.

234. The infectious agent of any of embodiments 231-233, wherein the wild-type IgSF domain is from an IgSF member selected from CD80, CD86, PD-L1, PD-L2, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R or NKp30.

235. The infectious agent of any of embodiments 231-234, wherein the wild-type IgSF domain is a human IgSF member.

236. The infectious agent of any of embodiments 231-235, wherein the transmembrane immunomodulatory protein has at least 90% sequence identity to the amino acid sequence selected from any of SEQ ID NOS: 381-407 and 409 or to a contiguous portion thereof containing the affinity-modified IgSF domain and a transmembrane domain.

237. The infectious agent of any of embodiments 231-236, wherein the transmembrane immunomodulatory protein is a chimeric receptor, wherein the endodomain is not the endodomain from the wild-type IgSF member comprising the wild-type IgSF domain.

238. The infectious agent of embodiment 237, wherein the endodomain comprises at least one ITAM (immunoreceptor tyrosine-based activation motif)-containing signaling domain.

239. The infectious agent of embodiment 238, wherein the endodomain comprises a CD3-zeta signaling domain.

240. The infectious agent of embodiment 238 or embodiment 239, wherein the endodomain further comprises at least one of: a CD28 costimulatory domain, an ICOS signaling domain, an OX40 signaling domain, and a 41BB signaling domain.

241. The infectious agent of any of embodiments 231-240, wherein the affinity modified IgSF domain differs by no more than ten amino acid substitutions or no more than five amino acid substitutions from the wildtype IgSF domain.

242. The infectious agent of any of embodiments 231-241, wherein the affinity-modified IgSF domain is or comprises an affinity modified IgV domain, affinity modified IgC1 domain or an affinity modified IgC2 domain or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

243. The infectious agent of any of embodiments 231-242, wherein the transmembrane domain is the native transmembrane domain from the corresponding wild-type IgSF member.

244. The infectious agent of any of embodiments 231-243, wherein the transmembrane domain is not the native transmembrane domain from the corresponding wild-type IgSF member.

245. The infectious agent of embodiment 244, wherein the transmembrane protein is a transmembrane protein derived from CD8.

246. The infectious agent of any of embodiments 230-245, wherein the infectious agent is a bacteria or a virus.

247. The infectious agent of embodiment 246, wherein the virus is an oncolytic virus.

248. The infectious agent of embodiment 247, 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.

249. The infectious agent of embodiment 246, wherein the virus specifically targets dendritic cells (DCs) and/or is dendritic cell-tropic.

250. The infectious agent of embodiment 249, wherein the virus is a lentiviral vector that is pseudotyped with a modified Sindbis virus envelope product.

251. The infectious agent of any of embodiments 230-250, 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.

252. The infectious agent of embodiment 251, 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 a reprogramming human somatic cells to pluripotency.

X. EXAMPLES

[0337] The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

[0338] Examples 1-12 describe the design, creation, and screening of exemplary affinity modified CD80 (B7-1), CD86 (B7-2), ICOSL, and NKp30 immunomodulatory proteins, which are components of the immune synapse (IS) that have a demonstrated dual role in both immune activation and inhibition. These examples demonstrate that affinity modification of IgSF domains yields proteins that can act to both increase and decrease immunological activity. This work also describes the various combinations of those domains fused in pairs (i.e., stacked) to form a Type II immunomodulatory protein to achieve immunomodulatory activity. The Examples also describe the generation of exemplary secretable immunomodulatory proteins containing such affinity-modified immunomodulatory proteins.

Example 1

Generation of Mutant DNA Constructs of IgSF Domains

[0339] Example 1 describes the generation of mutant DNA constructs of human CD80, CD86, ICOSL and NKp30 IgSF domains for translation and expression on the surface of yeast as yeast display libraries. The below examples exemplify binding and activity of affinity-modified domains of the exemplary IgSF proteins in an Fc-fusion format; such affinity-modified domains are contemplated in connection with a secretable immunomodulatory protein or transmembrane immunomodulatory protein as described.

A. Degenerate Libraries

[0340] For libraries that target specific residues of target protein for complete or partial randomization with degenerate codons, such as specific mixed base sets to code for various amino acid substitutions, the coding DNAs for the extracellular domains (ECD) of human CD80

(SEQ ID NO:28), ICOSL (SEQ ID NO:32), and NKp30 (SEQ ID NO:54) were ordered from Integrated DNA Technologies (Coralville, IA) as a set of overlapping oligonucleotides of up to 80 base pairs (bp) in length. To generate a library of diverse variants of each ECD, the oligonucleotides contained desired degenerate codons at desired amino acid positions. Degenerate codons were generated using an algorithm at the URL: rosettadesign.med.unc.edu/SwiftLib/.

[0341] In general, positions to mutate and degenerate codons were chosen from crystal structures (CD80, NKp30) or homology models (ICOSL) of the target-ligand pairs of interest were used to identify ligand contact residues as well as residues that are at the protein interaction interface. This analysis was performed using a structure viewer available at the URL:spdbv.vital-it.ch). For example, a crystal structure for CD80 bound to CTLA4 is publicly available at the URL:www.rcsb.org/pdb/explore/explore.do?structureId=1I8L and a targeted library was designed based on the CD80::CTLA4 interface for selection of improved binders to CTLA4. However, there are no CD80 structures available with ligands CD28 and PD-L1, so the same library was also used to select for binders of CD28 (binds the same region on CD80 as CTLA4) and PD-L1 (not known if PD-L1 binds the same site as CTLA4). The next step in library design was the alignment of human, mouse, rat and monkey CD80, ICOSL or NKp30 sequences to identify 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 included 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 at a time. These residues were a combination of contact residues and non-contact interface residues.

[0342] The oligonucleotides were dissolved in sterile water, mixed in equimolar ratios, heated to 95ºC for five minutes and slowly cooled to room temperature for annealing. ECD-specific oligonucleotide primers that anneal to the start and end of the ECDs, respectively, were then used to generate PCR product. The ECD-specific oligonucleotides which overlap by 40-50bp with a modified version of 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 electroporation. 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. To prepare for library insertion, a modified yeast display version of vector pBYDS03 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 for every electroporation with 4 μg of linearized vector in a total volume of 50 μL deionized and sterile water. An alternative way to generate targeted libraries was to carry out site-directed mutagenesis (Multisite kit, Agilent, USA) of target ECDs with oligonucleotides containing degenerate codons. This approach was used to generate sublibraries that only target specific stretches of the DNA for mutagenesis. In these cases, sublibraries were mixed before proceeding to the selection steps. In general, library sizes were in the range of $10x10^7$ to $10x10^8$ clones, except that sublibraries were only in the range of $10x10^4$ to $10x10^5$. Large libraries and sublibraries were generated for CD80, ICOSL, CD86 and NKp30. Sublibraries were generated for CD80, ICOSL and NKp30.

B. Random Libraries

[0343] Random libraries were also constructed to identify variants of the ECD of CD80 (SEQ ID NO:28), CD86 (SEQ ID NO: 29), ICOSL (SEQ ID NO:32) and NKp30 (SEQ ID NO:54. DNA encoding wild-type ECDs was cloned between the BamHI and KpnI restriction sites of modified yeast display vector pBYDS03 and in some cases, the DNA was released using the same restriction enzymes. The released DNA or undigested plasmid 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

[0344] Example 2 describes the introduction of CD80, CD86, ICOSL and NKp30 DNA libraries into yeast.

[0345] 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 step 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.

[0346] 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 into the same medium once more to minimize the fraction of untransformed cells. 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 $10x10^{10}$ per mL and frozen and stored at -80°C (frozen library stock).

[0347] One liter of SCD-Leu media consists of 14.7 grams of sodium citrate dihydrate, 4.29 grams of citric acid monohydrate, 20 grams of dextrose, 6.7 grams of Difco brand yeast nitrogen base, and 1.6 grams yeast synthetic drop-out media supplement without leucine. Media was filtered sterilized before use using a 0.2 μM vacuum filter device.

[0348] Library size was determined by plating dilutions of freshly recovered cells on SCD-Leu agar plates and then extrapolating library size from the number of single colonies from a plating that generate at least 50 colonies per plate.

[0349] To segregate plasmid from cells that contain two or more different library clones, a number of cells corresponding to 10 times the library size, were taken from the overnight SCD-Leu culture and subcultured 1/100 into fresh SCD-Leu medium and grown overnight. Cells from this overnight culture were resuspended in 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

[0350] Example 3 describes the selection of yeast expressing affinity modified variants of CD80, CD86, ICOSL and NKp30.

[0351] A number of cells equal to at least 10 times the 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 the SCDG-Leu induction media consists of 5.4 grams Na_2HPO_4, 8.56 grams of $NaH_2PO_4*H_20$, 20 grams galactose, 2.0 grams dextrose, 6.7 grams Difco yeast nitrogen base, and 1.6 grams of 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 for two days at 20°C to induce expression of library proteins on the yeast cell surface.

[0352] Cells were processed with magnetic beads to reduce non-binders and enrich for all CD80, CD86, ICOSL or NKp30 variants with the ability to bind their exogenous recombinant counter-structure proteins (cognate binding partners). For example, yeast displayed targeted or random CD80 libraries were selected against each of CD28, CTLA-4, PD-L1. ICOSL libraries were selected against ICOS and CD28 and NKp30 libraries were selected against B7-H6. This was then followed by two to three rounds of fluorescence activated cell sorting (FACS) using exogenous cognate binding partner 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 Keith D. Miller,1 Noah B. Pefaur,2 and Cheryl L. Baird1 Current Protocols in Cytometry 4.7.1-4.7.30, July 2008.

[0353] With CD80, CD86, ICOSL, 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, rICOS.Fc, and rB7H6.Fc. Magnetic streptavidin beads were obtained from New England Biolabs, USA. For biotinylation of cognate binding partner protein, biotinylation kit cat# 21955, Life Technologies, USA, was used. For two-color, flow cytometric sorting, a Becton Dickinson FACS Aria II sorter was used. CD80, CD86, ICOSL, or NKp30 display levels were monitored with an anti-hemagglutinin tag antibody labeled with Alexafluor 488 (Life Technologies, USA). Ligand binding Fc fusion proteins rCD28.Fc, rCTLA4.Fc, rPDL1.Fc, rICOS.Fc, or rB7-H6.Fc were 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 HA tag expression binding in FL1.

[0354] 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.

[0355] For ICOSL, the second sort outputs (F2) were compared to parental ICOSL yeast for binding of each rICOS.Fc, rCD28.Fc, and rCTLA4.Fc by double staining each population with anti-HA (hemagglutinin) tag expression and the anti-human Fc secondary to detect ligand binding.

[0356] In the case of ICOSL yeast variants selected for binding to ICOS, the F2 sort outputs gave Mean Fluorescence Intensity (MFI) values of 997, when stained with 5.6 nM rICOS.Fc, whereas the parental ICOSL strain MFI was measured at 397 when stained with the same concentration of rICOS.Fc. This represents a roughly three-fold improvement of the average binding in this F2 selected pool of clones, and it is predicted that individual clones from that pool will have much better improved MFI/affinity when individually tested.

[0357] In the case of ICOSL yeast variants selected for binding to CD28, the F2 sort outputs gave MFI values of 640 when stained with 100nM rCD28.Fc, whereas the parental ICOSL strain MFI was measured at 29 when stained with the same concentration of rCD28.Fc (22-fold improvement). In the case of ICOSL yeast variants selected for binding to CTLA4, the F2 sort outputs gave MFI values of 949 when stained with 100nM rCTLA4.Fc, whereas the parental ICOSL strain MFI was measured at 29 when stained with the same concentration of rCTLA4.Fc (32-fold improvement).

[0358] 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).

[0359] 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. Among the CD86 variants that were identified, was a variant that contained mutations Q35H/H90L/Q102H with reference to positions in the CD86 extracellular domain corresponding to positions set forth in SEQ ID NO:29.

[0360] Importantly, the MFIs of all F2 outputs described above when measured with the anti-HA tag antibody on FL1 did not increase and sometimes decreased compared to wild-type strains, indicating that increased binding was not a function of increased expression of the

selected variants on the surface of yeast, and validated gating strategies of only selecting mid to low expressors with high ligand binding.

Example 4

Reformatting Selection Outputs as Fc-Fusions and in Various Immunomodulatory Protein Types

[0361] Example 4 describes reformatting of selection outputs as immunomodulatory proteins containing an affinity modified (variant) extracellular domain (ECD) of CD80 or ICOSL fused to an Fc molecule (variant ECD-Fc fusion molecules).

[0362] Output cells from final flow cytometric CD80 and ICOSL sorts were grown to terminal density in SCD-Leu medium. Plasmid DNA from each output was isolated using a yeast plasmid DNA isolation kit (Zymo Research, 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's ECD. After restriction digestion, the PCR products were ligated into an appropriate Fc fusion vector followed by chemical transformation into strain *E. coli* strain XL1 Blue *E. coli* (Agilent, USA) or NEB5alpha (New England Biolabs, USA) as directed by supplier. Exemplary of an Fc fusion vector is pFUSE-hIgG1-Fc2 (InvivoGen, USA).

[0363] Dilutions of transformation reactions were plated on LB-agar containing 100 μg/mL carbenicillin (Teknova, USA) to generate single colonies. Up to 96 colonies from each transformation were then grown in 96 well plates to saturation overnight at 37°C in LB-broth (Teknova cat # L8112) and a small aliquot from each well was submitted for DNA sequencing of the ECD 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.

[0364] 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 5 mL liquid LB-broth containing 100 μg/mL carbenicillin (Teknova, USA) and 2 mL of each culture were then used for preparation of approximately 10 μg of miniprep plasmid DNA of each clone using a standard kit such as the Pureyield kit (Promega). Identification of clones of interest 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 ECD 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 sequenced were processed to generate alignments using Ugene software (http://ugene.net).

[0365] Clones of interest were then identified 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 clones that have been enriched by our sorting process most likely due to improved binding.

[0366] The methods generated immunomodulatory proteins containing an ECD of CD80 or ICOSL with at least one affinity-modified domain in which the encoding DNA was generated to encode a protein designed as follows: signal peptide followed by variant (mutant) ECD followed by a linker of three alanines (AAA) followed by a human IgG1 Fc set forth in SEQ ID NO:2084 containing the mutation N297G (N82G with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 226). The human IgG1 Fc also contained the mutations R292C and V302C (corresponding to R77C and V87C with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 226). Since the construct does not include any antibody light chains that can form a covalent bond with a cysteine, the human IgG1 Fc also contained replacement of the cysteine residues to a serine residue at position 220 (C220S) by EU numbering (corresponding to position 5 (C5S) with reference 5 (C5S) compared to the wild-type or unmodified Fc set forth in SEQ ID NO: 226.

[0367] In addition, Example 8 below describes further immunomodulatory proteins that were generated as stack constructs containing at least two different affinity modified domains from identified variant CD80, CD86, ICOSL, and NKp30 molecules linked together and fused to an Fc.

Example 5

Expression and Purification of Fc-Fusions

[0368] Example 5 describes the high throughput expression and purification of Fc-fusion proteins containing variant ECD CD80, CD86, ICOSL, and NKp30 as described in the above Examples.

[0369] Recombinant variant Fc fusion proteins were produced from suspension-adapted human embryonic kidney (HEK) 293 cells using the 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 3.4mL 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% CO2. Following a 5 day incubation, cells were pelleted and culture supernatants were retained.

[0370] Proteins were purified from supernatants using a high throughput 96 well Protein A purification kit using the manufacturer's protocol (Catalog number 45202, Life Technologies, USA). Resulting elution fractions were buffer exchanged into PBS using Zeba 96 well spin desalting plate (Catalog number 89807, Life Technologies, USA) using the manufacturer's protocol. Purified protein was 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 reducing conditions and subsequent gel electrophoresis. Proteins were visualized in gel using standard Coomassie staining.

Example 6

Assessment of Binding and Activity of Affinity-Matured IgSF Domain-Containing Molecules

A. Binding to Cell Surface-Expressed Cognate Binding Partners

[0371] This Example describes Fc-fusion binding studies of purified proteins from the above Examples to assess specificity and affinity of CD80 and ICOSL domain variant immunomodulatory proteins for cognate binding partners.

[0372] To produce cells expressing cognate binding partners, full-length mammalian surface expression constructs for each of human CD28, CTLA4, PD-L1, ICOS and B7-H6 were designed in pcDNA3.1 expression vector (Life Technologies) and sourced from Genscript, USA. Binding studies were carried out using the Expi293F transient transfection system (Life Technologies, USA) described above. The number of cells needed for the experiment was determined, and the appropriate 30 mL scale of transfection was performed using the manufacturer's suggested protocol. For each CD28, CTLA-4, PD-L1, ICOS, B7-H6, or mock 30 mL transfection, 75 million Expi293F cells were incubated with 30 μg expression construct DNA and 1.5mL diluted ExpiFectamine 293 reagent for 48 hours, at which point cells were harvested for staining.

[0373] For staining by flow cytometry, 200,000 cells of appropriate transient transfection or negative control 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 staining buffer containing 100nM to 1nM variant immunomodulatory protein, depending on the experiment of each candidate CD80 variant Fc, ICOSL variant Fc, or stacked IgSF variant Fc fusion protein in 50 μl. Primary staining was performed on ice for 45 minutes, before washing cells in staining buffer twice. 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 FACScan flow cytometer (Becton Dickinson, USA).

[0374] Mean Fluorescence Intensity (MFI) was calculated for each transfectant and negative parental line with Cell Quest Pro software (Becton Dickinson, USA).

B.Bioactivity Characterization

[0375] This Example further describes Fc-fusion variant protein bioactivity characterization in human primary T cell in vitro assays.

1. Mixed Lymphocyte Reaction (MLR)

[0376] Soluble rICOSL.Fc or rCD80.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 500U/mL rIL-4 (R&D Systems, USA) and 250U/mL rGM-CSF (R&D Systems, USA) in Ex-Vivo 15 media

(Lonza, Switzerland). 10,000 matured DC and 100,000 purified allogeneic CD4+ T cells (BenTech Bio, USA) were co-cultured with ICOSL variant fusion protein, CD80 variant Fc fusion protein, or controls in 96 well round bottom plates in 200µl final volume of Ex-Vivo 15 media. 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 by VMax ELISA Microplate Reader (Molecular Devices, USA) and quantitated against titrated rIFN-gamma standard included in the IFN-gamma Duo-set kit (R&D Systems, USA).

2. Anti-CD3 Coimmobilization Assay

[0377] Costimulatory bioactivity of ICOSL fusion variants and CD80 Fc fusion variants was determined in anti-CD3 coimmobilization assays. 1nM or 4nM mouse anti-human CD3 (OKT3, Biolegends, USA) was diluted in PBS with 1nM to80nM rICOSL.Fc or rCD80.Fc variant proteins. This mixture was added to tissue culture treated flat bottom 96 well plates (Corning, USA) overnight to facilitate adherence of the stimulatory proteins to the wells of the plate. The next day, unbound protein was washed off the plates and 100,000 purified human pan T cells (BenTech Bio, US) or human T cell clone BC3 (Astarte Biologics, USA) were added to each well in a final volume of 200µL of Ex-Vivo 15 media (Lonza, Switzerland). Cells were cultured 3 days before harvesting culture supernatants and measuring human IFN-gamma levels with Duoset ELISA kit (R&D Systems, USA) as mentioned above.

C.Results

[0378] Results for the binding and activity studies for exemplary tested variants are shown in Tables 12-15. In particular, Table 12 indicates exemplary IgSF domain amino acid substitutions (replacements) in the ECD of CD80 selected in the screen for affinity-maturation against the respective cognate structure CD28. Table 13 indicates exemplary IgSF domain amino acid substitutions (replacements) in the ECD of CD80 selected in the screen for affinity-maturation against the respective cognate structure PD-L1. Table 14 indicates exemplary IgSF domain amino acid substitutions (replacements) in the ECD of ICOSL selected in the screen for affinity-maturation against the respective cognate structures ICOS and CD28. For each Table, the exemplary amino acid substitutions are designated by amino acid position number corresponding to the respective reference unmodified ECD sequence as follows. For example, the reference unmodified ECD sequence in Tables 12 and 13 is the unmodified CD80 ECD sequence set forth in SEQ ID NO:28 and the reference unmodified ECD sequence in Table 14 is the unmodified ICOSL ECD sequence (SEQ ID NO:32). 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. Column 2 sets forth the SEQ ID NO identifier for the variant ECD for each variant ECD-Fc fusion molecule.

[0379] 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 binding partner ligand and the ratio of the MFI compared to the binding of the corresponding unmodified ECD-Fc fusion molecule not containing the amino acid substitution(s) to the same cell-expressed cognate binding partner 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 ECD-Fc fusion molecule coimmoblized with anti-CD3 or ii) with the indicated variant ECD-Fc fusion molecule in an MLR assay. The Tables also depict the ratio of IFN-gamma produced by each variant ECD-Fc compared to the corresponding unmodified ECD-Fc in both functional assays.

[0380] As shown, the selections resulted in the identification of a number of CD80 or ICOSL IgSF domain variants that were affinity-modified to exhibit increased binding for at least one, and in some cases more than one, cognate binding partner 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. For example, coimmobilization of the ligand likely provides a multivalent interaction with the cell to cluster or increase the avidity to favor agonist activity and increase T cell activation compared to the unmodified (e.g. wildtype) ECD-Fc molecule not containing the amino acid replacement(s). However, when the molecule is provided as a bivalent Fc molecule in solution, the same IgSF domain variants exhibited an antagonist activity to decrease T cell activation compared to the unmodified (e.g. wildtype) ECD-Fv molecule not containing the amino acid replacement(s).

Table 12: CD80 variants selected against CD28. Molecule sequences, binding data, and costimulatory bioactivity data.

CD80 mutation(s)	SEQ ID NO	Binding	Coimmobili-zation with anti-CD3	MLR

	(ECD)	CD28 MFI (parental ratio)	CTLA-4 MFI (parental ratio)	PD-L1 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
L70Q/A91G	55	125 (1.31)	283 (1.36)	6 (0.08)	93 (1.12)	716 (0.83)
L70Q/A91G/T130A	56	96 (1.01)	234 (1.13)	7 (0.10)	99 (1.19)	752 (0.87)
L70Q/A91G/I118A/ T120S/T130A	57	123 (1.29)	226 (1.09)	7 (0.10)	86 (1.03)	741 (0.86)
V4M/L70Q/A91G/ T120S/T130A	58	89 (0.94)	263 (1.26)	6 (0.09)	139 (1.67)	991 (1.14)
L70Q/A91G/T120S/ T130A	59	106 (1.12)	263 (1.26)	6 (0.09)	104 (1.25)	741 (0.86)
V20L/L70Q/A91S/ T120S/T130A	60	105 (1.11)	200 (0.96)	9 (0.13)	195 (2.34)	710 (0.82)
S44P/L70Q/A91G/ T130A	61	88 (0.92)	134 (0.64)	5 (0.07)	142 (1.71)	854 (0.99)
L70Q/A91G/E117G/ T120S/T130A	62	120 (1.27)	193 (0.93)	6 (0.08)	98 (1.05)	736 (0.85)
A91G/T120S/ T130A	63	84 (0.89)	231 (1.11)	44 (0.62)	276 (3.33)	714 (0.82)
L70R/A91G/T120S/ T130A	64	125 (1.32)	227 (1.09)	6 (0.09)	105 (1.26)	702 (0.81)
L70Q/E81A/A91G/ T120S/I127T/ T130A	65	140 (1.48)	185 (0.89)	18 (0.25)	98 (1.18)	772 (0.89)
L70Q/Y87N/A91G/ T130A	66	108 (1.13)	181 (0.87)	6 (0.08)	136 (1.63)	769 (0.89)
T28S/L70Q/A91G/ E95K/T120S/T130A	67	32 (0.34)	65 (0.31)	6 (0.08)	120 (1.44)	834 (0.96)
N63S/L70Q/A91G/ T120S/T130A	68	124 (1.30)	165 (0.79)	6 (0.08)	116 (1.39)	705 (0.81)
K36E/I67T/L70Q/ A91G/T120S/ T130A/N152T	69	8 (0.09)	21 (0.10)	5 (0.08)	53 (0.63)	852 (0.98)
E52G/L70Q/A91G/ T120S/T130A	70	113 (1.19)	245 (1.18)	6 (0.08)	94 (1.13)	874 (1.01)
K37E/F59S/L70Q/ A91G/T120S/ T130A	71	20 (0.21)	74 (0.36)	6 (0.08)	109 (1.31)	863 (1.00)
A91G/S103P	72	39 (0.41)	56 (0.27)	9 (0.13)	124 (1.49)	670 (0.77)
K89E/T130A	73	90 (0.95)	148 (0.71)	75 (1.07)	204 (2.45)	761 (0.88)
A91G	74	96 (1.01)	200 (0.96)	85 (1.21)	220 (2.65)	877 (1.01)
D60V/A91G/T120S/ T130A	75	111 (1.17)	222 (1.07)	12 (0.18)	120 (1.44)	744 (0.86)

Table 12: CD80 variants selected against CD28. Molecule sequences, binding data, and costimulatory bioactivity data.

CD80 mutation(s)	SEQ ID NO (ECD)	Binding			Coimmobilization with anti-CD3	MLR
		CD28 MFI (parental ratio)	CTLA-4 MFI (parental ratio)	PD-L1 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
K54M/A91G/T120S	76	68 (0.71)	131 (0.63)	5 (0.08)	152 (1.83)	685 (0.79)
M38T/L70Q/E77G/ A91G/T120S/ T130A/N152T	77	61 (0.64)	102 (0.49)	5 (0.07)	119 (1.43)	796 (0.92)
R29H/E52G/L70R/ E88G/A91G/T130A	78	100 (1.05)	119 (0.57)	5 (0.08)	200 (2.41)	740 (0.85)
Y31H/T41G/L70Q/ A91G/T120S/ T130A	79	85 (0.89)	85 (0.41)	6 (0.08)	288 (3.47)	782 (0.90)
V68A/T110A	80	103 (1.08)	233 (1.12)	48 (0.68)	163 (1,96)	861 (0.99)
S66H/D90G/T110A/ F116L	81	33 (0.35)	121 (0.58)	11 (0.15)	129 (1.55)	758 (0.88)
R29H/E52G/T120S/ T130A	82	66 (0.69)	141 (0.68)	11 (0.15)	124 (1.49)	800 (0.92)
A91G/L102S	83	6 (0.06)	6 (0.03)	5 (0.08)	75 (0.90)	698 (0.81)
I67T/L70Q/A91G/ T120S	84	98 (1.03)	160 (0.77)	5 (0.08)	1751 (21.1)	794 (0.92)
L70Q/A91G/T110A/ T120S/T130A	85	8 (0.09)	14 (0.07)	5 (0.07)	77 (0.93)	656 (0.76)
M38V/T41D/M43I/ W50G/D76G/V83A/ K89E/T120S/T130A	86	5 (0.06)	8 (0.04)	8 (0.11)	82 (0.99)	671 (0.78)
V22A/L70Q/S121P	87	5 (0.06)	7 (0.04)	5 (0.07)	105 (1.27)	976 (1.13)
A12V/S15F/Y31H/ T41G/T130A/P137L/ N152T	88	6 (0.06)	6 (0.03)	5 (0.08)	104 (1.25)	711 (0.82)
I67F/L70R/E88G/ A91G/T120S/T130A	89	5 (0.05)	6 (0.03)	6 (0.08)	62 (0.74)	1003 (1.16)
E24G/L25P/L70Q/ T120S	90	26 (0.27)	38 (0.18)	8 (0.11)	101 (1.21)	969 (1.12)
A91G/F92L/F108L/ T120S	91	50 (0.53)	128 (0.61)	16 (0.11)	59 (0.71)	665 (0.77)
WT CD80	28	95 (1.00)	208 (1.00)	70 (1.00)	83 (1.00)	866 (1.00)

Table 13: CD80 variants selected against PD-L1. Molecule sequences, binding data, and costimulatory bioactivity data.

CD80 mutation(s)	SEQ ID NO (ECD)	Binding			Coimmobilization with anti-CD3	MLR
		CD28 MFI (parental ratio)	CTLA-4 MFI (parental ratio)	PD-L1 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
R29D/Y31L/Q33H/ K36G/M38I/ T41A/ M43R/M47T/E81V/ L85R/K89N/A91T/ F92P/K93V/ R94L/ I118T/N149S	92	1071 (0.08)	1089 (0.02)	37245 (2.09)	387 (0.76)	5028 (0.26)
R29D/Y31L/Q33H/ K36G/M38I/T41A/ M43R/M47T/E81V/ L85R/K89N/A91T/ F92P/K93V/R94L/ N144S/N149S	93	1065 (0.08)	956 (0.02)	30713 (1.72)	400 (0.79)	7943 (0.41)
R29D/Y31L/Q33H/ K36G/M38I/T41A/ M42T/M43R/M47T/ E81V/L85R/K89N/ A91T/F92P/K93V/ R94L/L148S/N149S	94	926 (0.07)	954 (0.02)	47072 (2.64)	464 (0.91)	17387 (0.91)
E24G/R29D/Y31L/ Q33H/K36G/M38I/ T41A/M43R/M47T/ F59L/E81V/L85R/ K89N/A91T/F92P/ K93V/R94L/H96R	95	1074 (0.08)	1022 (0.02)	1121 (0.06)	406 (0.80)	13146 (0.69)
R29D/Y31L/Q33H/ K36G/M38I/T41A/ M43R/M47T/E81V/ L85R/K89N/A91T/ F92P/K93V/R94L/ N149S	96	1018 (0.08)	974 (0.02)	25434 (1.43)	405 (0.80)	24029 (1.25)
R29V/M43Q/E81R/ L85I/K89R/D90L/ A91E/F92N/K93Q/ R94G	97	1029 (0.08)	996 (0.02)	1575 (0.09)	342 (0.67)	11695 (0.61)
T41I/A91G	98	17890 (1.35)	50624 (1.01)	12562 (0.70)	433 (0.85)	26052 (1.36)
K89R/D90K/A91G/ F92Y/K93R/N122S/ N178S	99	41687 (3.15)	49429 (0.99)	20140 (1.13)	773 (1.52)	6345 (0.33)
K89R/D90K/A91G/ F92Y/K93R	100	51663 (3.91)	72214 (1.44)	26405 (1.48)	1125 (2.21)	9356 (0.49)

Table 13: CD80 variants selected against PD-L1. Molecule sequences, binding data, and costimulatory bioactivity data.

CD80 mutation(s)	SEQ ID NO (ECD)	Binding			Coimmobilization with anti-CD3	MLR
		CD28 MFI (parental ratio)	CTLA-4 MFI (parental ratio)	PD-L1 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
K36G/K37Q/M38I/ F59L/E81V/L85R/ K89N/A91T/F92P/ K93V/R94L/E99G/ T130A/N149S	101	1298 (0.10)	1271 (0.03)	3126 (0.18)	507 (1.00)	3095 (0.16)
AE88D/K89R/D90K/ A91G/F92Y/K93R	102	31535 (2.38)	50868 (1.02)	29077 (1.63)	944 (1.85)	5922 (0.31)
K36G/K37Q/M38I/ L40M	103	1170 (0.09)	1405 (0.03)	959 (0.05)	427 (0.84)	811 (0.04)
K36G	104	29766 (2.25)	58889 (1.18)	20143 (1.13)	699 (1.37)	30558 (1.59)
WTCD80	28	13224 (1.00)	50101 (1.00)	17846 (1.00)	509 (1.00)	19211 (1.00)

Table 14: ICOSL variants selected against CD28 or ICOS. Molecule sequences, binding data, and costimulatory bioactivity data.

ICOSL mutation(s)	SEQ ID NO (ECD)	Binding		Coimmobilization with anti-CD3	MLR
		ICOS OD (parental ratio)	CD28 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
N52S	109	1.33 (1.55)	162 (9.00)	1334 (1.93)	300 (0.44)
N52H	110	1.30 (1.51)	368 (20.44)	1268 (1.83)	39 (0.06)
N52D	111	1.59 (1.85)	130 (7.22)	1943 (2.80)	190 (0.28)
N52Y/N57Y/ F138L/L203P	112	1.02 (1.19)	398 (22.11)	510* (1.47*)	18 (0.03)
N52H/N57Y/ Q100P	113	1.57 (1.83)	447 (24.83)	2199 (3.18)	25 (0.04)
N52S/Y146C/ Y152C	114	1.26 (1.47)	39 (2.17)	1647 (2.38)	152 (0.22)
N52H/C198R	115	1.16 (1.35)	363 (20.17)	744* (2.15*)	ND (ND)
N52H/C140del/ T225A	1563	ND (ND)	154 (8.56)	522* (1.51*)	ND (ND)
N52H/C198R/ T225A	117	1.41 (1.64)	344 (19.11)	778* (2.25*)	0 (0)
N52H/K92R	118	1.48	347	288*	89

Table 14: ICOSL variants selected against CD28 or ICOS. Molecule sequences, binding data, and costimulatory bioactivity data.

ICOSL mutation(s)	SEQ ID NO (ECD)	Binding		Coimmobilization with anti-CD3	MLR
		ICOS OD (parental ratio)	CD28 MFI (parental ratio)	IFN-gamma pg/mL (parental ratio)	IFN-gamma levels pg/mL (parental ratio)
		(1.72)	(19.28)	(0.83*)	(0.13)
N52H/S99G	119	0.09 (0.10)	29 (1.61)	184* (0.53*)	421 (0.61)
N52Y	120	0.08 (0.09)	18 (1.00)	184* (0.53*)	568 (0.83)
N57Y	121	1.40 (1.63)	101 (5.61)	580* (1.68*)	176 (0.26)
N57Y/Q100P	122	0.62 (0.72)	285 (15.83)	301* (0.87*)	177 (0.26)
N52S/S130G/ Y152C	123	0.16 (0.19)	24 (1.33)	266* (0.77*)	1617 (2.35)
N52S/Y152C	124	0.18 (0.21)	29 (1.61)	238* (0.69*)	363 (0.53)
N52S/C198R	125	1.80 (2.09)	82 (4.56)	1427 (2.06)	201 (0.29)
N52Y/N57Y/ Y152C	126	0.08 (0.09)	56 (3.11)	377* (1.09*)	439 (0.64)
N52Y/N57Y/ H129P/C198R	127	ND (ND)	449 (24.94)	1192 (1.72)	ND (ND)
N52H/L161P/ C198R	128	0.18 (0.21)	343 (19.05)	643* (1.86*)	447 (0.65)
N52S/T113E	129	1.51 (1.76)	54 (3.00)	451* (1.30*)	345 (0.50)
S54A	130	1.62 (1.88)	48 (2.67)	386* (1.12*)	771 (1.12)
N52S/S54P	1564	1.50 (1.74)	38 (2.11)	476* (1.38*)	227 (0.33)
N52K/L208P	132	1.91 (2.22)	291 (16.17)	1509 (2.18)	137 (0.20)
N52S/Y152H	133	0.85 (0.99)	68 (3.78)	2158 (3.12)	221 (0.32)
N52D/V151A	134	0.90 (1.05)	19 (1.06)	341* (0.99*)	450 (0.66)
N52H/I143T	135	1.83 (2.13)	350 (19.44)	2216 (3.20)	112 (0.16)
N52S/L80P	136	0.09 (0.10)	22 (1.22)	192* (0.55*)	340 (0.49)
F120S/Y152H/ N201S	137	0.63 (0.73)	16 (0.89)	351* (1.01*)	712 (1.04)
N52S/R75Q/L203P	138	1.71 (1.99)	12 (0.67)	1996 (2.88)	136 (0.20)
N52S/D158G	139	1.33 (1.55)	39 (2.17)	325* (0.94*)	277 (0.40)
N52D/Q133H	140	1.53 (1.78)	104 (5.78)	365* (1.05*)	178 (0.26)
WT ICOSL	32	0.86 (1.00)	18 (1.00)	692 / 346* (1.00)	687 (1.00)

*: Parental ratio calculated using 346 pg/mL IFN-gamma for WT ICOSL

Example 7

Ligand Binding Competition Assay

[0381] As shown in Example 6, several CD80 variant molecules exhibited improved binding to one or both of CD28 and PD-L1. To further assess the binding activity of CD80 to ligands CD28 and PD-L1, this Example describes a ligand competition assay assessing the non-competitive nature of exemplary CD80 variants to bind both CD28 and PD-L1.

[0382] An ELISA based binding assay was set up incorporating plate-bound CD80 variant A91G ECD-Fc to assess the ability of CD80 to simultaneously bind CD28 and PD-L1. Maxisorp 96 well ELISA plates (Nunc, USA) were coated overnight with 100nM human recombinant CD80 variant A91G ECD-Fc fusion protein in PBS. The following day unbound protein was washed out, and the plate was blocked with 1% bovine serum albumin (Millipore, USA)/PBS for 1 hour at room temperature. This blocking reagent was washed out three times with PBS/ 0.05% Tween, which included a two minute incubation on a platform shaker for each wash.

[0383] In one arm of the competition assay, CD80 was incubated with CD28, and then CD28-bound CD80 was then assessed for competitive binding in the presence of either the other known CD80 cognate binding partner PD-L1 or CTLA-4 or negative control ligand PD-L2. Specifically, biotinylated recombinant human CD28 Fc fusion protein (rCD28.Fc; R&D Systems) was titrated into the wells starting at 10nM, diluting out for eight points with 1:2 dilutions in 25 µL volume. Immediately after adding the biotinylated rCD28.Fc, unlabeled competitive binders, recombinant human PD-L1 monomeric his- tagged protein, recombinant human CTLA-4 monomeric his-tagged protein, or a negative control human recombinant PD-L2 Fc fusion protein (R&D Systems) were added to wells at 2000/1000/500nM respectively in 25 µL volume for a final volume of 50 µL. These proteins were incubated together for one hour before repeating the three wash steps as described above.

[0384] After washing, 2.5 ng per well of HRP-conjugated streptavidin (Jackson Immunoresearch, USA) was diluted in 1%BSA/PBS and added to wells to detect bound biotinylated rCD28.Fc. After one hour incubation, wells were washed again three times as described above. To detect signal, 50 µL of TMB substrate (Pierce, USA) was added to wells following wash and incubated for 7 minutes, before adding 50ul 2M sulfuric acid stop solution.

Optical density was determined on an Emax Plus microplate reader (Molecular Devices, USA). Optical density values were graphed in Prism (Graphpad, USA).

[0385] The results are set forth in FIG. 1A. The results showed decreased binding of biotinylated rCD28.Fc to the CD80 variant A91G ECD-Fc fusion protein with titration of the rCD28.Fc. When rCD28.Fc binding was performed in the presence of non-competitive control protein, rPDL2, there was no decrease in CD28 binding for CD80 (solid triangle). In contrast, a competitive control protein, rCTLA-4, when incubated with the CD28.Fc, did result in decreased CD28 binding for CD80 as expected (x line). When recombinant PD-L1 was incubated with CD28.Fc, no decrease in CD28 binding to CD80 was observed, which demonstrated that the epitopes of CD28 and PD-L1 for CD80 are non-competitive. Binding of the recombinant PD-L1 protein used in the CD28 competition assay to CD80 was confirmed by incubating the biotinylated PD-L1in the presence of non-biotinylated rCD28.Fc (square).

[0386] The reverse competition also was set up in which CD80 was incubated with PD-L1, and then PD-L1-bound CD80 was then assessed for competitive binding in the presence of either the other known CD80 cognate binding partners CD28 or CTLA-4 or negative control ligand PD-L2. Specifically, the assay was performed by titrating biotinylated recombinant human PD-L1-his monomeric protein into wells containing the recombinant CD80 variant. Because binding is weaker with this ligand, titrations started at 5000nM with similar 1:2 dilutions over eight points in 25 μL. When the rPD-L1-his was used to detect binding, the competitive ligands human rCD28.Fc, human rCTLA-4.Fc, or human rPD-L2.Fc control were added at 2.5nM final concentration in 25 μL for a total volume of 50 μL. The subsequent washes, detection, and OD measurements were the same as described above.

[0387] The results are set forth in FIG. 1B. Titrated PD-L1-his binding alone confirmed that PD-L1 bound to the CD80 variant A91G ECD-Fc fusion molecule immobilized on the plate (square). When PD-L1-his binding was performed in the presence of non-competitive control protein, rPDL2, there was no decrease in PD-L1 binding for CD80 (triangle). The CD28-competitive control protein, rCTLA-4, when incubated with the PD-L1-his, did not result in decreased PD-L1 binding for CD80 (x line), even though CTLA-4 is competitive for CD28. This result further demonstrated that lack of competition between CD28 and PD-L1 for CD80 binding. Finally, when PD-L1-his was incubated with CD28.Fc, no decrease in PD-L1 binding to CD80 was observed, which demonstrated that the epitopes of CD28 and PD-L1 for CD80 are non-competitive.

[0388] Thus, the results showed that CTLA-4, but not PD-L1 or the negative control PD-L2, competed for binding of CD28 to CD80 (FIG. 1A) and that CD28, CTLA-4, and PD-L2 did not compete for binding of PD-L1 to CD80 (FIG. 1B). Thus, these results demonstrated that CD28 and PD-L1 are non-competitive binders of CD80, and that this non-competitive binding can be demonstrated independently of which ligand is being detected in the ELISA.

Example 8

Generation and Assessment of Stacked Molecules Containing Different Affinity-Modified Domains

[0389] Selected variant molecules described above that were affinity-modified for one or more cognate binding partners were used to generate "stack" molecule (i.e., Type II immunomodulatory protein) containing two or more affinity-modified IgSF domains. Stack constructs were obtained as geneblocks (Integrated DNA Technologies, Coralville, IA) that encode the stack in a format that enables its fusion to Fc by standard Gibson assembly using a Gibson assembly kit (New England Biolabs). As above, this example exemplifies binding and activity of a molecule containing the affinity-modified domains in an Fc-fusion format; such stack molecules containing two or more affinity-modified domains are contemplated in connection with a secretable immunomodulatory protein or transmembrane immunomodulatory protein as described.

[0390] The encoding nucleic acid molecule of all stacks was generated to encode a protein designed as follows: Signal peptide, followed by the first variant IgV of interest, followed by a 15 amino acid linker which is composed of three GGGGS(G4S) motifs (SEQ ID NO:228), followed by the second IgV of interest, followed by two GGGGS linkers (SEQ ID NO: 229) followed by three alanines (AAA), followed by a human IgG1 Fc as described above. To maximize the chance for correct folding of the IgV domains in each stack, the first IgV was preceded by all residues that normally occur in the wild-type protein between this IgV and the signal peptide (leading sequence). Similarly, the first IgV was followed by all residues that normally connect it in the wild-type protein to either the next Ig domain (typically an IgC domain) or if such a second IgV domain is absent, the residues that connect it to the transmembrane domain (trailing sequence). The same design principle was applied to the second IgV domain except that when both IgV domains were derived from same parental protein (e.g. a CD80 IgV stacked with another CD80 IgV), the linker between both was not duplicated.

[0391] Table 15 sets forth the design for exemplary stacked constructs. The exemplary stack molecules shown in Table 15 contain the IgV domains as indicated and additionally leading or trailing sequences as described above. In the Table, the following components are present in order: signal peptide (SP; SEQ ID NO:225), IgV domain 1 (IgV1), trailing sequence 1 (TS1), linker 1 (LR1; SEQ ID NO:228), IgV domain 2(IgV2), trailing sequence 2 (TS2), linker 2 (LR2; SEQ ID NO:230) and Fc domain (SEQ ID NO:226 containing C5S/N82G amino acid substitution). In some cases, a leading sequence 1(LS1) is present between the signal peptide and IgV1 and in some cases a leading sequence 2 (LS2) is present between the linker and IgV2.

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs

	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
NKp30 WT ICOSL WT	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	+
NKp30 L30V/A60V/S64P/ S86G ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	-	SEQ ID NO: 212	SEQ ID NO: 233	+	+
NKp30 L30V/A60V/S64P/ S86G) ICOSL N52D	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	+
NKp30 L30V/A60V/S64P/ S86G ICOSL N52H/N57Y/Q100 P	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+
ICOSL WT Nkp30 WT	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	+
ICOSL N52D NKp30 L30V/A60V/S64P/ S86G	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	+
ICOSL N52H/N57Y/Q100 P NKp30 L30V/A60V/S64P/ S86G	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
Domain 1: NKp30 WT Domain 2: CD80 WT	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	+
Domain 1: NKp30 WT Domain 2: CD86 WT	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	+
Domain 1: NKp30 L30V/A60V/S64P/ S86G Domain 2: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+
Domain 1: NKp30 L30V/A60V/S64P/ S86G Domain 2: CD80 I67T/L70Q/A91G/ T120S	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	+
Domain 1: NKp30 L30V/A60V/S64P/ S86G Domain 2: CD86 Q35H/H90L/Q102 H	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+
Domain 1: CD80 WT Domain 2: Nkp30 WT	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	+
Domain 1: CD86 WT Domain 2: Nkp30 WT	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	-	SEQ ID NO: 214	SEQ ID NO: 235	+	+
Domain 1: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S Domain 2: NKp30 L30V/A60V/S64P/ S86G	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	+
Domain 1: CD80 I67T/L70Q/A91G/	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
T120S Domain 2: NKp30 L30V/A60V/S64P/ S86G										
Domain 1: CD86 Q35H/H90L/Q102 H Domain 2: NKp30 L30V/A60V/S64P/ S86G	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	-	SEQ ID NO: 215	SEQ ID NO: 235	+	+
Domain 1: CD80 WT Domain 2: ICOSL WT	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	+
Domain 1: CD80 WT Domain 2: CD86 WT	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	+
Domain 1: CD80 WT Domain 2: CD80 WT	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	+
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: CD80 I67T/L70Q/A91G/	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
T120S										
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: CD86 Q35H/H90L/Q102 H	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: CD86 Q35H/H90L/Q102 H	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: ICOSL N52D	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	+
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: ICOSL N52H/N57Y/Q100 P	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: ICOSL	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
N52H/N57Y/Q100P										
Domain 1: ICOSL WT Domain 2: CD80 WT	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	+
Domain 1: CD86 WT Domain 2: CD80 WT	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	-	SEQ ID NO: 152	SEQ ID NO: 231	+	+
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: CD86 Q35H/H90L/Q102H Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: CD86	+	SEQ	SEQ ID	SEQ ID	+	-	SEQ ID	SEQ ID	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
Q35H/H90L/Q102H Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T		ID NO: 236	NO: 221	NO: 237			NO: 193	NO: 231		
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52D Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52D Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
Domain 1: CD80 V68M/L70P/L72P/ K86E Domain 2: CD80 E88D/K89R/D90K /A91G/F92Y/K93R	+	-	SEQ ID NO: 195	SEQ ID NO: 231	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: CD80 R29V/Y31F/K36G/ M38L/M43Q/E81R /V83I/L85I/K89R/ D90L/A91E/F92N/ K93Q/R94G Domain 2: CD80 E88D/K89R/D90K /A91G/F92Y/K93R	+	-	SEQ ID NO: 194	SEQ ID NO: 231	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	+
Domain 1: CD80 V68M/L70P/L72P/ K86E Domain 2: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T	+	-	SEQ ID NO: 195	SEQ ID NO: 231	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: CD80 R29V/Y31F/K36G/ M38L/M43Q/E81R /V83I/L85I/K89R/ D90L/A91E/F92N/ K93Q/R94G Domain 2: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T	+	-	SEQ ID NO: 194	SEQ ID NO: 231	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	+
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: CD80 V68M/L70P/L72P/ K86E	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	-	SEQ ID NO: 195	SEQ ID NO: 231	+	+
Domain 1: CD80 E88D/K89R/D90K /A91G/F92Y/K93R Domain 2: CD80 R29V/Y31F/K36G/ M38L/M43Q/E81R /V83I/L85I/K89R/ D90L/A91E/F92N/ K93Q/R94G	+	-	SEQ ID NO: 189	SEQ ID NO: 231	+	-	SEQ ID NO: 194	SEQ ID NO: 231	+	+
Domain 1: CD80 A12T/H18L/M43V	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 195	SEQ ID NO: 231	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
/F59L/E77K/P109S /I118T Domain 2: CD80 V68M/L70P/L72P/ K86E										
Domain 1: CD80 A12T/H18L/M43V /F59L/E77K/P109S /I118T Domain 2: CD80 R29V/Y31F/K36G/ M38L/M43Q/E81R /V83I/ L85I/K89R/D90L/ A91E/F92N/K93Q/ R94G	+	-	SEQ ID NO: 193	SEQ ID NO: 231	+	-	SEQ ID NO: 194	SEQ ID NO: 231	+	+
Domain 1: CD86 WT Domain 2: ICOSL WT	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	+
Domain 1: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S Domain 2: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	+
Domain 1: CD80 I67T/L70Q/A91G/ T120S Domain 2: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	+
Domain 1: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S Domain 2: ICOSL N52D	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	+
Domain 1: CD80 I67T/L70Q/A91G/ T120S	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
Domain 2: ICOSL N52D										
Domain 1: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E /D90N/A91G/P109 S Domain 2: ICOSL N52H/N57Y/Q100 P	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+
Domain 1: CD80 I67T/L70Q/A91G/ T120S Domain 2: ICOSL N52H/N57Y/Q100 P	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+
Domain 1: CD86 Q35H/H90L/Q102 H Domain 2: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	+
Domain 1: CD86 Q35H/H90L/Q102 H Domain 2: ICOSL N52D	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	+
Domain 1: CD86 Q35H/H90L/Q102 H Domain 2: ICOSL N52H/N57Y/Q100 P	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	+
Domain 1: ICOSL WT Domain 2: CD86 WT	+	-	SEQ ID NO: 196	SEQ ID NO: 233	+	SEQ ID NO: 236	SEQ ID NO: 220	SEQ ID NO: 237	+	+
Domain 1: ICOSL N52S/N57Y/H94D /L96F/L98F/Q100 R/G103E/ F120S Domain 2: CD80 R29H/Y31H/T41G /Y87N/E88G/K89E	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
/D90N/A91G/P109S										
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S Domain 2: CD80 I67T/L70Q/A91G/T120S	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52D Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52D Domain 2: CD80 I67T/L70Q/A91G/T120S	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	-	SEQ ID NO: 175	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	-	SEQ ID NO: 192	SEQ ID NO: 231	+	+
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S Domain 2: CD86 Q35H/H90L/Q102H	+	-	SEQ ID NO: 213	SEQ ID NO: 233	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+
Domain 1: ICOSL N52D Domain 2: CD86 Q35H/H90L/Q102H	+	-	SEQ ID NO: 199	SEQ ID NO: 233	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD86 Q35H/H90L/Q102	+	-	SEQ ID NO: 201	SEQ ID NO: 233	+	SEQ ID NO: 236	SEQ ID NO: 221	SEQ ID NO: 237	+	+

Table 15: Amino acid sequence (SEQ ID NO) of components of exemplary stacked constructs										
	SP	First domain			LR1	Second domain			LR2	Fc
		LS1	IgV1	TS1		LS2	IgV2	TS2		
H										

[0392] High throughput expression and purification of the variant IgV-stacked-Fc fusion molecules containing various combinations of variant IgV domains from CD80, CD86, ICOSL or NKp30 containing at least one affinity-modified IgV domain were generated as described in Example 5. Binding of the variant IgV-stacked-Fc fusion molecules to respective cognate binding partners and functional activity by anti-CD3 coimmobilization assay also were assessed as described in Example 6. For example, costimulatory bioactivy of the stacked IgSF Fc fusion proteins was determined in a similar immobilized anti-CD3 assay as above. In this case, 4nM of anti-CD3 (OKT3, Biolegend, USA) was coimmobilized with 4nM to 120nM of human rB7-H6.Fc (R&D Systems, USA) or human rPD-L1.Fc (R&D Systems, USA) overnight on tissue-culture treated 96 well plates (Corning, USA). The following day unbound protein was washed off with PBS and 100,000 purified pan T cells were added to each well in 100ul Ex-Vivo 15 media (Lonza, Switzerland). The stacked IgSF domains were subsequently added at concentrations ranging from 8nM to 40nM in a volume of 100ul for 200ul volume total. Cells were cultured 3 days before harvesting culture supernatants and measuring human IFN-gamma levels with Duoset ELISA kit (R&D Systems, USA) as mentioned above.

[0393] The results are set forth in Tables 16-20. Specifically, Table 16 sets forth binding and functional activity results for variant IgV-stacked-Fc fusion molecules containing an NKp30 IgV domain and an ICOSL IgV domain. Table 17 sets forth binding and functional activity results for variant IgV-stacked-Fv fusion molecules containing an NKp30 IgV domain and a CD80 or CD86 IgV domain. Table 18 sets forth binding and functional activity results for variant IgV-stacked-Fc fusion molecules containing a variant CD80 IgV domain and a CD80, CD86 or ICOSL IgV domain. Table 19 sets forth binding and functional activity results for variant IgV-stacked-Fc fusion molecules containing two variant CD80 IgV domains. Table 20 sets forth results for variant IgV-stacked Fc fusion molecules containing a variant CD80 or CD86 IgV domain and a variant ICOSL IgV domain.

[0394] For each of Tables 16-20, Column 1 indicates the structural organization and orientation of the stacked, affinity modified or wild-type (WT) domains beginning with the amino terminal (N terminal) domain, followed by the middle WT or affinity modified domain located before the C terminal human IgG1 Fc domains. Column 2 sets forth the SEQ ID NO

identifier for the sequence of each IgV domain contained in a respective "stack" molecule. Column 3 shows the binding partners which the indicated affinity modified stacked domains from column 1 were selected against.

[0395] Also shown is the binding activity as measured by the Mean Fluorescence Intensity (MFI) value for binding of each stack molecule to cells engineered to express various cognate binding partners and the ratio of the MFI compared to the binding of the corresponding stack molecule containing unmodified IgV domains not containing the amino acid substitution(s) to the same cell-expressed cognate binding partner. The functional activity of the variant stack 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 with the indicated variant stack molecule in solution and the appropriate ligand coimmoblized with anti-CD3 as described in Example 6. The Tables also depict the ratio of IFN-gamma produced by each variant stack molecule compared to the corresponding unmodified stack molecule in the coimmobilization assay.

[0396] As shown, the results showed that it was possible to generate stack molecules containing at least one variant IgSF domains that exhibited affinity-modified activity of increased binding for at least one cognate binding partner compared to a corresponding stack molecule containing the respective unmodified (e.g. wild-type) IgV domain. In some cases, the stack molecule, either from one or a combination of both variant IgSF domains in the molecule, exhibited increased binding for more than one cognate binding partner. The results also showed that the order of the IgV domains in the stacked molecules could, in some cases, alter the degree of improved binding activity. In some cases, functional T cell activity also was altered when assessed in the targeted coimmobilization assay.

TABLE 16: Stacked variant IgV Fc fusion proteins containing an NKp30 IgV domain and an ICOSL IgV domain

Domain Structure N terminal to C terminal: domain 1/domain 2/Fc	SEQ ID NO (IgV)	cognate binding partner selected against	Binding Activity			Anti-CD3 coimmobilization assay
			B7H6 MFI (WT parental MFI ratio)	ICOS MFI (WT parental MFI ratio)	CD28 MFI (WT parental MFI ratio)	pg/mL IFN-gamma (WT parental IFN-gamma ratio)
Domain 1: NKp30 WT Domain 2: ICOSL WT	214 196	-	64538 (1.00)	26235 (1.00)	6337 (1.00)	235 (1.00)
Domain 1: NKp30 (L30V A60V S64P S86G)	215	B7-H6	59684 (0.92)	12762 (0.49)	9775 (1.54)	214 (0.91)

Domain 2: ICOSL (N52S N57Y H94D L96F L98F Q100R)	212	ICOS-CD28				
Domain 1: NKp30 (L30V A60V S64P S86G) Domain 2: ICOSL (N52D)	215 199	B7-H6 ICOS-CD28	65470 (1.01)	30272 (1.15)	9505 (1.50)	219 (0.93)
Domain 1: NKp30 (L30V A60V S64P S86G)/ Domain 2: ICOSL (N52H N57Y Q100P)	215 201	B7-H6 ICOS-CD28	38153 (0.59)	27903 (1.06)	11300 (1.78)	189 (0.80)
Domain 1: ICOSL WT Domain 2: Nkp30 WT	196 214	-	117853 (1.0)	70320 (1.0)	7916 (1.0)	231 (1.0)
Domain 1:ICOSL (N52D) Domain 2: NKp30 (L30V A60V S64P S86G)	199 215	ICOS-CD28 B7-H6	100396 (0.85)	83912 (1.19)	20778 (2.62)	228 (0.98)
Domain 1: ICOSL (N52H N57Y Q100P) Domain 2: NKp30 (L30V A60V S64P S86G)	201 215	ICOS-CD28 B7-H6	82792 (0.70)	68874 (0.98)	72269 (9.12)	561 (2.43)

TABLE 17: Stacked variant IgV Fc fusion proteins containing an NKp30 IgV domain and a CD80 or CD86 IgV domain

Domain Structure **N terminal to C terminal:** **domain 1/domain 2/Fc**	**SEQ ID NO (IgV)**	**cognate binding partner selected against**	**Binding Activity**		**Anti-CD3 coimmobilization assay** **pg/mL IFN-gamma** **(WT parental IFN-gamma ratio)**
			B7H6 MFI **(WT parental MFI ratio)**	**CD28 MFI** **(WT parental MFI ratio)**	
Domain 1: NKp30 WT Domain 2: CD80 WT	214 152	-	88823 (1.00)	7022 (1.00)	68 (1.00)
Domain 1: NKp30 WT Domain 2: CD86 WT	214 220	-	14052 (1.00)	1690 (1.00)	92 (1.00)
Domain 1: NKp30 (L30V A60V S64P S86G) Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	215 192	B7-H6 CD28	53279 (0.60)	9027 (1.29)	94 (1.38)
Domain 1: NKp30 (L30V (A60V/S64P/S86G) Domain 2: CD80 (I67T/L70Q/A91G/T120S)	215 175	B7-H6 CD28	41370 (0.47)	11240 (1.60)	60 (0.88)
Domain 1: NKp30 (L30V	215	B7-H6	68480	9115	110

(A60V/S64P/S86G) Domain 2: CD86 (Q35H/H90L/Q102H)	221	CD28	(4.87)	(5.39)	(1.19)
Domain 1: CD80 WT Domain 2: Nkp30 WT	152 214	-	110461 (1.00)	13654 (1.00)	288 (1.00)
Domain 1: CD86 WT Domain 2: Nkp30 WT	220 214	CD28 B7-H6	128899 (1.00)	26467 (1.00)	213 (1.00)
Domain 1: CD80 (R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S) Domain 2: NKp30 (L30V/A60V/S64P.S86G)	192 215	CD28 B7-H6	55727 (0.50)	4342 (0.32)	100 (0.35)
Domain 1: CD80 (I67T/L70Q/A91G/T120S) Domain 2: NKp30 (L30V/A60V/S64P/S86G)	175 215	CD28 B7-H6	40412 (0.37)	7094 (0.52)	84 (0.29)
Domain 1: CD86 (Q35H/H90L/Q102H) Domain 2: NKp30 (L30V/A60V/S64P/S86G)	221 215	CD28 B7-H6	220836 (1.71)	11590 (0.44)	113 (0.53)

TABLE 18: Stacked variant IgV Fc fusion proteins containing a CD80 IgV domain and a CD80, CD86, or ICOSL IgV domain

Domain Structure **N terminal to C terminal:** **domain 1/domain 2/Fc**	**SEQ ID NO** **(IgV)**	**cognate binding partner selected against**	**Binding Activity**			**Anti-CD3 coimmobilization assay** **pg/mL IFN-gamma** **(WT parental IFN-gamma ratio)**
			CD28 MFI **(WT parental MFI ratio)**	**PD-L1 MFI** **(WT parental MFI ratio)**	**ICOS MFI** **(WT parental MFI ratio)**	
Domain 1: CD80 WT Domain 2: ICOSL WT	152 196		1230 (1.00)	2657 (1.00)	11122 (1.00)	69 (1.00)
Domain 1: CD80 WT Domain 2: CD86 WT	152 220		60278 (1.00)	2085 (1.00)		59 (1.00)
Domain 1: CD80 WT Domain 2: CD80 WT	152 152		1634 (1.00)	6297 (1.00)		98 (1.00)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	189 192	PD-L1 CD28	4308 (2.64)	4234 (0.67)		214 (2.18)

Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	193 192	PD-L1 CD28	7613 (4.66)	2030 (0.32)		137 (1.40)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: CD80 I67T/L70Q/A91G/T120S	193 175	PD-L1 CD28	3851 (2.36)	3657 (0.58)		81 (0.83)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: CD86 Q35H/H90L/Q102H	189 221	PD-L1 CD28	4117 (0.07)	2914 (1.40)		96 (1.63)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: CD86 Q35H/H90L/Q102H	193 221	PD-L1 CD28	2868 (0.05)	3611 (1.73)		94 (1.60)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S	189 213	PD-L1 ICOS/CD28	3383 (2.75)	4515 (1.70)	5158 (0.46)	90 (1.30)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S	193 213	PD-L1 ICOS/CD28	2230 (1.81)	2148 (0.81)	3860 (0.35)	112 (1.62)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: ICOSL N52D	193 199	PD-L1 ICOS/CD28	5665 (4.61)	6446 (2.43)	15730 (1.41)	126 (1.83)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: ICOSL N52H/N57Y/Q100P	189 201	PD-L1 ICOS/CD28	6260 (5.09)	4543 (1.71)	11995 (1.08)	269 (3.90)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	193	PD-L1	3359 (2.73)	3874 (1.46)	8541 (0.77)	97 (1.41)

Domain 2: ICOSL N52H/N57Y/Q100P	201	ICOS/CD 28				
Domain 1: ICOSL WT Domain 2: CD80 WT	196 152		3000 (1.00)	2966 (1.00)	14366 (1.00)	101 (1.00)
Domain 1: CD86 WT Domain 2: CD80 WT	220 152		4946 (1.00)	1517 (1.00)		125 (1.00)
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	192 189	CD28 PD-L1	2832 (1.73)	3672 (0.58)		114 (1.16)
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	192 193	CD28 PD-L1	4542 (2.78)	2878 (0.45)		142 (1.45)
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	175 189	CD28 PD-L1	938 (0.57)	995 (0.16)		102 (1.04)
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	175 193	CD28 PD-L1	4153 (2.54)	2827 (0.45)		108 (1.10)
Domain 1: CD86 Q35H/H90L/Q102H Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	221 189	CD28 PD-L1	14608 (2.95)	2535 (1.67)		257 (2.06)
Domain 1: CD86 Q35H/H90L/Q102H Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	221 193	CD28 PD-L1	2088 (0.42)	2110 (1.39)		101 (0.81)
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/F120S Domain 2: CD80 E88D/K89R/D90K/A91G/F92Y/K93R	213 189	ICOS/CD 28 PD-L1	3634 (1.21)	4893 (1.65)	6403 (0.45)	123 (1.22)
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L9	213	ICOS/CD 28	1095 (0.37)	5929 (2.0)	7923 (0.55)	127 (1.26)

8F/Q100R/G103E/ F120S Domain 2: CD80 A12T/H18L/M43V/F59L/E7 7K/P109S/I118T	 193	 PD-L1				
Domain 1: ICOSL N52D Domain 2: CD80 E88D/K89R/D90K/A91G/F9 2Y/K93R	199 189	ICOSL/C D28 PD-L1	 2023 (0.67)	 5093 (1.72)	 16987 (1.18)	 125 (1.24)
Domain 1: ICOSL N52D Domain 2: CD80 A12T/H18L/M43V/F59L/E7 7K/P109S/I118T	199 193	ICOS/CD 28 PD-L1	 3441 (1.15)	 3414 (1.15)	 20889 (1.45)	 165 (1.63)
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 E88D/K89R/D90K/A91G/F9 2Y/K93R	201 189	ICOS/CD 28 PD-L1	 7835 (2.61)	 6634 (2.24)	 20779 (1.45)	 95 (0.94)
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 A12T/H18L/M43V/F59L/E7 7K/P109S/I118T	201 193	ICOS/CD 28 PD-L1	 8472 (2.82)	 3789 (1.28)	 13974 (0.97)	 106 (1.05)

TABLE 19: Stacked variant IgV Fc fusion proteins containing two CD80 IgV domains

Domain Structure **N terminal to C terminal:** **domain 1/domain 2/Fc**	**SEQ ID NO** **(IgV)**	**Cognate binding partner selected against**	**Binding Activity**		**Functional Activity MLR IFN-gamma pg/mL**
			PD-L1 MFI **(WT parental MFI ratio)**	**CTLA-4 MFI** **(WT parental MFI ratio)**	
Domain 1: CD80 WT Domain 2: CD80 WT	152 152		6297 (1.00)	4698 (1.00)	35166 (1.00)
Domain 1: CD80 V68M/L70P/L72P/K86E Domain 2: CD80 E88D/K89R/D90K/A91G/F9 2Y/K93R	195 189	CTLA-4 PD-L1	 2464 (0.39)	 4955 (1.05)	 5705 (0.16)
Domain 1: CD80 R29V/Y31F/K36G/M38L/M 43Q/E81R/V83I/L85I/K89R/ D90L/A91E/F92N/K93Q/R9 4G Domain 2: CD80 E88D/K89R/D90K/A91G/F9 2Y/K93R	194 189	CTLA-4 PD-L1	 1928 (0.31)	 1992 (0.42)	 1560 (0.04)

Domain 1: CD80 V68M/L70P/L72P/K86E Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	195 193	CTLA-4 PD-L1	1215 (0.19)	1382 (0.29)	2171 (0.06)
Domain 1: CD80 R29V/Y31F/K36G/M38L/M43Q/E81R/V83I/L85I/K89R/D90L/A91E/F92N/K93Q/R94G Domain 2: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T	194 193	CTLA-4 PD-L1	1592 (0.25)	1962 (0.42)	1512 (0.04)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: CD80 V68M/L70P/L72P/K86E	189 195	PD-L1 CTLA-4	1747 (0.28)	2057 (0.44)	9739 (0.28)
Domain 1: CD80 E88D/K89R/D90K/A91G/F92Y/K93R Domain 2: CD80 R29V/Y31F/K36G/M38L/M43Q/E81R/V83I/L85I/K89R/D90L/A91E/F92N/K93Q/R94G	189 194	PD-L1 CTLA-4	1752 (0.28)	1772 (0.38)	5412 (0.15)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: CD80 V68M/L70P/L72P/K86E	193 195	PD-L1 CTLA-4	1636 (0.26)	1887 (0.40)	7608 (0.22)
Domain 1: CD80 A12T/H18L/M43V/F59L/E77K/P109S/I118T Domain 2: CD80 R29V/Y31F/K36G/M38L/M43Q/E81R/V83I/L85I/K89R/D90L/A91E/F92N/K93Q/R94G	193 194	PD-L1 CTLA-4	2037 (0.32)	4822 (1.03)	11158 (0.32)

TABLE 20: Stacked variant IgV Fc fusion proteins containing a CD80 or CD86 IgV domain and an ICOSL IgV domain

Domain Structure **N terminal to C terminal:** **domain 1/domain 2/Fc**	**SEQ ID NO** **(IgV)**	**Cognate binding partner selected against**	**Binding Activity**		**Functional Activity MLR IFN-gamma pg/mL**
			PD-L1 MFI **(WT parental MFI ratio)**	**CTLA-4 MFI** **(WT parental MFI ratio)**	
Domain 1: CD80 WT	152		1230 (1.00)	11122 (1.00)	1756 (1.00)

Domain 2: ICOSL WT	196				
Domain 1: CD86 WT Domain 2: ICOSL WT	220 196		29343 (1.00)	55193 (1.00)	6305 (1.00)
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S	192 213	CD28 ICOS/CD28	2280 (1.85)	3181 (0.29)	2281 (1.30)
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S	175 213	CD28 ICOS/CD28	2309 (1.88)	26982 (2.43)	1561 (0.89)
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: ICOSL N52D	192 199	CD28 ICOS/CD28	4285 (3.48)	22744 (2.04)	1612 (0.92)
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: ICOSL N52D	175 199	CD28 ICOS/CD28	3024 (2.46)	16916 (1.52)	3857 (2.20)
Domain 1: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S Domain 2: ICOSL N52H/N57Y/Q100P	192 201	CD28 ICOS/CD28	6503 (5.29)	7240 (0.65)	6886 (3.92)
Domain 1: CD80 I67T/L70Q/A91G/T120S Domain 2: ICOSL N52H/N57Y/Q100P	175 201	CD28 ICOS/CD28	3110 (2.53)	4848 (0.44)	3393 (1.93)
Domain 1: CD86 Q35H/H90L/Q102H Domain 2: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S	221 213	CD28 ICOS/CD28	11662 (0.40)	21165 (0.38)	880 (0.14)
Domain 1: CD86 Q35H/H90L/Q102H Domain 2: ICOSL N52D	221 199	CD28 ICOS/CD28	24230 (0.83)	73287 (1.33)	1110 (0.18)
Domain 1: CD86 Q35H/H90L/Q102H	221	CD28 ICOS/CD	1962 (0.07)	1630 (0.03)	587 (0.09)

Domain 2: ICOSL N52H/N57Y/Q100P	201	28			
Domain 1: ICOSL WT Domain 2: CD80 WT	196 152		3000 (1.00)	14366 (1.00)	4113 (1.00)
Domain 1: ICOSL WT Domain 2: CD86 WT	196 220		18005 (1.00)	53602 (1.00)	18393 (1.00)
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	213 192	ICOSL/CD28 CD28	10426 (3.48)	51286 (3.57)	18680 (4.54)
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S Domain 2: CD80 I67T/L70Q/A91G/T120S	213 175	ICOS/CD28 CD28	17751 (5.92)	29790 (2.07)	10637 (2.59)
Domain 1: ICOSL N52D Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	199 192	ICOS/CD28 CD28	2788 (0.93)	25870 (1.80)	6205 (1.51)
Domain 1: ICOSL N52D Domain 2: CD80 I67T/L70Q/A91G/T120S	199 175	ICOS/CD28 CD28	2522 (0.84)	13569 (0.94)	5447 (1.32)
Domain 1: ICOSL N52H/N57Y/Q100P Domain 2: CD80 R29H/Y31H/T41G/Y87N/E88G/K89E/D90N/A91G/P109S	201 192	ICOS/CD28 CD28	9701 (3.23)	9187 (0.64)	5690 (1.38)
Domain 1: ICOSL N52S/N57Y/H94D/L96F/L98F/Q100R/G103E/ F120S Domain 2: CD86 Q35H/H90L/Q102H	213 221	ICOS/CD28 CD28	27050 (1.50)	21257 (0.40)	8131 (0.44)
Domain 1: ICOSL N52D Domain 2: CD86 Q35H/H90L/Q102H	199 221	ICOS/CD28 CD28	34803 (1.93)	80210 (1.50)	6747 (0.37)
Domain 1: ICOSL N52H/N57Y/Q100P	201	ICOS/CD28	5948 (0.33)	4268 (0.08)	26219 (1.43)

Domain 2: CD86 Q35H/H90L/Q102H	221	CD28			

Example 9

Generation, Selection and Screening of Affinity-modified IgSF Domain Variants of CD155

[0397] Affinity-modified IgSF domain variants of CD155 were generated substantially as described in Examples 1-6 above with some slight modifications. For example, for the generation of CD155 variants, only the IgV domain, and not the other two domains of the ECD, was included in the generated proteins. The example exemplifies binding and activity of the exemplary affinity-modified domains in an Fc-fusion format; such affinity-modified domains are contemplated in connection with a secretable immunomodulatory protein or transmembrane immunomodulatory protein as described.

[0398] To generate a library targeting specific residues of CD155 by complete or partial randomization with degenerate codons, the coding DNA for the immunoglobulin-like V-type (IgV) domain of human CD155 (SEQ ID NO:241) was ordered from Integrated DNA Technologies (Coralville, IA) as a set of overlapping oligonucleotides of up to 80 base pairs (bp) in length. In general, to generate a library of diverse variants of the IgV domain, the oligonucleotides contained desired degenerate codons at desired amino acid positions. Degenerate codons were generated using an algorithm at the URL: rosettadesign.med.unc.edu/SwiftLib/. In general, positions to mutate and degenerate codons were chosen from crystal structure information (PDB: 3UDW) or homology models built from this structure containing the target-ligand pairs of interest to identify ligand contact residues as well as residues that are at the protein interaction interface. For example, a crystal structure of CD155 bound to TIGIT is publicly available at the URL: www.rcsb.org/pdb/explore/explore.do?structureId=3UDW for Protein Data Base code 3UDW. This analysis was performed using a structure viewer available at the URL: spdbv.vital-it.ch).

[0399] The oligonucleotides were used for PCR amplification to generate library DNA inserts for insertion into the modified yeast display version of vector pBYDS03 substantially as described in Example 1. 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 incorporated 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. The library of DNA inserts were prepared for library insertion substantially as descried in Example 1 and electroporation-ready DNA was prepared.

[0400] As alternative approaches, either sublibraries generated by site-directed mutagenesis to target specific residues of the IgV domain of CD155 or random libraries of the IgV domain of CD155 were generated to further identify variants of the IgV domain of CD155 substantially as described in Example 1.

[0401] The degenerate or random library DNA was inserted into yeast substantially as described in Example 2. Yeast expressing affinity modified variants of CD155 were selected using the method substantially described in Example 3. For the selection, the following target ligand proteins were employed: human rTIGIT.Fc (i.e., recombinant TIGIT-Fc fusion protein) and rCD226.Fc. Magnetic Protein A beads were obtained from New England Biolabs, USA. For two-color, flow cytometric sorting, a Bio-Rad S3e sorter was used. CD155 display levels were monitored with an anti-hemagglutinin antibody labeled with Alexafluor 488 (Life Technologies, USA). Ligand binding of Fc fusion proteins, rTIGIT.Fc or rCD226.Fc, were 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.

[0402] Second sort outputs (F2) were obtained substantially as described in Example 3 by expanding and re-inducing expression of sort outputs that had been assayed for higher specific binding affinity and were used to assess binding compared to the parental, wild-type yeast strain. For CD155, the second FACS outputs (F2) were compared to parental CD155 yeast for binding rTIGIT.Fc or rCD226.Fc by double staining each population with anti-HA (hemagglutinin) tag expression and the anti-human Fc secondary to detect ligand binding.

[0403] Selected outputs were reformatted as immunomodulatory proteins containing an affinity modified (variant) immunoglobulin-like V-type (IgV) domain of CD155 fused to an Fc molecule (variant IgV domain -Fc fusion molecules) substantially as described in Example 4, except including only the IgV domain and not the full ECD domain. In some alternative methods for the CD155 outputs, DNA from the outputs were PCR amplified with primers containing 40 bp overlap regions on either end with an 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).

[0404] After transformation, samples were prepared for DNA sequencing substantially as described in Example 4. The sequences were then manually curated as described in Example 4, except that they were manually curated so that they start at the beginning of the IgV coding region. The curated sequences were batch-translated and aligned as described in Example 4. Clones of interest were identified using the criteria as described in Example 4. Table 21 sets forth the identified variant CD155 affinity-modified molecules, including the amino acid substitutions contained in each variant.

[0405] The methods generated immunomodulatory proteins containing an affinity-modified IgV domain of CD155 in which the encoding DNA was generated to encode a protein as follows: signal peptide followed by variant (mutant) IgV domain followed by a linker of three alanines (AAA) followed by a human IgG1 Fc containing the mutation N297G (N82G with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 226). The human IgG1 Fc also contained the mutations R292C and V302C by EU numbering (corresponding to R77C and V87C with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 226). Since the construct does not include any antibody light chains that can form a covalent bond with a cysteine, the human IgG1 Fc also contained 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: 226.

[0406] Recombinant variant CD155 Fc fusion proteins were expressed and purified substantially as described in Example 5. Binding and activity of the affinity-modified variant CD155 Fc fusion proteins was assessed substantially as described in Example 6, except that cells expressing full length human CD226 and TIGIT cognate binding partners were generated. Cells were stained by flow cytometry with CD155 Fc variant and mean fluorescence intensity (MFI) was determined as described in Example 5. For bioactivity characterization, recombinant CD155 Fc variants were assessed in an anti-CD3 coimmobilization assay substantially as described in Example 5.

[0407] The results for the binding and activity studies are set forth in Table 21. The Table indicates exemplary IgSF domain amino acid substitutions (replacements) in the IgV domain of CD155 selected in the screen for affinity-maturation against the respective cognate structures

TIGIT and CD226. The exemplary amino acid substitutions are designated by amino acid position number corresponding to position of the unmodified sequence set forth in SEQ ID NO: 241 (IgV). 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. Column 2 sets forth the SEQ ID NO identifier for the variant for each variant ECD-Fc fusion molecule.

[0408] 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 binding partner as the ratio of the MFI compared to the binding of the corresponding unmodified ECD-Fc fusion molecule not containing the amino acid substitution(s) to the same cell-expressed cognate binding partner. 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 with the indicated variant Fc fusion molecule coimmoblized with anti-CD3 as a ratio of IFN-gamma produced by each variant CD155 IgV-Fc compared to the corresponding unmodified CD155 IgV-Fc in both functional assays.

TABLE 21: CD155 variants 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	653	497825 (133.7)	247219 (91.1)	140065 (45.4)	3528 (1.2)	270.1 (0.7)
P18S, F91S, L104P	654	26210 (7.0)	75176 (27.7)	10867 (3.5)	2130 (0.7)	364.2 (0.9)
L44P	655	581289 (156.1)	261931 (96.5)	152252 (49.4)	3414 (1.2)	277.6 (0.7)
A56V	656	455297 (122.3)	280265 (103.2)	161162 (52.2)	2601 (0.9)	548.2 (1.4)
P18L, L79V, F91S	657	5135 (1.4)	4073 (1.5)	3279 (1.1)	2719 (0.9)	1241.5 (3.2)
P18S, F91S	658	408623 (109.8)	284190 (104.7)	147463 (47.8)	3348 (1.1)	760.6 (2.0)
P18T, F91S	659	401283 (107.8)	223985 (82.5)	157644 (51.1)	3065 (1.1)	814.7 (2.1)
P18T, S42P, F91S	660	554105 (148.8)	223887 (82.5)	135395 (43.9)	3796 (1.3)	539.7 (1.4)
G7E, P18T, Y30C, F91S	661	12903 (3.5)	12984 (4.8)	7906 (2.6)	2671 (0.9)	275.9 (0.7)
P18T, F91S, G111D	662	438327	287315	167583	4012	307.2

TABLE 21: CD155 variants 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)
		(117.7)	(105.8)	(54.3)	(1.4)	(0.8)
P18S, F91P	663	4154 (1.1)	3220 (1.2)	2678 (0.9)	2816 (1.0)	365.7 (0.9)
P18T, F91S, F108L	664	394546 (106.0)	298680 (110.0)	193122 (62.6)	2926 (1.0)	775.4 (2.0)
P18T, T45A, F91S	665	435847 (117.1)	222044 (81.8)	191026 (61.9)	2948 (1.0)	1546.8 (4.0)
P18T, F91S, R94H	666	3589 (1.0)	2942 (1.1)	2509 (0.8)	2390 (0.8)	1273.2 (3.3)
P18S, Y30C, F91S	667	382352 (102.7)	276358 (101.8)	56934 (18.5)	3540 (1.2)	426.5 (1.1)
A81V, L83P	668	4169 (1.1)	2912 (1.1)	2616 (0.8)	2993 (1.0)	339.7 (0.9)
L88P	669	65120 (17.5)	74845 (27.6)	35280 (11.4)	2140 (0.7)	969.2 (2.5)
Wild type	652	3723 (1.0)	2715 (1.0)	3085 (1.0)	2913 (1.0)	389.6 (1.0)
R94H	670	18905 (5.1)	104013 (38.3)	11727 (3.8)	1663 (0.6)	372.6 (1.0)
A13E, P18S, A56V, F91S	671	357808 (96.1)	179060 (66.0)	118570 (38.4)	2844 (1.0)	349.2 (0.9)
P18T, F91S, V115A	672	38487 (10.3)	46313 (17.1)	22718 (7.4)	2070 (0.7)	1574.5 (4.0)
P18T, Q60K	673	238266 (64.0)	173730 (64.0)	154448 (50.1)	4778 (1.6)	427.2 (1.1)

Example 10

Generation, Selection and Screening of Affinity-modified IgSF Domain Variants of CD112

[0409] Affinity-modified IgSF domain variants of CD112 were generated substantially as described in Examples 1-6 above with some slight modifications. For example, for the generation of CD112 variants, only the IgV domain, and not the other two domains of the ECD, was included in the generated proteins. The example exemplifies binding and activity of the exemplary affinity-modified domains in an Fc-fusion format; such affinity-modified domains are contemplated in connection with a secretable immunomodulatory protein or transmembrane immunomodulatory protein as described.

[0410] To generate a library targeting specific residues of CD155 by complete or partial randomization with degenerate codons, the coding DNA for the immunoglobulin-like V-type

(IgV) domain of human CD112 (SEQ ID NO:286) was ordered from Integrated DNA Technologies (Coralville, IA) as a set of overlapping oligonucleotides of up to 80 base pairs (bp) in length. In general, to generate a library of diverse variants of the IgV domain, the oligonucleotides contained desired degenerate codons at desired amino acid positions. Degenerate codons were generated using an algorithm at the URL: rosettadesign.med.unc.edu/SwiftLib/. In general, positions to mutate and degenerate codons were chosen from crystal structure information (PDB: 3UDW) or homology models built from this structure containing the target-ligand pairs of interest to identify ligand contact residues as well as residues that are at the protein interaction interface.

[0411] The oligonucleotides were used for PCR amplification to generate library DNA inserts for insertion into the modified yeast display version of vector pBYDS03 substantially as described in Example 1. 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 incorporated 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. The library of DNA inserts were prepared for library insertion substantially as descried in Example 1 and electroporation-ready DNA was prepared.

[0412] As alternative approaches, either sublibraries generated by site-directed mutagenesis to target specific residues of the IgV domain of CD112 or random libraries of the IgV domain of CD112 were generated to further identify variants of the IgV domain of CD112 substantially as described in Example 1.

[0413] The degenerate or random library DNA was inserted into yeast substantially as described in Example 2. Yeast expressing affinity modified variants of CD112 were selected using the method substantially described in Example 3. For the selection, the following target ligand proteins were employed: human rTIGIT.Fc (i.e., recombinant TIGIT-Fc fusion protein), rCD226.Fc and rCD112R.Fc. Magnetic Protein A beads were obtained from New England Biolabs, USA. For two-color, flow cytometric sorting, a Bio-Rad S3e sorter was used. CD112 display levels were monitored with an anti-hemagglutinin antibody labeled with Alexafluor 488 (Life Technologies, USA). Ligand binding of Fc fusion proteins, rTIGIT.Fc, rCD226.Fc, or

rCD112R.Fc, were 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.

[0414] Second sort outputs (F2) were obtained substantially as described in Example 3 by expanding and re-inducing expression of sort outputs that had been assayed for higher specific binding affinity and were used to assess binding compared to the parental, wild-type yeast strain. For CD112, the second FACS outputs (F2) were compared to parental CD112 yeast for binding of each rTIGIT.Fc, rCD226.Fc, and rCD112R by double staining each population with anti-HA (hemagglutinin) tag expression and the anti-human Fc secondary to detect ligand binding.

[0415] Selected outputs were reformatted as immunomodulatory proteins containing an affinity modified (variant) immunoglobulin-like V-type (IgV) domain of CD112 fused to an Fc molecule (variant IgV domain -Fc fusion molecules) substantially as described in Example 4, except including only the IgV domain and not the full ECD domain. In some alternative methods for the CD112 outputs, DNA from the outputs were PCR amplified with primers containing 40 bp overlap regions on either end with an 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).

[0416] After transformation, samples were prepared for DNA sequencing substantially as described in Example 4. The sequences were then manually curated as described in Example 4, except that they were manually curated so that they start at the beginning of the IgV coding region. The curated sequences were batch-translated and aligned as described in Example 4. Clones of interest were identified using the criteria as described in Example 4. Table 22 sets forth the identified variant CD112 affinity-modified molecules, including the amino acid substitutions contained in each variant.

[0417] The methods generated immunomodulatory proteins containing an affinity-modified IgV domain of CD112 in which the encoding DNA was generated to encode a protein as follows: signal peptide followed by variant (mutant) IgV domain followed by a linker of three alanines (AAA) followed by a human IgG1 Fc containing the mutation N297G (N82G with reference to wild-type human IgG1 Fc set forth in SEQ ID NO: 226). The human IgG1 Fc also contained the mutations R292C and V302C (corresponding to R77C and V87C with reference to

wild-type human IgG1 Fc set forth in SEQ ID NO: 226). Since the construct does not include any antibody light chains that can form a covalent bond with a cysteine, the human IgG1 Fc also 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: 226.

[0418] Recombinant variant CD112 Fc fusion proteins were expressed and purified substantially as described in Example 5. Binding and activity of the affinity-modified variant CD112 Fc fusion proteins was assessed substantially as described in Example 6, except that cells expressing full length human CD226, TIGIT and CD112R cognate binding partners were generated. Cells were stained by flow cytometry with CD112 Fc variant and mean fluorescence intensity (MFI) was determined as described in Example 5. For bioactivity characterization, recombinant CD112 Fc variants were assessed in an anti-CD3 coimmobilization assay substantially as described in Example 5.

[0419] The results for the binding and activity studies are set forth in Table 22. The Table indicates exemplary IgSF domain amino acid substitutions (replacements) in the IgV domain of CD112 selected in the screen for affinity-maturation against the respective cognate structures TIGIT, CD226 and CD112R. The exemplary amino acid substitutions are designated by amino acid position number corresponding to position of the unmodified sequence set forth in SEQ ID NO: 286. 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. Column 2 sets forth the SEQ ID NO identifier for the variant ECD for each variant IgV-Fc fusion molecule.

[0420] 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 binding partner as the ratio of the MFI compared to the binding of the corresponding unmodified IgV-Fc fusion molecule not containing the amino acid substitution(s) to the same cell-expressed cognate binding partner. 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 with the indicated variant Fc fusion molecule coimmoblized with anti-CD3 as a ratio of IFN-gamma produced by each variant CD112 IgV-Fc compared to the corresponding unmodified CD112 IgV-Fc in both functional assays.

TABLE 22: CD112 variants selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.

CD112 mutations	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	965	210829 (1.00)	1452 (1.00)	265392 (1.00)	1112 (1.00)	676.6 (1.00)
Y33H, A112V, G117D	966	12948 (0.06)	1552 (1.07)	1368 (0.01)	1241 (1.12)	164.8 (0.24)
V19A, Y33H, S64G, S80G, G98S, N106Y, A112V	967	48356 (0.23)	1709 (1.18)	2831 (0.01)	1098 (0.99)	
L32P, A112V	968	191432 (0.91)	1557 (1.07)	11095 (0.04)	1259 (1.13)	390.4 (0.58)
A95V, A112I	969	238418 (1.13)	1706 (1.17)	51944 (0.20)	1215 (1.09)	282.5 (0.42)
P28S, A112V	970	251116 (1.19)	1985 (1.37)	153382 (0.58)	1189 (1.07)	503.4 (0.74)
P27A, T38N, V101A, A112V	971	255803 (1.21)	2138 (1.47)	222822 (0.84)	1399 (1.26)	240.7 (0.36)
S118F	972	11356 (0.05)	5857 (4.03)	6938 (0.03)	1270 (1.14)	271.7 (0.40)
R12W, H48Y, F54S, S118F	973	10940 (0.05)	3474 (2.39)	5161 (0.02)	1069 (0.96)	
R12W, Q79R, S118F	974	2339 (0.01)	7370 (5.08)	1880 (0.01)	1338 (1.20)	447.4 (0.66)
T113S, S118Y	975	6212 (0.03)	6823 (4.70)	1554 (0.01)	1214 (1.09)	225.1 (0.33)
S118Y	976	2921 (0.01)	6535 (4.50)	2003 (0.01)	1463 (1.32)	190.4 (0.28)
N106I, S118Y	977	2750 (0.01)	7729 (5.32)	1815 (0.01)	1222 (1.10)	265.8 (0.39)
N106I, S118F	978	1841 (0.01)	9944 (6.85)	1529 (0.01)	1308 (1.18)	437.9 (0.65)
A95T, L96P, S118Y	979	2352 (0.01)	4493 (3.09)	1412 (0.01)	1329 (1.19)	292.4 (0.43)
Y33H, P67S, N106Y, A112V	980	225015 (1.07)	3259 (2.24)	204434 (0.77)	1296 (1.17)	618.8 (0.91)
N106Y, A112V	981	6036 (0.03)	1974 (1.36)	15334 (0.06)	1108 (1.00)	409.9 (0.61)
T18S, Y33H, A112V	982	252647 (1.20)	1347 (0.93)	183181 (0.69)	1412 (1.27)	601.8 (0.89)
P9S, Y33H, N47S, A112V	983	240467 (1.14)	1418 (0.98)	203608 (0.77)	1361 (1.22)	449.1 (0.66)
P42S, P67H, A112V	984	204484 (0.97)	1610 (1.11)	188647 (0.71)	1174 (1.06)	530.6 (0.78)
P27L, L32P, P42S, A112V	985	219883 (1.04)	1963 (1.35)	84319 (0.32)	1900 (1.71)	251.6 (0.37)
G98D, A112V	986	4879 (0.02)	2369 (1.63)	6100 (0.02)	1729 (1.55)	387.0 (0.57)
Y33H, S35P, N106Y, A112V	987	250724 (1.19)	1715 (1.18)	94373 (0.36)	1495 (1.34)	516.2 (0.76)
L32P, P42S, T100A, A112V	988	242675 (1.15)	1742 (1.20)	202567 (0.76)	1748 (1.57)	435.3 (0.64)

TABLE 22: CD112 variants selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.

CD112 mutations	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)
P27S, P45S, N106I, A112V	989	223557 (1.06)	1799 (1.24)	84836 (0.32)	1574 (1.42)	277.5 (0.41)
Y33H, N47K, A112V	990	251339 (1.19)	1525 (1.05)	199601 (0.75)	1325 (1.19)	483.2 (0.71)
Y33H, N106Y, A112V	991	297169 (1.41)	1782 (1.23)	258315 (0.97)	1440 (1.30)	485.4 (0.72)
K78R, D84G, A112V, F114S	992	236662 (1.12)	1638 (1.13)	24850 (0.09)	1345 (1.21)	142.5 (0.21)
Y33H, N47K, F54L, A112V	993	14483 (0.07)	1617 (1.11)	2371 (0.01)	1353 (1.22)	352.8 (0.52)
Y33H, A112V	994	98954 (0.47)	1216 (0.84)	1726 (0.01)	1298 (1.17)	
A95V, A112V	995	168521 (0.80)	2021 (1.39)	200789 (0.76)	1459 (1.31)	412.9 (0.61)
R12W, A112V	996	135635 (0.64)	1582 (1.09)	23378 (0.09)	1412 (1.27)	165.8 (0.24)
A112V	1002	213576 (1.01)	1986 (1.37)	151900 (0.57)	1409 (1.27)	211.4 (0.31)
Y33H, A112V	994	250667 (1.19)	1628 (1.12)	230578 (0.87)	1216 (1.09)	612.7 (0.91)
R12W, P27S, A112V	997	3653 (0.02)	1308 (0.90)	9105 (0.03)	1051 (0.94)	
Y33H, V51M, A112V	998	218698 (1.04)	1384 (0.95)	195450 (0.74)	1170 (1.05)	709.4 (1.05)
Y33H, A112V, S118T	999	219384 (1.04)	1566 (1.08)	192645 (0.73)	1313 (1.18)	396.3 (0.59)
Y33H, V101A, A112V, P115S	1000	5605 (0.03)	1582 (1.09)	5079 (0.02)	1197 (1.08)	
H24R, T38N, D43G, A112V	1001	227095 (1.08)	1537 (1.06)	229311 (0.86)	1336 (1.20)	858.6 (1.27)
A112V	1002	4056 (0.02)	1356 (0.93)	10365 (0.04)	986 (0.89)	
P27A, A112V	1003	193537 (0.92)	1531 (1.05)	230708 (0.87)	3084 (2.77)	355.1 (0.52)
A112V, S118T	1004	233173 (1.11)	1659 (1.14)	121817 (0.46)	845 (0.76)	533.3 (0.79)
R12W, A112V, M122I	1005	235935 (1.12)	1463 (1.01)	217748 (0.82)	1350 (1.21)	528.0 (0.78)
Q83K, N106Y, A112V	1006	205948 (0.98)	2042 (1.41)	234958 (0.89)	1551 (1.39)	481.4 (0.71)
R12W, P27S, A112V, S118T	1007	11985 (0.06)	2667 (1.84)	12756 (0.05)	1257 (1.13)	334.4 (0.49)
P28S, Y33H, A112V	1008	4711 (0.02)	1412 (0.97)	3968 (0.01)	955 (0.86)	
P27S, Q90R, A112V	1009	3295 (0.02)	1338 (0.92)	6755 (0.03)	1048 (0.94)	
L15V, P27A, A112V, S118T	1010	209888 (1.00)	1489 (1.03)	84224 (0.32)	1251 (1.13)	512.3 0.76)

TABLE 22: CD112 variants selected against cognate binding partners. Molecule sequences, binding data, and costimulatory bioactivity data.						
CD112 mutations	**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	1011	Not tested				
Y33H, P56L, V75M, V101M, A112V	1012	Not tested				

Example 11

Additional Affinity Modified IgSF Domains

[0421] This examples describe the design, creation, and screening of additional affinity modified CD80, CD155, CD112, PD-L1, PD-L2, 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. Also described are generation and screening of Nkp30 variants. 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 fused in pairs (i.e., stacked) with a variant affinity modified CD80 to form a Type II immunomodulatory protein to achieve immunomodulatory activity. The example exemplifies binding and activity of the exemplary affinity-modified domains in an Fc-fusion format; such affinity-modified domains are contemplated in connection with a secretable immunomodulatory protein or transmembrane immunomodulatory protein as described.

[0422] Mutant DNA constructs of encoding a variant of the IgV domain of human CD80, CD155, CD112, PD-L1, PD-L2, CD86 (B7-2), and NKp30 for translation and expression as yeast display libraries were generated substantially as described in Example 1. For 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:578), IgV of CD112 (SEQ ID NO: 965), CD155(SEQ ID NO: 652), PD-L1 (SEQ ID NO:1332), and variants of the IgV of PD-L2 (SEQ ID NO:1393) substantially as described in Example 1. Similar methods also were used to generate libraries of the IgC-like domain of NKp30 (SEQ ID NO:1566).

[0423] 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, CD155, CD112, PD-L1, PD-L2, CD86 (B7-2), and NKp30 substantially as described in Example 3. Cells were processed to reduce non-binders and to enrich for CD80, CD155, CD112, PD-L1 or PD-L2 variants with the ability to bind their exogenous recombinant counter-structure proteins substantially as described in Example 3.

[0424] 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.

[0425] 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).

[0426] 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.

[0427] For CD155 variants provided in Table 23A-E, 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.

[0428] For additional CD112 variants provided in Table 24A-B, 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.

[0429] For PD-L1 and PD-L2 variants provided in Table 25 and 26A-B, yeast display targeted or random PD-L1 or 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. Alternatively, for PD-L1, 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. 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.

[0430] For CD80 variants provided in Tables 27A-B, CD80 libraries consisted of positive selection with the desired counter structure CTLA4 and negative selection with the counter structure CD28.

[0431] Exemplary selection outputs were reformatted as immunomodulatory proteins containing an affinity modified (variant) IgV of CD80, variant IgV of CD155, variant IgV of CD112, variant IgV of PD-L1, variant IgV of PD-L2, each fused to an Fc molecule (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. In some cases, Fc-fusion proteins were generated containing: affinity-modified IgSF domain followed by a GSGGGGS linker followed by a human IgG1 Fc containing the mutations L234A, L235E, G237A, E356D and M358L by EU numbering (SEQ ID NO:2153).

[0432] Binding of exemplary IgSF domain variants to cell-expressed counter structures (cognate binding partners) 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.

[0433] As above, for each Table, the exemplary amino acid substitutions are designated by amino acid position number corresponding to the respective reference unmodified ECD s (see Table 1). 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.

[0434] 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 PD-L2 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 with the indicated variant Fc fusion molecule in an MLR assay. Table 26B also depicts the ratio of IFN-gamma produced by each variant IgV-Fc compared to the corresponding unmodified IgV-Fc in an MLR assay.

[0435] As shown, the selections resulted in the identification of a number of CD80, CD155, CD112, PD-L1, and PD-L2 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.

TABLE 23A: 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
S52M	868	1865.3	0.00	1901.0	0.01	1553.4	0.87	1609.8	0.02
T45Q, S52L, L104E, G111R	869	2287.0	0.01	2390.4	0.01	1735.1	0.97	1575.1	0.02
S42G	879	4837.5	0.01	2448.1	0.01	1815.4	1.02	1699.6	0.02
Q62F	871	2209.5	0.01	2572.1	0.01	2706.5	1.52	2760.7	0.03
S52Q	872	2288.1	0.01	2022.3	0.01	1790.1	1.00	1822.3	0.02
S42A, L104Q, G111R	873	1923.7	0.00	1901.7	0.01	1815.1	1.02	1703.8	0.02
S42A, S52Q, L104Q, G111R	874	1807.5	0.00	2157.2	0.01	1894.4	1.06	1644.0	0.02
S52W, L104E	875	1938.2	0.00	1905.6	0.01	2070.6	1.16	1629.5	0.02

TABLE 23A: 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
S42C	876	1914.0	0.00	2096.1	0.01	1685.0	0.95	1592.4	0.02
S52W	877	1991.6	0.00	2037.3	0.01	1612.8	0.90	1712.9	0.02
S52M, L104Q	878	2666.6	0.01	2252.2	0.01	1706.0	0.96	1633.1	0.02
S42L, S52L, Q62F, L104Q	879	2021.4	0.00	2643.8	0.02	1730.1	0.97	2318.7	0.02
S42W	880	2434.5	0.01	2133.4	0.01	2325.7	1.30	2555.4	0.03
S42Q	881	2073.5	0.00	2225.9	0.01	1905.1	1.07	2143.1	0.02
S52L	882	2224.8	0.01	2676.3	0.02	2038.6	1.14	2043.2	0.02
S52R	883	4395.4	0.01	3964.4	0.02	2741.7	1.54	4846.9	0.05
L104E	884	3135.4	0.01	2264.2	0.01	1803.5	1.01	1556.7	0.02
G111R	885	2082.7	0.00	2791.3	0.02	2470.9	1.39	3317.1	0.03
S52E	886	2655.4	0.01	2599.8	0.02	1904.9	1.07	1799.0	0.02
Q62Y	887	2528.6	0.01	2621.4	0.02	1918.4	1.08	1827.5	0.02
T45Q, S52M, L104E	888	79498.2	0.19	143238.5	0.83	2600.6	1.46	6310.4	0.06
S42N, L104Q, G111R	889	2432.1	0.01	2311.3	0.01	1847.4	1.04	1958.3	0.02
S52M, V57L	890	1760.7	0.00	2431.6	0.01	2006.9	1.13	1858.7	0.02
S42N, S52Q, Q62F	891	2402.7	0.01	2152.0	0.01	1855.0	1.04	1737.6	0.02
S42A, S52L, L104E, G111R	892	2262.7	0.01	1889.4	0.01	1783.2	1.00	1606.2	0.02
S42W, S52Q, V57L, Q62Y	893	1961.4	0.00	2138.3	0.01	1844.9	1.03	1699.6	0.02
L104Q	894	10314.4	0.02	3791.4	0.02	2119.9	1.19	1542.6	0.02
S42L, S52Q, L104E	895	1946.9	0.00	6474.3	0.04	1749.0	0.98	1702.2	0.02
S42C, S52L	896	1762.5	0.00	2147.3	0.01	1663.4	0.93	1484.7	0.01
S42W, S52R, Q62Y, L104Q	897	1918.8	0.00	2300.1	0.01	1824.6	1.02	1756.0	0.02
T45Q, S52R, L104E	898	121636.9	0.29	142381.2	0.82	2617.9	1.47	3748.2	0.04
S52R, Q62F, L104Q, G111R	899	2969.2	0.01	3171.6	0.02	1725.4	0.97	2362.3	0.02
T45Q, S52L, V57L, L104E	900	2857.7	0.01	5943.5	0.03	1496.8	0.84	1533.3	0.02
S52M, Q62Y	901	1926.6	0.00	2000.3	0.01	1771.6	0.99	1651.1	0.02
Q62F, L104E, G111R	902	1966.4	0.00	2043.5	0.01	1701.9	0.95	1524.8	0.02
T45Q, S52Q	903	4812.8	0.01	5787.5	0.03	1765.6	0.99	2451.3	0.02
S52L, L104E	904	4317.8	0.01	2213.9	0.01	1756.9	0.99	1829.3	0.02
S42V, S52E	905	2055.0	0.00	2272.6	0.01	1808.0	1.01	2530.2	0.03
T45Q, S52R, G111R	906	4092.3	0.01	2075.2	0.01	1793.6	1.01	2336.6	0.02
S42G, S52Q, L104E, G111R	907	2010.1	0.00	2019.2	0.01	1706.4	0.96	1707.6	0.02
S42N, S52E, V57L,	908	1784.2	0.00	1743.6	0.01	1690.1	0.95	1538.7	0.02

TABLE 23A: 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
L104E									
Wildtype	652	1964.7	0.00	2317.1	0.01	2169.6	1.22	1893.4	0.02
S42C, S52M, Q62F	909	1861.0	0.00	2084.2	0.01	1592.3	0.89	1481.3	0.01
S42L	910	1930.4	0.00	2187.2	0.01	1743.2	0.98	1618.4	0.02
Wildtype	652	2182.6	0.01	2374.5	0.01	1743.1	0.98	1680.4	0.02
S42A	911	1929.2	0.00	2188.6	0.01	1733.7	0.97	1623.6	0.02
S42G, S52L, Q62F, L104Q	912	1924.3	0.00	2157.6	0.01	1661.3	0.93	1642.1	0.02
S42N	913	1817.4	0.00	1910.9	0.01	1699.7	0.95	1691.5	0.02
CD155 IgV Fc	652 (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 23B: 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	914	297843	1.99	351195	3.22	128180	1.68
P18F, T39A, T45Q, T61R, S65N, S67L, E73G, R78G	915	Little to no protein produced					
P18T, T45Q, T61R, S65N, S67L	916	224682	1.50	270175	2.48	22820	0.30
P18F, S65A, S67V, F91S	917	534106	3.57	350410	3.21	144069	1.89
P18F, T45Q, T61R, S65N, S67L, F91S, L104P	918	Little to no protein produced					
P18S, L79P, L104M	919	342549	2.29	320823	2.94	107532	1.41
P18S, L104M	920	449066	3.00	295126	2.70	121266	1.59
L79P, L104M	921	3210	0.02	8323	0.08	2894	0.04
P18T, T45Q, L79P	922	542878	3.63	371498	3.40	193719	2.55
P18T, T45Q, T61R, S65H, S67H	923	312337	2.09	225439	2.07	152903	2.01
P18T, A81E	924	Little to no protein produced					
P18S, D23Y, E37P, S52G, Q62M, G80S, A81P, G99Y, S112N	925	Little to no protein produced					
A13R, D23Y, E37P, S42P, Q62Y, A81E	926	4161	0.03	11673	0.11	5762	0.08

TABLE 23B: 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
A13R, D23Y, E37P, G99Y, S112N	927	Little to no protein produced					
A13R, D23Y, E37P, Q62M, A77V, G80S, A81P, G99Y	928	Little to no protein produced					
P18L, E37S, Q62M, G80S, A81P, G99Y, S112N	929	5900	0.04	14642	0.13	3345	0.04
P18S, L104T	930	321741	2.15	367470	3.37	108569	1.43
P18S, Q62H, L79Q, F91S	931	283357	1.89	324877	2.98	125541	1.65
P18S, F91S	658	222780	1.49	300049	2.75	48542	0.64
T45Q, S52K, Q62F, L104Q, G111R	932	Little to no protein produced					
T45Q, S52Q, Q62Y, L104Q, G111R	933	Little to no protein produced					
T45Q, S52Q, Q62Y, L104E, G111R	934	Little to no protein produced					
V57A, T61M, S65W, S67A, E96D, L104T	935	Little to no protein produced					
P18L, V57T, T61S, S65Y, S67A, L104T	936	278178	1.86	276870	2.54	121499	1.60
P18T, T45Q	937	326769	2.18	357515	3.28	92389	1.21
P18L, V57A, T61M, S65W, S67A, L104T	938	Little to no protein produced					
T61M, S65W, S67A, L104T	939	360915	2.41	417897	3.83	148954	1.96
P18S, V41A, S42G, T45G, L104N	940	3821	0.03	11449	0.10	3087	0.04
P18H, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104N	941	5066	0.03	177351	1.63	3700	0.05
P18S, S42G, T45V, F58L, S67W, L104N	942	14137	0.09	15175	0.14	15324	0.20
P18S, T45I, L104N	943	141745	0.95	298011	2.73	97246	1.28
P18S, S42G, T45G, L104N, V106A	944	29387	0.20	117965	1.08	15884	0.21
P18H, H40R, S42G, T45I, S52T, G53R, S54H, V57L, H59E, T61S, S65D, E68G, L104Y, V106L, F108H	945	12335	0.08	14657	0.13	15779	0.21
E37V, S42G, T45G, L104N	946	Little to no protein produced					
P18S, T45Q, L79P, L104T	947	206674	1.38	285512	2.62	87790	1.15
P18L, Q62R	948	66939	0.45	25063	0.23	10928	0.14
A13R, D23Y, E37P, S42L, S52G, Q62Y, A81E	949	Little to no protein produced					
P18L, H49R, L104T, D116N	950	167980	1.12	214677	1.97	62451	0.82

TABLE 23B: 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
A13R, D23Y, E37P, Q62M, G80S, A81P, L104T	951	Little to no protein produced					
S65T, L104T	952	205942	1.38	187147	1.71	65207	0.86
A13R, D23Y, E37P, S52G, V57A, Q62M, K70E, L104T	953	Little to no protein produced					
P18L, A47V, Q62Y, E73D, L104T	954	146142	0.98	248926	2.28	73956	0.97
H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, D97G, E98S, L104T, D116N	955	Little to no protein produced					
P18L, S42P, T45Q, T61G, S65H, S67E, L104T, D116N	956	153536	1.03	402503	3.69	53044	0.70
P18S, H40T, V41M, A47V, S52Q, Q62L, S65T, E73R, L104M, V106A	957	Little to no protein produced					
H40T, V41M, A47V, S52Q, Q62L, S65T, E68G, E73R, D97G, E98S, L104T	958	Little to no protein produced					
T45Q, S52E, L104E	959	Little to no protein produced					
T45Q, S52E, Q62F, L104E	960	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 23C: 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	961	117327	1.2	1613	0.1	1629	0.1
P18S, T45S, T61K, S65W, S67A, F91S, G111R	962	124936	1.3	2114	0.1	2223	0.1
P18S, L79P, L104M, T107M	963	110512	1.1	18337	0.9	22793	1.3
P18S, S65W, S67A, M90V, V95A, L104Q, G111R	964	101726	1.0	1605	0.1	2571	0.1
Wildtype CD155-ECD	47 (ECD)	98935	1.0	20029	1.0	17410	1.0

TABLE 23D: 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	1678	56,409	1.19	1,191	0.08	25,362	1.49
P18T, D23G, S24A, N35D, H49L, L79P, F91S, L104M, G111R	1679	128,536	2.72	987	0.06	3,497	0.20
V9L, P18S, Q60R, V75L, L79P, R89K, F91S, L104E, G111R	1680	125,329	2.65	986	0.06	959	0.06
P18S, H49R, E73D, L79P, N85D, F91S, V95A, L104M, G111R	1681	Little to no protein produced					
V11A, P18S, L79P, F91S, L104M, G111R	1682	48,246	1.02	974	0.06	923	0.05
V11A, P18S, S54R, Q60P, Q62K, L79P, N85D, F91S, T107M	1683	190,392	4.02	1,019	0.07	1,129	0.07
P18T, S52P, S65A, S67V, L79P, F91S, L104M, G111R	1684	121,611	2.57	986	0.06	16,507	0.97
P18T, M36T, L79P, F91S, G111R	1685	150,015	3.17	1,029	0.07	2,514	0.15
D8G, P18S, M36I, V38A, H49Q, A76E, F91S, L104M, T107A, R113W	1686	79,333	1.68	1,026	0.07	2,313	0.14
P18S, S52P, S65A, S67V, L79P, F91S, L104M, T107S, R113W	1687	23,766	0.50	1,004	0.07	1,080	0.06
T15I, P18T, L79P, F91S, L104M, G111R	1688	55,498	1.17	1,516	0.10	1,030	0.06
P18F, T26M, L44V, Q62K, L79P, E82D, F91S, L104M, G111D	1689	213,640	4.51	991	0.06	1,276	0.07
P18T, E37G, G53R, Q62K, L79P, F91S, E98D, L104M, T107M	1690	251,288	5.31	2,001	0.13	45,878	2.69
P18L, K70E, L79P, F91S, V95A, G111R	1691	62,608	1.32	1,117	0.07	973	0.06
V9I, Q12K, P18F, S65A, S67V, L79P, L104T, G111R, S112I	1692	81,932	1.73	803	0.05	68,295	4.00
P18F, S65A, S67V, F91S, L104M, G111R	1693	30,661	0.65	901	0.06	3,193	0.19

TABLE 23D: 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
V9I, V10I, P18S, F20S, T45A, L79P, F91S, L104M, F108Y, G111R, S112V	1694	151,489	3.20	973	0.06	974	0.06
V9L, P18L, L79P, M90I, F91S, T102S, L104M, G111R	1695	155,279	3.28	910	0.06	10,568	0.62
P18C, T26M, L44V, M55I, Q62K, L79P, F91S, L104M, T107M	1696	137,521	2.91	973	0.06	111,085	6.51
V9I, P18T, D23G, L79P, F91S, G111R	1697	151,426	3.20	897	0.06	2,725	0.16
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1698	125,639	2.66	917	0.06	3,939	0.23
P18F, L79P, M90L, F91S, V95A, L104M, G111R	1698	115,156	2.43	1,073	0.07	2,464	0.14
P18T, M36T, S65A, S67E, L79Q, A81T, F91S, G111R	1699	10,616	0.22	1,130	0.07	963	0.06
V9L, P18T, Q62R, L79P, F91S, L104M, G111R	1700	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	-	2,298	0.05	1,133	0.07	996	0.06

TABLE 23E: 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	1819	905	0.02	748	0.02	1276	1.56	726	0.01
V9L, P18L, M55V, S69L, L79P, A81E, F91S, T107M	1820	58656	1.34	11166	0.29	920	1.13	67364	1.39
P18F, H40Q, T61K, Q62K, L79P, F91S, L104M, T107V	1821	108441	2.48	853	0.02	918	1.13	8035	0.17

TABLE 23E: 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
P18S, Q32R, Q62K, R78G, L79P, F91S, T107A, R113W	1822	5772	0.13	701	0.02	843	1.03	831	0.02
Q12H, P18T, L21S, G22S, V57A, Q62R, L79P, F91S, T107M	1823	1084	0.02	687	0.02	876	1.07	818	0.02
V9I, P18S, S24P, H49Q, F58Y, Q60R, Q62K, L79P, F91S, T107M	1824	69926	1.60	1089	0.03	1026	1.26	43856	0.90
P18T, W46C, H49R, S65A, S67V, A76T, L79P, S87T, L104M	1825	918	0.02	640	0.02	803	0.98	717	0.01
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1826	12630	0.29	707	0.02	857	1.05	1050	0.02
P18S, S42T, E51G, L79P, F91S, G92W, T107M	1826	7476	0.17	851	0.02	935	1.15	924	0.02
V10F, T15S, P18L, R48Q, L79P, F91S, T107M, V115M	1827	1168	0.03	792	0.02	901	1.10	998	0.02
P18S, L21M, Y30F, N35D, R84W, F91S, T107M, D116G	1828	1377	0.03	743	0.02	946	1.16	1033	0.02
P18F, E51V, S54G, Q60R, L79Q, E82G, S87T, M90I, F91S, G92R, T107M	1829	46090	1.05	15701	0.41	1012	1.24	61814	1.27
Q16H, P18F, F91S, T107M	1830	Little to no protein produced							
P18T, D23G, Q60R, S67L, L79P, F91S, T107M, V115A	1831	64091	1.47	30931	0.81	874	1.07	108875	2.24
D8G, V9I, V11A, P18T, T26M, S52P, L79P, F91S, G92A, T107L, V115A	1832	52508	1.20	9483	0.25	817	1.00	97770	2.01
V9I, P18F, A47E, G50S, E68G, L79P, F91S, T107M	1833	55167	1.26	54341	1.43	752	0.92	102115	2.10
P18S, M55I, Q62K, S69P, L79P, F91S, T107M	1834	Little to no protein produced							
P18T, T39S, S52P, S54R, L79P, F91S, T107M	1835	45927	1.05	744	0.02	1038	1.27	1225	0.03

TABLE 23E: 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
P18S, D23N, L79P, F91S, T107M, S114N	1836	Little to no protein produced							
P18S, P34S, E51V, L79P, F91S, G111R	1837	7917	0.18	769	0.02	853	1.04	892	0.02
P18S, H59N, V75A, L79P, A81T, F91S, L104M, T107M	1838	800	0.02	676	0.02	915	1.12	759	0.02
P18S, W46R, E68D, L79P, F91S, T107M, R113G	1839	1359	0.03	717	0.02	798	0.98	737	0.02
V9L, P18F, T45A, S65A, S67V, R78K, L79V, F91S, T107M, S114T	1840	130274	2.98	153569	4.04	812	1.00	85605	1.76
P18T, M55L, T61R, L79P, F91S, V106I, T107M	1841	133399	3.05	1906	0.05	827	1.01	57927	1.19
T15I, P18S, V33M, N35F, T39S, M55L, R78S, L79P, F91S, T107M	1842	7550	0.17	1015	0.03	789	0.97	2709	0.06
P18S, Q62K, K70E, L79P, F91S, G92E, R113W	1843	11173	0.26	691	0.02	735	0.90	1951	0.04
P18F, F20I, T26M, A47V, E51K, L79P, F91S	1844	136088	3.11	54026	1.42	1401	1.72	96629	1.99
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1845	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	1846	1599	0.04	1030	0.03	1115	1.37	1944	0.04
A13E, P18S, M36R, Q62K, S67T, L79P, N85D, F91S, T107M	1847	Little to no protein produced							
V9I, P18T, H49R, L79P, N85D, F91S, L104T, T107M	1848	46375	1.06	76851	2.02	794	0.97	80210	1.65
V9A, P18F, T61S, Q62L, L79P, F91S, G111R	1849	26109	0.60	891	0.02	825	1.01	2633	0.05
D8E, P18T, T61A, L79P, F91S, T107M	1850	Little to no protein produced							
P18S, V41A, H49R, S54C, L79S, N85Y, L88P, F91S, L104M, T107M	1851	1098	0.03	830	0.02	876	1.07	1678	0.03
V11E, P18H, F20Y, V25E, N35S, H49R, L79P, F91S, T107M, G111R	1852	979	0.02	846	0.02	844	1.03	928	0.02
V11A, P18F, D23A, L79P,	1853	45249	1.04	913	0.02	830	1.02	33883	0.70

TABLE 23E: 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
G80D, V95A, T107M									
P18S, K70R, L79P, F91S, G111R	1854	16180	0.37	793	0.02	854	1.05	1182	0.02
P18T, D23A, Q60H, L79P, M90V, F91S, T107M	1845	175673	4.02	161958	4.26	879	1.08	50981	1.05
V9L, V11M, P18S, N35S, S54G, Q62K, L79P, L104M, T107M, V115M	1855	2999	0.07	2315	0.06	893	1.09	925	0.02
V9L, P18Y, V25A, V38G, M55V, A77T, L79P, M90I, F91S, L104M	1856	138011	3.16	26015	0.68	919	1.13	17970	0.37
V10G, P18T, L72Q, L79P, F91S, T107M	1857	4253	0.10	1584	0.04	863	1.06	3643	0.07
P18S, H59R, A76G, R78S, L79P	1858	130622	2.99	79435	2.09	1009	1.24	44493	0.91
V9A, P18S, M36T, S65G, L79P, F91S, L104T, G111R, S112I	1859	92503	2.12	989	0.03	886	1.09	7850	0.16
P18T, S52A, V57A, Q60R, Q62K, S65C, L79P, F91T, N100Y, T107M	1860	187338	4.29	10579	0.28	908	1.11	3791	0.08
V11A, P18F, N35D, A47E, Q62K, L79P, F91S, G99D, T107M, S114N	1861	Little to no protein produced							
V11A, P18T, N35S, L79P, S87T, F91S	1862	218660	5.00	273825	7.20	1269	1.56	69871	1.44
V9D, V11M, Q12L, P18S, E37V, M55I, Q60R, K70Q, L79P, F91S, L104M, T107M	1863	8693	0.20	790	0.02	852	1.04	1991	0.04
T15S, P18S, Y30H, Q32L, Q62R, L79P, F91S, T107M	1864	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	965	1289		824		17819		1172	0.02

TABLE 24A: 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	972	1763	0.02	1645	0.08	2974	0.61	1659	0.19
N47K, Q79R, S118F	1095	1738	0.02	1689	0.09	2637	0.54	1647	0.19

TABLE 24A: 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
Q40R, P60T, A112V, S118T	1096	4980	0.06	1608	0.08	2399	0.50	2724	0.32
F114Y, S118F	1097	110506	1.34	7325	0.37	1502	0.31	1553	0.18
N106I, S118Y	977	1981	0.02	1700	0.09	2394	0.49	1582	0.19
S118Y	976	101296	1.23	9990	0.50	1429	0.30	1551	0.18
Y33H, K78R, S118Y	1098	2276	0.03	2115	0.11	3429	0.71	2082	0.24
N106I, S118F	978	1875	0.02	1675	0.08	2365	0.49	1662	0.19
R12W, A46T, K66M, Q79R, N106I, T113A, S118F	1099	3357	0.04	1808	0.09	1664	0.34	4057	0.48
Y33H, A112V, S118F	1100	3376	0.04	2886	0.15	3574	0.74	3685	0.43
R12W, Y33H, N106I, S118F	1101	100624	1.22	24513	1.24	1490	0.31	2060	0.24
L15V, Q90R, S118F	1102	5791	0.07	4169	0.21	2752	0.57	4458	0.52
N47K, D84G, N106I, S118Y	1103	3334	0.04	2819	0.14	2528	0.52	3498	0.41
L32P, S118F	1104	3881	0.05	2506	0.13	2659	0.55	2518	0.29
Y33H, Q79R, A112V, S118Y	1105								
T18A, N106I, S118T	1106	84035	1.02	10208	0.52	1585	0.33	1590	0.19
L15V, Y33H, N106Y, A112V, S118F	1107								
V37M, S118F	1108	96986	1.18	2523	0.13	1985	0.41	1849	0.22
N47K, A112V, S118Y	1109	1980	0.02	1859	0.09	2733	0.56	1825	0.21
A46T, A112V	1110	4224	0.05	4685	0.24	3288	0.68	4273	0.50
P28S, Y33H, N106I, S118Y	1111	6094	0.07	2181	0.11	1891	0.39	3021	0.35
P30S, Y33H, N47K, V75M, Q79R, N106I, S118Y	1112	2247	0.03	2044	0.10	1796	0.37	2658	0.31
V19A, N47K, N106Y, K116E, S118Y	1113	2504	0.03	2395	0.12	2174	0.45	2852	0.33
Q79R, T85A, A112V, S118Y	1114	2192	0.03	1741	0.09	2367	0.49	1620	0.19
Y33H, A112V	994	20646	0.25	1465	0.07	1794	0.37	2589	0.30
V101M, N106I, S118Y	1115	55274	0.67	6625	0.33	1357	0.28	1494	0.17

TABLE 24A: 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
Y33H, Q79R, N106I, A112V, S118T	1116	6095	0.07	1760	0.09	2393	0.49	3033	0.36
Q79R, A112V	1117	1571	0.02	1490	0.08	2284	0.47	1326	0.16
Y33H, A46T, Q79R, N106I, S118F	1118	90813	1.10	15626	0.79	1298	0.27	3571	0.42
A112V, G121S	1119	95674	1.16	19992	1.01	1252	0.26	4005	0.47
Y33H, Q79R, N106I, S118Y	1120	36246	0.44	2118	0.11	1970	0.41	3250	0.38
Y33H, N106I, A112V	1121	47352	0.57	4217	0.21	2641	0.55	1488	0.17
Y33H, A46T, V101M, A112V, S118T	1122	14413	0.17	1596	0.08	2335	0.48	1441	0.17
L32P, L99M, N106I, S118F	1123	3056	0.04	1791	0.09	2210	0.46	2000	0.23
L32P, T108A, S118F	1124	104685	1.27	4531	0.23	2308	0.48	1518	0.18
A112V	1002	4937	0.06	1903	0.10	1646	0.34	3011	0.35
R12W, Q79R, A112V	1125	55539	0.67	6918	0.35	1386	0.29	1740	0.20
Y33H, N106Y, E110G, A112V	1126	2786	0.03	2517	0.13	1787	0.37	2023	0.24
Y33H, N106I, S118Y	1127	1967	0.02	1579	0.08	2601	0.54	1517	0.18
Q79R, S118F	1128	82055	1.00	7582	0.38	1298	0.27	1970	0.23
Y33H, Q79R, G98D, V101M, A112V	1129	21940	0.27	1632	0.08	1141	0.24	18423	2.16
N47K, T81S, V101M, A112V, S118F	1130	6889	0.08	1311	0.07	1303	0.27	1145	0.13
G82S, S118Y	1131	4267	0.05	1938	0.10	2140	0.44	2812	0.33
Y33H, A112V, S118Y	1132	14450	0.18	1532	0.08	2353	0.49	3004	0.35
Y33H, N47K, Q79R, N106Y, A112V	1133	70440	0.85	3557	0.18	1447	0.30	1679	0.20
Y33H, S118T	1134	113896	1.38	17724	0.89	1252	0.26	5001	0.59
R12W, Y33H, Q79R, V101M, A112V	1135	3376	0.04	2727	0.14	2047	0.42	2339	0.27
S118F	972	2685	0.03	1864	0.09	2520	0.52	1566	0.18
Wildtype CD112-IgV Fc	965 (IgV)	82414	1.00	19803	1.00	4842	1.00	8541	1.00
CD112 ECD-Fc	48	29157	0.35	8755	0.44	1107	0.23	1103	0.13

TABLE 24A: 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
	(ECD)								
Anti-hFc PE	-	1383	0.02	1461	0.07	1358	0.28	1468	0.17

TABLE 24B: 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	977	1288	0.04	1334	0.12	6920	4.16	1102	0.44
Y33H, Q83K, A112V, S118T	1631	115690	3.31	10046	0.93	1128	0.68	2053	0.82
R12W, Q79R, S118F	974	1436	0.04	1296	0.12	6546	3.93	1046	0.42
V29M, Y33H, N106I, S118F	1632	Not tested							
Y33H, A46T, A112V	1633	111256	3.18	14974	1.39	1148	0.69	3333	1.34
Y33H, Q79R, S118F	1634	1483	0.04	1326	0.12	7425	4.46	1138	0.46
Y33H, N47K, F74L, S118F	1635	1338	0.04	1159	0.11	1516	0.91	1140	0.46
R12W, V101M, N106I, S118Y	1636	1378	0.04	1249	0.12	5980	3.59	1182	0.47
A46T, V101A, N106I, S118Y	1637	1359	0.04	1199	0.11	6729	4.04	1173	0.47
Y33H, N106Y, A112V	991	113580	3.25	17771	1.65	1207	0.72	2476	0.99
N106Y, A112V, S118T	1638	Not tested							
S76P, T81I, V101M, N106Y, A112V, S118F	1639	Not tested							
N106Y, A112V	981	29015	0.83	2760	0.26	1159	0.70	1639	0.66
P9R, L21V, P22L, I34M, S69F, F74L, A87V, A112V, L125A	1640	1920	0.05	1218	0.11	1107	0.66	1074	0.43
Y33H, V101M, A112V	1641	126266	3.61	24408	2.27	1150	0.69	4535	1.82
N106I, S118F	978	1776	0.05	1385	0.13	9058	5.44	1370	0.55

TABLE 24B: 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
V29A, L32P, S118F	1642	1265	0.04	1148	0.11	5057	3.04	1194	0.48
A112V	1002	69673	1.99	6387	0.59	1140	0.68	1214	0.49
Y33H, V101M, A112V	1641	133815	3.83	24992	2.32	1184	0.71	6338	2.54
P28S, Y33H, N106I, S118Y	1111	2745	0.08	1689	0.16	6625	3.98	1978	0.79
Y33H, V101M, N106I, A112V	1643	118654	3.40	21828	2.03	1253	0.75	3871	1.55
R12W, Y33H, N47K, Q79R, S118Y	1644	171390	4.91	5077	0.47	1124	0.68	2636	1.06
A112V, S118T	1004	103203	2.95	15076	1.40	1155	0.69	1426	0.57
Y33H, A46T, A112V, S118T	1645	141859	4.06	29436	2.74	1184	0.71	5760	2.31
Y33H, A112V, F114L, S118T	1646	5161	0.15	1734	0.16	1184	0.71	1249	0.50
A112V	1002	78902	2.26	6224	0.58	1114	0.67	1181	0.47
Y33H, T38A, A46T, V101M, A112V	1647	111293	3.19	25702	2.39	1192	0.72	99015	39.69
Q79R, A112V	1117	96674	2.77	7264	0.67	1130	0.68	1216	0.49
Y33H, N106I, S118Y	1127	5720	0.16	1453	0.14	6543	3.93	1248	0.50
P28S, Y33H, S69P, N106I, A112V, S118Y	1648	22393	0.64	1378	0.13	1550	0.93	19174	7.68
Y33H, P42L, N47K, V101M, A112V	1649	214116	6.13	13878	1.29	1315	0.79	4753	1.91
Y33H, N47K, F74S, Q83K, N106I, F111L, A112V, S118T	1650	6719	0.19	1319	0.12	1305	0.78	1278	0.51
Y33H, A112V, S118T, V119A	1651	184794	5.29	10204	0.95	1269	0.76	4321	1.73
Y33H, N106I, A112V, S118F	1652	6872	0.20	1591	0.15	2308	1.39	2796	1.12
Y33H, K66M, S118F, W124L	1653	1724	0.05	1259	0.12	6782	4.07	1197	0.48
S118F	972	1325	0.04	1213	0.11	7029	4.22	1135	0.46
N106I, A112V	1654	111342	3.19	4241	0.39	1546	0.93	1178	0.47
Y33H, A112V	994	177926	5.09	13761	1.28	1152	0.69	3117	1.25
WT CD112 IgV	965	34932	1.00	10762	1.00	1665	1.00	2495	1.00

TABLE 24B: 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
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 25A: 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	1267	12585	2.4
I20L, I36T, N45D, I47T	1268	3119	0.6
I20L, M41K, K44E	1269	9206	1.8
P6S, N45T, N78I, I83T	1270	419	0.1
N78I	1271	2249	0.4
M41K, N78I	1272	Little or no protein produced	
I20L, I36T, N45D	1277	Little or no protein produced	
N17D, N45T, V50A, D72G	1278	Little or no protein produced	
I20L, F49S	1279	Little or no protein produced	
N45T, V50A	1280	23887	4.6
I20L, N45T, N78I	1281	29104	5.6
N45T, N78I	1273	24865	4.7
I20L, N45T	1274	24279	4.6
I20L, N45T, V50A	1282	34158	6.5
N45T	1275	6687	1.3
M41K	1276	5079	1.0
M41V, N45T	1283	Little or no protein produced	
M41K, N45T	1284	Little or no protein produced	
A33D, S75P, D85E	1285	685	0.1
M18I, M41K, D43G, H51R, N78I	1286	20731	4.0
V11E, I20L, I36T, N45D, H60R, S75P	1287	3313	0.6
A33D, V50A	1288	Little or no protein produced	
S16G, A33D, K71E, S75P	1289	Little or no protein produced	
E27G, N45T, M97I	1290	881	0.2
E27G, N45T, K57R	1291	5022	1.0
A33D, E53V	1292	650	0.1
D43G, N45D, V58A	1293	63960	12.2
E40G, D43V, N45T, V50A	1294	809	0.2
Y14S, K28E, N45T	1295	16232	3.1

TABLE 25A: 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
A33D, N78S	1296	1725	0.3
A33D, N78I	1297	8482	1.6
A33D, N45T	1298	17220	3.3
A33D,N45T, N78I	1299		
E27G, N45T, V50A	1300	25267	4.8
N45T, V50A, N78S	1301	28572	5.4
N45T, V50A	1280	18717	3.6
I20L, N45T, V110M	1302	464	0.1
I20L, I36T, N45T, V50A	1303	7658	1.5
N45T, L74P, S75P	1304	5251	1.0
N45T, S75P	1305	12200	2.3
S75P, K106R	1306	388	0.1
S75P	1307	1230	0.2
A33D, S75P	1308	306	0.1
A33D, S75P, D104G	1309	251	0.0
A33D, S75P	1310	1786	0.3
I20L, E27G, N45T, V50A	1311	29843	5.7
I20L, E27G, D43G, N45D, V58A, N78I	1312	69486	13.3
I20L, D43G, N45D, V58A, N78I	1313	72738	13.9
I20L, A33D, D43G, N45D, V58A, N78I	1314	80205	15.3
I20L, D43G, N45D, N78I	1315	67018	12.8
E27G, N45T, V50A, N78I	1316	30677	5.9
N45T, V50A, N78I	1317	32165	6.1
V11A, I20L, E27G, D43G, N45D, H51Y, S99G	1318	73727	14.1
I20L, E27G, D43G, N45T, V50A	1319	36739	7.0
I20L, K28E, D43G, N45D, V58A, Q89R, G101G-ins	1320	80549	15.4
I20L, I36T, N45D	1321	16870	3.2
I20L, K28E, D43G, N45D, E53G, V58A, N78I	1322	139	0.0
A33D, D43G, N45D, V58A, S75P	1323	58484	11.2
K23R, D43G, N45D	1324	67559	12.9
I20L, D43G, N45D, V58A, N78I, D90G, G101D	1325	259	0.0
D43G, N45D, L56Q, V58A, G101G-ins (G101GG)	1326	88277	16.8
I20L, K23E, D43G, N45D, V58A, N78I	1327	89608	17.1
I20L, K23E, D43G, N45D, V50A, N78I	1328	88829	16.9
T19I, E27G, N45I, V50A, N78I, M97K	1329	25496	4.9

TABLE 25A: 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, M41K, D43G, N45D	1330	599	0.1
K23R, N45T, N78I	1331	84980	16.2
Full length PD-L1 Fc	-	18465	3.5
Wild type PD-L1 IgV	1332	5243	1.0
Anti-PD-1 monoclonal antibody (nivolumab)	-	79787	15.2
Human IgG	-	198	0.0

Table 25B: 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	1875	2953	0.9	16253	121.3
K57R, S99G, F189L	1876	1930	0.6	12906	96.3
M18V, M97L, F193S, R195G, E200K, H202Q	1877	69	0.0	241	1.8
I36S, M41K, M97L, K144Q, R195G, E200K, H202Q, L206F	1878	3498	1.1	68715	512.8
C22R, Q65L, L124S, K144Q, R195G, E200N, H202Q, T221L	1879	Little or no protein produced			
M18V, I98L, L124S, P198T, L206F	1880	2187	0.7	143	1.1
S99G, N117S, I148V, K171R, R180S	1881	Little or no protein produced			
I36T, M97L, A103V, Q155H	1882	120	0.0	128	1.0
K28I, S99G	1883	830	0.3	693	5.2
R195S	1884	3191	1.0	138	1.0
A79T, S99G, T185A, R195G, E200K, H202Q, L206F	1885	1963	0.6	643	4.8
K57R, S99G, L124S, K144Q	1886	2081	0.7	14106	105.3
K57R, S99G, R195G	1887	2479	0.8	10955	81.8
D55V, M97L, S99G	1888	11907	3.8	71242	531.7
E27G, I36T, D55N, M97L, K111E	1889	1904	0.6	88724	662.1
E54G, M97L, S99G	1890	8414	2.7	51905	387.4
G15A, I36T, M97L, K111E, H202Q	1891	112	0.0	13530	101.0
G15A, I36T, V129D	1892	114	0.0	136	1.0
G15A, I36T, V129D, R195G	1893	125	0.0	134	1.0
G15A, V129D	1894	2075	0.7	128	1.0
I36S, M97L	1895	3459	1.1	44551	332.5

Table 25B: 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, D55N, M97L, K111E, A204T	1896	265	0.1	62697	467.9
I36T, D55N, M97L, K111E, V129A, F173L	1897	393	0.1	72641	542.1
I36T, D55S, M97L, K111E, I148V, R180S	1898	94	0.0	30704	229.1
I36T, G52R, M97L, V112A, K144E, V175A, P198T	1899	81	0.0	149	1.1
I36T, I46V, D55G, M97L, K106E, K144E, T185A, R195G	1900	69	0.0	190	1.4
I36T, I83T, M97L, K144E, P198T	1901	62	0.0	6216	46.4
I36T, M97L, K111E	1902	Little or no protein produced			
I36T, M97L, K144E, P198T	1903	197	0.1	40989	305.9
I36T, M97L, Q155H, F193S, N201Y	1904	69	0.0	1251	9.3
I36T, M97L, V129D	1905	523	0.2	50905	379.9
L35P, I36S, M97L, K111E	1906	190	0.1	155	1.2
M18I, I36T, E53G, M97L, K144E, E199G, V207A	1907	104	0.0	47358	353.4
M18T, I36T, D55N, M97L, K111E	1908	138	0.0	71440	533.1
M18V, M97L, T176N, R195G	1909	1301	0.4	45300	338.1
M97L, S99G	1910	12906	4.1	81630	609.2
N17D, M97L, S99G	1911	10079	3.2	73249	546.6
S99G, T185A, R195G, P198T	1912	2606	0.8	22062	164.6
V129D, H202Q	1913	2001	0.6	219	1.6
V129D, P198T	1914	3245	1.0	152	1.1
V129D, T150A	1915	1941	0.6	142	1.1
V93E, V129D	1916	1221	0.4	150	1.1
Y10F, M18V, S99G, Q138R, T203A	1917	70	0.0	412	3.1
WT PD-L1 (IgV+IgC) Fc	-	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	-	59	N/A	132	N/A

TABLE 25C. Additional Affinity-Matured IgSF Domain-Containing Molecules			
PD-L1 Mutation(s)	SEQ ID NO (ECD)	PD-L1 Mutation(s)	SEQ ID NO (ECD)
N45D	1918	N45D, G102D, R194W, R195G	1943

K160M, R195G	1919	N45D, G52V, Q121L, P198S	1943
N45D, K144E	1920	N45D, I148V, R195G, N201D	1944
N45D, P198S	1921	N45D, K111T, T183A, I188V	1945
N45D, P198T	1922	N45D, Q89R, F189S, P198S	1946
N45D, R195G	1923	N45D, S99G, C137R, V207A	1947
N45D, R195S	1924	N45D, T163I, K167R, R195G	1948
N45D, S131F	1925	N45D, T183A, T192S, R194G	1949
N45D, V58D	1926	N45D, V50A, I119T, K144E	1950
V129D, R195S	1927	T19A, N45D, K144E, R195G	1951
I98T, F173Y, L196S	1928	V11E, N45D, T130A, P198T	1952
N45D, E134G, L213P	1929	V26A, N45D, T163I, T185A	1953
N45D, F173I, S177C	1930	K23N, N45D, L124S, K167T, R195G	1954
N45D, I148V, R195G	1931	K23N, N45D, Q73R, T163I	1955
N45D, K111T, R195G	1932	K28E, N45D, W149R, S158G, P198T	1956
N45D, N113Y, R195S	1933	K28R, N45D, K57E, I98V, R195S	1957
N45D, N165Y, E170G	1934	K28R, N45D, V129D, T163N, R195T	1958
N45D, Q89R, I98V	1935	M41K, D43G, N45D, R64S, R195G	1959
N45D, S131F, P198S	1936	M41K, D43G, N45D, R64S, S99G	1960
N45D, S75P, P198S	1937	N45D, R68L, F173L, D197G, P198S	1961
N45D, V50A, R195T	1938	N45D, V50A, I148V, R195G, N201D	1962
E27D, N45D, T183A, I188V	1939	M41K, D43G, K44E, N45D, R195G, N201D	1963
F173Y, T183I, L196S, T203A	1940	N45D, V50A, L124S, K144E, L179P, R195G	1964
K23N, N45D, S75P, N120S	1941		

TABLE 26A: 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	1487	15998	1.63	0.007
N24D	1488	1414	0.14	-0.039
E44D	1489	2928	0.3	-0.006
V89D	1490	3361	0.34	0.005
Q82R,V89D	1491	44977	4.57	1.111
E59G,Q82R	1492	12667	1.29	-0.028
S39I,V89D	1493	26130	2.65	0.26
S67L,V89D	1494	15991	1.62	0.608
S67L,I85F	1495	529	0.05	-0.005
S67L,I86T	1496	6833	0.69	0.141
H15Q,K65R	1497	13497	1.37	-0.001
H15Q,Q72H,V89D	1498	12629	1.28	0.718
H15Q,S67L,R76G	1499	47201	4.8	0.418
H15Q,R76G,I85F	1500	2941	0.3	-0.038

TABLE 26A: 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,T47A,Q82R	1501	65174	6.62	0.194
H15Q,Q82R,V89D	1502	49652	5.04	1.198
H15Q,C23S,I86T	1503	830	0.08	-0.026
H15Q,S39I,I86T	1504	1027	0.1	0.309
H15Q,R76G,I85F	1505	1894	0.19	-0.006
E44D,V89D,W91R	1506	614	0.06	-0.048
I13V,S67L,V89D	1507	26200	2.66	1.42
H15Q,S67L,I86T	1508	15952	1.62	0.988
I13V,H15Q,S67L,I86T	1509	21570	2.19	1.391
I13V,H15Q,E44D,V89D	1510	23958	2.43	1.399
I13V,S39I,E44D,Q82R,V89D	1511	71423	7.26	0.697
I13V,E44D,Q82R,V89D	1512	45191	4.59	1.283
I13V,Q72H,R76G,I86T	1513	10429	1.06	0.733
I13V,H15Q,R76G,I85F	1514	4736	0.48	-0.04
H15Q,S67L,R76G,I85F	1516	2869	0.29	0.025
H15Q,S39I,R76G,V89D	1515	Little or no protein produced		
H15Q,T47A,Q72H,R76G,I86T	1517	32103	3.26	0.512
H15Q,T47A,Q72H,R76G	1518	16500	1.68	0.327
I13V,H15Q,T47A,Q72H,R76G	1519	73412	7.46	0.896
H15Q,E44D,R76G,I85F	1520	2885	0.29	-0.013
H15Q,S39I,S67L,V89D	1521	45502	4.62	1.174
H15Q,N32D,S67L,V89D	1522	25880	2.63	1.407
N32D,S67L,V89D	1523	31753	3.23	1.155
H15Q,S67L,Q72H,R76G,V89D	1524	40180	4.08	1.464
H15Q,Q72H,Q74R,R76G,I86T	1525	4049	0.41	0.093
G28V,Q72H,R76G,I86T	1526	5563	0.57	0.003
I13V,H15Q,S39I,E44D,S67L	1527	63508	6.45	0.889
E44D,S67L,Q72H,Q82R,V89D	1528	51467	5.23	1.061
H15Q,V89D	1529	17672	1.8	0.31
H15Q,T47A	1530	26578	2.7	0.016
I13V,H15Q,Q82R	1531	76146	7.74	0.655
I13V,H15Q,V89D	1532	28745	2.92	1.331
I13V,S67L,Q82R,V89D	1533	58992	5.99	1.391
I13V,H15Q,Q82R,V89D	1534	49523	5.03	1.419
H15Q,V31M,S67L,Q82R,V89D	1535	67401	6.85	1.37
I13V,H15Q,T47A,Q82R	1536	89126	9.05	0.652
I13V,H15Q,V31A,N45S,Q82R,V89D	1537	68016	6.91	1.327
I13V,T20A,T47A,K65X,Q82R,V89D	1538	Not tested		
H15Q,T47A,H69L,Q82R,V89D	1539	65598	6.66	1.44
I13V,H15Q,T47A,H69L,R76G,V89D	1540	54340	5.52	1.719

TABLE 26A: 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	
I12V,I13V,H15Q,T47A,Q82R,V89D	1541	61207	6.22	1.453
I13V,H15Q,R76G,D77N,Q82R,V89D	1542	33079	3.36	0.065
I13V,H15Q,T47A,R76G,V89D	1543	53668	5.45	1.596
I13V,H15Q,T47A,Q82R,V89D	1544	63320	6.43	1.418
I13V,H15Q,T47A,Q82R,V89D	1545	60980	6.2	1.448
I13V,H15Q,I36V,T47A,S67L,V89D	1546	52835	5.37	1.627
H15Q,T47A,K65R,S67L,Q82R,V89D	1547	79692	8.1	1.453
H15Q,L33P,T47A,S67L,P71S,V89D	1548	45726	4.65	1.467
I13V,H15Q,Q72H,R76G,I86T	1549	24450	2.48	1.355
H15Q,T47A,S67L,Q82R,V89D	1550	67962	6.9	1.479
F2L,H15Q,D46E,T47A,Q72H,R76G,Q82R,V89D	1551	23039	2.34	1.045
I13V,H15Q,L33F,T47A,Q82R,V89D	1552	62254	6.32	1.379
I13V,H15Q,T47A,E58G,S67L,Q82R,V89D	1543	Not tested		
H15Q,N24S,T47A,Q72H,R76G,V89D	1554	32077	3.26	0.4
I13V,H15Q,E44V,T47A,Q82R,V89D	1555	61005	6.2	1.329
H15Q,N18D,T47A,Q72H,V73A,R76G,I86T,V89D	1556	48317	4.91	0.475
I13V,H15Q,T37A,E44D,S48C,S67L,Q82R,V89D	1557	47605	4.84	1.255
H15Q,L33H,S67L,R76G,Q82R,V89D	1558	62326	6.33	1.507
I13V,H15Q,T47A,Q72H,R76G,I86T	1559	49016	4.98	1.477
H15Q,S39I,E44D,Q72H,V75G,R76G,Q82R,V89D	1560	43713	4.44	0.646
H15Q,T47A,S67L,R76G,Q82R,V89D	1561	71897	7.3	1.539
I13V,H15Q,T47A,S67L,Q72H,R76G,Q82R,V89D	1562	71755	7.29	1.536
Wild Type PD-L2 IgV	1393	9843	1	-0.024
Full length ECD of PD-L2	31 (ECD)	2145	0.22	0.071
Full length ECD of PD-L1 (R&D Systems)	-	23769	2.41	1.263
Anti-PD-1 monoclonal antibody (nivolumab)	-	87002	8.84	0.899

TABLE 26B: 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	1487	1817.1	1.32
N24D	1488	1976.3	1.44
E44D	1489	1499.4	1.09
V89D	1490	1168.1	0.85
Q82R,V89D	1491	1617	1.17
E59G,Q82R	1492	1511.3	1.1
S39I,V89D	1493	1314.5	0.95

TABLE 26B: 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**
S67L,V89D	1494	1230.1	0.89
S67L,I85F	1495	1281.9	0.93
S67L,I86T	1496	1020.4	0.74
H15Q,K65R	1497	1510.8	1.1
H15Q,Q72H,V89D	1498	1272.2	0.92
H15Q,S67L,R76G	1499	1426.2	1.04
H15Q,R76G,I85F	1500	1725.7	1.25
H15Q,T47A,Q82R	1501	1317.9	0.96
H15Q,Q82R,V89D	1502	1081.2	0.79
H15Q,C23S,I86T	1503	1847.2	1.34
H15Q,S39I,I86T	1504	1415.2	1.03
H15Q,R76G,I85F	1505	1437.8	1.04
E44D,V89D,W91R	1506	1560.1	1.13
I13V,S67L,V89D	1507	867.5	0.63
H15Q,S67L,I86T	1508	1034.2	0.75
I13V,H15Q,S67L,I86T	1509	1014.4	0.74
I13V,H15Q,E44D,V89D	1510	1384.2	1.01
I13V,S39I,E44D,Q82R,V89D	1511	935.6	0.68
I13V,E44D,Q82R,V89D	1512	1009.5	0.73
I13V,Q72H,R76G,I86T	1513	1953	1.42
I13V,H15Q,R76G,I85F	1514	1528.5	1.11
H15Q,S67L,R76G,I85F	1516	1318.7	0.96
H15Q,T47A,Q72H,R76G,I86T	1517	1599.6	1.16
H15Q,T47A,Q72H,R76G	1518	1462.5	1.06
I13V,H15Q,T47A,Q72H,R76G	1519	1469.8	1.07
H15Q,E44D,R76G,I85F	1520	1391.6	1.01
H15Q,S39I,S67L,V89D	1521	1227	0.89
H15Q,N32D,S67L,V89D	1522	1285.7	0.93
N32D,S67L,V89D	1523	1194	0.87
H15Q,S67L,Q72H,R76G,V89D	1524	1061.2	0.77
H15Q,Q72H,Q74R,R76G,I86T	1525	933.8	0.68
G28V,Q72H,R76G,I86T	1526	1781.6	1.29
I13V,H15Q,S39I,E44D,S67L	1527	1256.9	0.91
E44D,S67L,Q72H,Q82R,V89D	1528	1281.4	0.93
H15Q,V89D	1529	1495.4	1.09
H15Q,T47A	1530	1637.2	1.19
I13V,H15Q,Q82R	1531	1432.9	1.04
I13V,H15Q,V89D	1532	1123	0.82
I13V,S67L,Q82R,V89D	1533	1372.8	1

TABLE 26B: 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,Q82R,V89D	1534	1596.6	1.16
H15Q,V31M,S67L,Q82R,V89D	1535	1206.5	0.88
I13V,H15Q,T47A,Q82R	1536	1703.3	1.24
I13V,H15Q,V31A,N45S,Q82R,V89D	1537	1723.1	1.25
H15Q,T47A,H69L,Q82R,V89D	1539	1732.5	1.26
I13V,H15Q,T47A,H69L,R76G,V89D	1540	1075.5	0.78
I12V,I13V,H15Q,T47A,Q82R,V89D	1541	1533.2	1.11
I13V,H15Q,R76G,D77N,Q82R,V89D	1542	1187.9	0.86
I13V,H15Q,T47A,R76G,V89D	1543	1253.7	0.91
I13V,H15Q,T47A,Q82R,V89D	1544	1445.5	1.05
I13V,H15Q,T47A,Q82R,V89D	1545	1737	1.26
I13V,H15Q,I36V,T47A,S67L,V89D	1546	1357.4	0.99
H15Q,T47A,K65R,S67L,Q82R,V89D	1547	1335.3	0.97
H15Q,L33P,T47A,S67L,P71S,V89D	1548	1289.1	0.94
I13V,H15Q,Q72H,R76G,I86T	1549	1221	0.89
H15Q,T47A,S67L,Q82R,V89D	1550	1197.1	0.87
F2L,H15Q,D46E,T47A,Q72H,R76G,Q82R,V89D	1551	1170.7	0.85
I13V,H15Q,L33F,T47A,Q82R,V89D	1552	1468.4	1.07
I13V,H15Q,T47A,E58G,S67L,Q82R,V89D	1543	836.1	0.61
H15Q,N24S,T47A,Q72H,R76G,V89D	1554	1091.8	0.79
I13V,H15Q,E44V,T47A,Q82R,V89D	1555	1270.5	0.92
H15Q,N18D,T47A,Q72H,V73A,R76G,I86T,V89D	1556	1065.8	0.77
I13V,H15Q,T37A,E44D,S48C,S67L,Q82R,V89D	1557	1751.7	1.27
H15Q,L33H,S67L,R76G,Q82R,V89D	1558	1502	1.09
I13V,H15Q,T47A,Q72H,R76G,I86T	1559	1088.1	0.79
H15Q,S39I,E44D,Q72H,V75G,R76G,Q82R,V89D	1560	940.9	0.68
H15Q,T47A,S67L,R76G,Q82R,V89D	1561	1097.8	0.8
I13V,H15Q,T47A,S67L,Q72H,R76G,Q82R,V89D	1562	1559.6	1.13
Wild Type PD-L2 IgV	1393	1376.8	1
Full length ECD of PD-L2	31 (ECD)	1173.2	0.85
Full length ECD of PD-L1	2118 (ECD)	2190.9	1.59
Nivolumab (anti-PD-1)	-	418.9	0.3

TABLE 27A: Variant CD80 Binding to HEK293 Cells Transfected with CTLA4, CD28 or PD-L1								
CD80 mutation(s)	SEQ ID NO (IgV)	CTLA4		CD28		PD-L1		Ratio of CTLA 4:CD28
		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	
L70P	579	Not tested						
I30F/L70P	580	Not tested						
Q27H/T41S/A71D	581	368176	2.3	25051	1.01	24181	N/A	14.7
I30T/L70R	582	2234	0.0	2596	0.10	5163	N/A	0.9
T13R/C16R/L70Q/A71D	583	197357	1.2	16082	0.65	9516	N/A	12.3
T57I	584	393810	2.4	23569	0.95	3375	N/A	16.7
M43I/C82R	585	3638	0.0	3078	0.12	7405	N/A	1.2
V22L/M38V/M47T/A71D/ L85M	586	175235	1.1	3027	0.12	6144	N/A	57.9
I30V/T57I/L70P/A71D/ A91T	587	116085	0.7	10129	0.41	5886	N/A	11.5
V22I/L70M/A71D	588	163825	1.0	22843	0.92	33404	N/A	7.2
N55D/L70P/E77G	589	Not tested						
T57A/I69T	590	Not tested						
N55D/K86M	591	3539	0.0	3119	0.13	5091	N/A	1.1
L72P/T79I	592	50176	0.3	3397	0.14	6023	N/A	14.8
L70P/F92S	593	4035	0.0	2948	0.12	6173	N/A	1.4
T79P	594	2005	0.0	2665	0.11	4412	N/A	0.8
E35D/M47I/L65P/D90N	595	4411	0.0	2526	0.10	4034	N/A	1.7
L25S/E35D/M47I/D90N	596	61265	0.4	4845	0.20	20902	N/A	12.6
Q27X*/S44P/I67T/P74S/ E81G/E95D	597	195637	1.2	17524	0.71	17509	N/A	11.2
A71D	598	220090	1.4	16785	0.68	29642	N/A	13.1
T13A/Q27X*/I61N/A71D	599	195061	1.2	17519	0.71	21717	N/A	11.1
E81K/A91S	600	98467	0.6	3309	0.13	44557	N/A	29.8
A12V/M47V/L70M	601	81616	0.5	7400	0.30	31077	N/A	11.0
K34E/T41A/L72V	602	88982	0.6	3755	0.15	35293	N/A	23.7
T41S/A71D/V84A	603	103010	0.6	5573	0.22	83541	N/A	18.5
E35D/A71D	604	106069	0.7	18206	0.73	40151	N/A	5.8
E35D/M47I	605	353590	2.2	14350	0.58	149916	N/A	24.6
K36R/G78A	606	11937	0.1	2611	0.11	5715	N/A	4.6
Q33E/T41A	607	8292	0.1	2442	0.10	3958	N/A	3.4
M47V/N48H	608	207012	1.3	14623	0.59	145529	N/A	14.2
M47L/V68A	609	74238	0.5	13259	0.53	11223	N/A	5.6
S44P/A71D	610	8839	0.1	2744	0.11	6309	N/A	3.2
Q27H/M43I/A71D/R73S	611	136251	0.8	12391	0.50	8242	N/A	11.0
E35D/T57I/L70Q/A71D	613	121901	0.8	21284	0.86	2419	N/A	5.7
M47I/E88D	614	105192	0.7	7337	0.30	97695	N/A	14.3
M42I/I61V/A71D	615	54478	0.3	6074	0.24	4226	N/A	9.0
P51A/A71D	616	67256	0.4	4262	0.17	5532	N/A	15.8

TABLE 27A: 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 CTLA 4:CD2 8
H18Y/M47I/T57I/A71G	617	136455	0.8	20081	0.81	13749	N/A	6.8
V20I/M47V/T57I/V84I	618	183516	1.1	26922	1.08	3583	N/A	6.8
WT	578	161423	1.0	24836	1.00	Not tested	N/A	6.5

*Stop codon at indicated position

TABLE 27B: 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	619	149937	7.23	15090	9.33	9710	5.48	9.9
A71D/L72V/E95K	620	140306	6.77	6314	3.90	8417	4.75	22.2
V22L/E35G/A71D/L72P	621	152588	7.36	8150	5.04	1403	0.79	18.7
E35D/A71D	622	150330	7.25	14982	9.26	13781	7.77	10.0
E35D/I67L/A71D	623	146087	7.04	11175	6.91	9354	5.28	13.1
T13R/M42V/M47I/A71D	625	108900	5.25	16713	10.33	1869	1.05	6.5
E35D	626	116494	5.62	3453	2.13	25492	14.38	33.7
E35D/M47I/L70M	627	116531	5.62	14395	8.90	49131	27.71	8.1
E35D/A71/L72V	628	134252	6.47	11634	7.19	13125	7.40	11.5
E35D/M43L/L70M	629	102499	4.94	3112	1.92	40632	22.92	32.9
A26P/E35D/M43I/L85Q/ E88D	630	83139	4.01	5406	3.34	9506	5.36	15.4
E35D/D46V/L85Q	631	85989	4.15	7510	4.64	38133	21.51	11.4
Q27L/E35D/M47I/T57I/ L70Q/E88D	632	59793	2.88	14011	8.66	1050	0.59	4.3
Q27H/E35G/A71D/L72P/ T79I	624	85117	4.10	10317	6.38	1452	0.82	8.3
M47V/I69F/A71D/V83I	633	76944	3.71	15906	9.83	3399	1.92	4.8
E35D/T57A/A71D/L85Q	634	85724	4.13	3383	2.09	1764	0.99	25.3
H18Y/A26T/E35D/A71D/ L85Q	635	70878	3.42	6487	4.01	8026	4.53	10.9
E35D/M47L	636	82410	3.97	11508	7.11	58645	33.08	7.2
E23D/M42V/M43I/I58V/ L70R	637	37331	1.80	10910	6.74	2251	1.27	3.4
V68M/L70M/A71D/E95K	638	56479	2.72	10541	6.51	38182	21.53	5.4
N55I/T57I/I69F	639	2855	0.14	1901	1.17	14759	8.32	1.5
E35D/M43I/A71D	640	63789	3.08	6369	3.94	27290	15.39	10.0
T41S/T57I/L70R	641	59844	2.89	4902	3.03	19527	11.01	12.2
H18Y/A71D/L72P/E88V	642	68391	3.30	8862	5.48	1085	0.61	7.7
V20I/A71D	643	60323	2.91	10500	6.49	3551	2.00	5.7

TABLE 27B: 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
E23G/A26S/E35D/T62N/ A71D/L72V/L85M	644	59025	2.85	5484	3.39	10662	6.01	10.8
A12T/E24D/E35D/D46V/ I61V/L72P/E95V	645	63738	3.07	7411	4.58	1221	0.69	8.6
V22L/E35D/M43L/A71G/ D76H	646	2970	0.14	1498	0.93	1851	1.04	2.0
E35G/K54E/A71D/L72P	647	71899	3.47	3697	2.29	1575	0.89	19.4
L70Q/A71D	648	45012	2.17	18615	11.50	1692	0.95	2.4
A26E/E35D/M47L/L85Q	649	40325	1.94	2266	1.40	55548	31.33	17.8
D46E/A71D	650	69674	3.36	16770	10.36	22777	12.85	4.2
Y31H/E35D/T41S/V68L/ K93R/R94W	651	3379	0.16	2446	1.51	18863	10.64	1.4
CD80 IgV Fc	578 (IgV)	20739	1.00	1618	1.00	1773	1.00	12.8
CD80 ECD Fc	28 (ECD)	72506	3.50	3072	1.90	4418	2.49	23.6

Example 12

Generation of Secreted Immunomodulatory Protein

[0436] To generate a PD-L2 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: 1571-1573, 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-L2 IgV wildtype amino acid sequence set forth in SEQ ID NO:1393 or variant PD-L2 IgV set forth in SEQ ID NO:1535 (H15Q,V31M,S67L,Q82R,V89D), SEQ ID NO:1547 (H15Q,T47A,K65R,S67L,Q82R,V89D) or SEQ ID NO: 1561 (H15Q,T47A,S67L,R76G,Q82R,V89D), also including in all cases the PD-L2 signal peptide MIFLLLMLSLELQLHQIAA as set forth in SEQ ID NO: 1567; DNA encoding Avitag as set forth in SEQ ID NO:1568 (GLNDIFEAQKIEWHE); DNA encoding His tag as set forth in SEQ

ID NO: 1569 (HHHHHH); TAA stop codon; second restriction site- 41 base pair overlap with pRRL beyond second restriction site.

[0437] 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 37ºC for 24 hours. After 24 hours, media was aspirated from the dishes and replaced with 10mL of fresh DMEM media and then incubated at 37ºC. 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: 2160 (encoded by the sequence in set forth in SEQ ID NO: 2161) containing the scFv set forth in SEQ ID NO:1576, the CD8-derived hinge and transmembrane domain set forth in SEQ ID NO: 1574, and the CD3zeta set forth in SEQ ID NO:1575.

[0438] Pan T-cells were transduced with the viral vectors encoding the PD-L2 SIPs. T-cells were thawed and activated with anti-CD3/anti-CD28 beads (Dynal) at a 1:1 ratio. The T-cells (1 x 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-L2 SIPs 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 30ºC. 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.

[0439] Transduction also was carried out on HEK-293 cells, which were resuspended at $2x10^5$ cells with 1mL of the lentiviral supernatant encoding the indicated PD-L2 SIPs. To the cells, 3mL of DMEM media was added and cells were fed every two days with fresh media.

[0440] To assess the amount of secreted SIP, a cell-based assay was performed to assess binding of the secretable variant PD-L2 to PD-1. Approximately, 100,000 PD-1+ Jurkat cells were plated per well in the presence of 50µL of culture supernatant containing PD-L2 SIP obtained from transduced cells above and incubated at 4ºC for 30 minutes. To generate a standard curve, 50 µL of the respective variant PD-L2 protein was added to PD-1+ Jurkat cells at 10µg/mL, 3µg/mL, 1µg/mL, 0.3µg/mL, 0.1µg/mL, and 0µg/mL and also incubated at 4ºC for 30 minutes. Cells were washed and 50 µL of anti-his-APC were added (1:50) and this was incubated at 4ºC for 30 minutes. Surface bound PD-L2 protein was detected by flow cytometry and the concentration of SIP in the supernatant sample was determined by comparison to the standard curve. As shown in FIG. 2A and 2B, SIP proteins were detected in the supernatant of transduced T cells and transduced HEK293 cell, but were not detected from supernatant samples from mock transduced or cells transduced without SIPs.

Example 13

Assessment of Proliferation and Bioactivity of Pan T cells transduced with PD-L2 SIP

[0441] Pan T-cells were transduced essentially as described in Example 12 with the viral vectors encoding the PD-L2 SIPs. T-cells were thawed and activated with anti-CD3/anti-CD28 beads (Dynal) at a 1:1 ratio. The T-cells (1 x 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-L2 SIPs 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 30ºC. 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.

[0442] 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 5 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-L2 SIP are shown in FIG. 3A.

[0443] Levels of IFN-gamma released into the supernatant were measured by ELISA on day 5 after re-stimulation. Results for the bioactivity studies for T cells transduced with exemplary tested variant PD-L2 SIP are shown in FIG. 3B. The T cells transduced with PD-L2 variant SIP are identified with reference to the amino acid substitutions in the IgV of PD-L2 with reference to positions corresponding to positions of the unmodified (wildtype) PD-L2 ECD sequence set forth in SEQ ID NO:31. As shown in FIG. 3A and 3B, proliferation and improved activities to increase immunological activity was observed.

[0444] A similar study was carried out except that T cells were co-transduced with the anti-CD19 CAR and a lentiviral vector encoding a SIP, either a variant PD-L2 IgV or wild-type (WT) PD-L2 IgV. Following stimulation of transduced T cells with Nalm6 PDL1+ cells as described above, the proliferation of T cells was measured at day 3 by determining the fraction of the cells that showed dilution of the dye. As shown in FIG. 3C, cells engineered with the variant PD-L2 SIP improved proliferation compared to proliferation of T cells only expressing the CAR, and the improved proliferation was also greater than the proliferation of T cells expressing the wild-type PD-L2 SIP.

Example 14

Generation of Secreted Immunomodulatory Protein and Assessment of Proliferation of Pan T cells transduced with PD-L1 SIP

[0445] 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 PD-L1 SIP constructs were generated to encode a protein set forth in SEQ ID NO: 2155-2156, 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: 1332 or variant PD-L1 IgV set forth in SEQ ID NO: 1326 (D43G/N45D/L56Q/V58A/G101G-ins (G101GG),

also including in all cases the signal peptide MGSTAILALLLAVLQGVSA as set forth in SEQ ID NO: 2157; DNA encoding Flag-tag as set forth in SEQ ID NO:2154 (DYKDDDDK); DNA encoding His tag as set forth in SEQ ID NO: 1569 (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.

[0446] 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 37ºC for 24 hours. After 24 hours, media was aspirated from the dishes and replaced with 10mL of fresh DMEM media and then incubated at 37ºC. 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: 2160 (encoded by the sequence in set forth in SEQ ID NO: 2161) containing the scFv set forth in SEQ ID NO:1576, the CD8-derived hinge and transmembrane domain set forth in SEQ ID NO: 1574, and the CD3zeta set forth in SEQ ID NO:1575.

[0447] 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 30ºC. 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.

[0448] 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. 5.

Example 15

Detection of Secreted Immunomodulatory Protein in Supernatant of Transduced Cells

[0449] A cell-based assay was employed to detect the presence of SIPs in culture supernatant. HEK-293 cells were transduced with a lentiviral vector encoding exemplary SIPs, variant PD-L1 IgV (D43G/N45D/L56Q/V58A/G101G-ins(G101GG) set forth in SEQ ID NO:1326), wild-type PD-L1 IgV (set forth in SEQ ID NO:1332), variant PD-L2 IgV (H15Q/T47A/K65R/S67L/Q82R/V89D set forth in SEQ ID NO:1547) or wild-type PD-L2 IgV (set forth in SEQ ID NO:1393), as described in Examples 12 and 14. Four days after transduction, supernatant was collected. Approximately 50 µL of supernatant, diluted 1:2, 1:4, 1:8, 1:16, 1:32, 1:64, 1:128 or neat, was added to 1 x 10^5 K562 cells transduced to express PD-1 (K562 PD-1+) in a 96-well round bottom plate, and incubated at 4ºC for 30 minutes. To generate a standard curve, PD-L2 his tag protein, diluted to 10,000 pg/mL, 1,000 pg/mL, 100 pg/mL, 10 pg/mL, 1 pg/mL and 0.1 pg/mL and also incubated with K562 PD-1+ cells at 4ºC for 30 minutes. Cells were washed and 50 µL of anti-his-APC were added (1:50) and this was incubated at 4ºC for 30 minutes. Surface bound PD-L2 protein was detected by flow cytometry and the concentration of SIP in the supernatant sample was determined by comparison to the standard curve. As shown in FIG. 6, the variant PD-L1 and variant PD-L2 SIPs, but not the wild-type proteins, were detected in the supernatant of cells.

[0450] The cell-based assay described above was used to assess the presence of PD-L2 SIP in supernatant of T cells following culture with antigen-expressing target cells. T cells were activated and transduced with a lentiviral vector encoding an anti-CD19 CAR and a lentiviral vector encoding either variant PD-L2 H15Q/T47A/K65R/S67L/Q82R/V89D set forth in SEQ ID NO:1547) or wild-type PD-L2 IgV (set forth in SEQ ID NO:1393), as described in Example 9.

At 14 days after activation, transduced T cells were cultured with CD19-expressing Nalm6 PD-L1+ cells or Raji cells. At days 3, 6, 9 and 12 after initiation of culture of T cells, supernatant was collected and the presence of PD-L2 was detected as described above. The variant PD-L2 SIP, but not the wild-type PD-L2 SIP, was detected in supernatant following stimulation with target antigen-expressing cells using this assay. This result may be due to the wild-type PD-L2 SIP not having a high enough affinity to bind to the K562/PD-1+ cells. The variant PD-L2 SIP was detected at substantially higher levels in supernatant of T cells stimulated with Raji cells compared to Nalm6 PD-L1 cells, and the level of variant PD-L2 SIP in the supernatant following stimulation with Raji cells was sustained throughout the time course of this study.

[0451] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. An engineered immune cell comprising a nucleic acid molecule that encodes an immunomodulatory protein, wherein:

the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain of an IgSF family member, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

the engineered immune cell expresses and secretes the immunomodulatory protein.

2. The engineered immune cell of claim 1, wherein the immunomodulatory protein does not comprise a transmembrane domain.

3. The engineered immune cell of claim 1 or claim 2, wherein the nucleic acid molecule comprises a sequence encoding a secretory signal peptide operably linked to the sequence encoding the immunomodulatory protein.

4. The engineered immune cell of claim 3, wherein the signal peptide is the native signal peptide from the corresponding wild-type IgSF member.

5. The engineered immune cell of claim 3, wherein the signal peptide is a non-native signal sequence.

6. The engineered immune cell of claim 3 or claim 5, wherein the signal peptide is an IgG-kappa signal peptide, an IL-2 signal peptide, or a CD33 signal peptide.

7. The engineered immune cell of any of claims 1-6, wherein the nucleic acid molecule further comprises at least one promoter operably linked to control expression of the immunomodulatory protein.

8. The engineered immune cell of claim 7, wherein the promoter is a constitutively active promoter.

9. The engineered immune cell of claim 7, wherein the promoter is an inducible promoter.

10. The engineered immune cell of claim 7 or claim 9, wherein the promoter is responsive to an element responsive to T-cell activation signaling.

11. The engineered immune cell of any of claims 7, 9, and 10, wherein the promoter comprises a binding site for NFAT or a binding site for NF-κB.

12. The engineered immune cell of any one of claims 1-11, wherein the immune cell is a lymphocyte.

13. The engineered immune cell of claim 12, wherein the lymphocyte is a T cell, a B cell or an NK cell.

14. The engineered immune cell of any of claims 1-13, wherein the immune cell is a T cell.

15. The engineered immune cell of claim 14, wherein the T cell is CD4+ or CD8+.

16. The engineered immune cell of any of claims 1-15, wherein the immune cell is an antigen presenting cell.

17. The engineered immune cell of any of claims 1-16, wherein the immune cell is a primary cell obtained from a subject.

18. The engineered immune cell of claim 17, wherein the subject is a human subject.

19. The engineered immune cell of any of claims 1-18, wherein the at least one affinity-modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the binding affinity of the wild-type IgSF domain for the at least one cell surface cognate binding partner.

20. The engineered immune cell of any of claims 1-19, wherein the wild-type IgSF domain is from an IgSF family member of a family selected from B7 family, 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, 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.

21. The engineered immune cell of any of claims 1-20, wherein the wild-type IgSF domain is from an IgSF member selected from the group consisting of PD-L1, PD-L2, CD80, CD86, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R, NKp30, VISTA, VSIG3, and VSIG8.

22. The engineered immune cell of any of claims 1-21, wherein the wild-type IgSF domain is a human IgSF domain.

23. The engineered immune cell of any of claims 1-22, wherein the wild-type IgSF domain is from an IgSF member that is a ligand of an stimulatory receptor, wherein the stimulatory receptor comprises a costimulatory signaling domain.

24. The engineered immune cell of any of claims 1-23, wherein the at least one cell surface cognate binding partner is a stimulatory receptor expressed on a T-cell and the at least

one affinity-modified IgSF domain has increased binding affinity to the stimulatory receptor compared to the binding affinity of the wild-type IgSF domain to the stimulatory receptor.

25. The engineered immune cell of claim 23 or claim 24, wherein the stimulatory receptor is CD28, ICOS, or CD226.

26. The engineered immune cell of any of claims 1-22, wherein the wild-type IgSF domain is from an IgSF member that is a ligand of an inhibitory receptor, wherein the inhibitory receptor comprising an ITIM signaling domain.

27. The engineered immune cell of any one of claims 1-22 and 26, wherein the at least one cell surface cognate binding partner is an inhibitory receptor expressed on a T-cell and the at least one affinity-modified IgSF domain has increased binding affinity to the inhibitory receptor compared to the binding affinity of the wild-type IgSF domain to the inhibitory receptor.

28. The engineered immune cell of claim 25 or claim 26, wherein:

the inhibitory receptor is PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of a ligand of PD-1, CTLA-4, LAG3, TIGIT, TIM-3, BTLA, VSIG3, or VSIG8, respectively; or

the ligand of the inhibitory receptor is PD-L1, PD-L2, B7-1, B7-2, MHC class II, CD155, CD112, CEACAM-1, GAL9 or VISTA and the at least one affinity-modified IgSF domain is an affinity-modified IgSF domain of PD-L1, PD-L2, B7-1, B7-2, MHC class II, CD155, CD112, CEACAM-1, GAL9 or VISTA, respectively.

29. The engineered immune cell of any of claims 26-28, wherein the inhibitory receptor is PD-1 and the at least one affinity-modified IgSF domain is an affinity-modified IgSF of PD-L1 or is an affinity-modified IgSF of PD-L2.

30. The engineered immune cell of any of claims 1-28, wherein the affinity modified IgSF domain is an affinity modified CD155 IgSF domain or an affinity modified CD112 IgSF domain and the at least one cell surface cognate binding partner is CD226, TIGIT or CD112R.

31. The engineered immune cell of any of claims 1-30, wherein the affinity modified IgSF domain differs by no more than ten amino acid substitutions from the wildtype IgSF domain.

32. The engineered immune cell of any of claims 1-30, wherein the affinity-modified IgSF domain differs by no more than five amino acid substitutions from the wildtype IgSF domain.

33. The engineered immune cell of any of claims 1-32, wherein the one or more affinity-modified IgSF domain is or comprises an affinity modified IgV domain, an affinity modified IgC1 domain, or an affinity modified IgC2 domain, or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

34. The engineered immune cell of any of claims 1-33, wherein the immunomodulatory protein further comprises one or more non-affinity modified IgSF domains.

35. The engineered cell of any of claims 1-34, wherein the engineered immune cell further comprises a chimeric antigen receptor (CAR) or an engineered T-cell receptor (TCR).

36. An infectious agent, comprising a nucleic acid molecule that encodes an immunomodulatory protein, wherein:

the immunomodulatory protein comprises at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitutions in a wild-type IgSF domain of an IgSF family member, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

the infectious agent expresses and secretes the immunomodulatory protein.

37. The infectious agent of claim 36, wherein the immunomodulatory protein does not comprise a transmembrane domain.

38. An infectious agent, comprising a nucleic acid molecule encoding a transmembrane immunomodulatory protein (TIP), wherein the TIP comprises:

(i) an ectodomain comprising at least one non-immunoglobulin affinity-modified immunoglobulin superfamily (IgSF) domain comprising one or more amino acid substitution(s) in a wild-type IgSF domain of an IgSF family member, wherein the at least one affinity-modified IgSF domain specifically binds at least one cell surface cognate binding partner of the wild-type IgSF domain; and

(ii) a transmembrane domain.

39. The infectious agent of claim 38, wherein the transmembrane domain is the native transmembrane domain from the corresponding wild-type IgSF member.

40. The infectious agent of claim 38 or claim 39, wherein the transmembrane domain is not the native transmembrane domain from the corresponding wild-type IgSF member.

41. The infectious agent of claim 40, wherein the transmembrane domain is a transmembrane domain derived from CD8.

42. The infectious agent of any of claims 36-41, wherein the at least one affinity-modified IgSF domain has increased binding affinity to the at least one cell surface cognate binding partner compared with the binding affinity of the wild-type IgSF domain for the at least one cell surface cognate binding partner.

43. The infectious agent of any of claims 36-42, wherein the wild-type IgSF domain is from an IgSF family member of a family selected from B7 family, 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, 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.

44. The infectious agent of any of claims 36-43, wherein the wild-type IgSF domain is from an IgSF member selected from PD-L1, PD-L2, CD80, CD86, ICOS Ligand, B7-H3, B7-H4, CD28, CTLA4, PD-1, ICOS, BTLA, CD4, CD8-alpha, CD8-beta, LAG3, TIM-3, CEACAM1, TIGIT, PVR, PVRL2, CD226, CD2, CD160, CD200, CD200R or NKp30.

45. The infectious agent of any of claims 36-44, wherein the wild-type IgSF domain is a human IgSF member.

46. The infectious agent of any of claims 36-45, wherein the affinity-modified IgSF domain differs by no more than ten amino acid substitutions or no more than five amino acid substitutions from the wildtype IgSF domain.

47. The infectious agent of any of claims 36-46, wherein the affinity-modified IgSF domain is or comprises an affinity-modified IgV domain, an affinity-modified IgC1 domain or an affinity-modified IgC2 domain or is a specific binding fragment thereof comprising the one or more amino acid substitutions.

48. The infectious agent of any of claims 36-47, wherein the infectious agent is a bacteria or a virus.

49. The infectious agent of claim 48, wherein infectious agent is a virus and the virus is an oncolytic virus.

50. The infectious agent of claim 49, 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.

51. The infectious agent of claim 48, wherein the infectious agent is a virus and the virus specifically targets dendritic cells (DCs) and/or is dendritic cell-tropic.

52. The infectious agent of claim 48 or claim 51, wherein the virus is a lentiviral vector that is pseudotyped with a modified Sindbis virus envelope product.

53. The infectious agent of any of claims 36-52, further comprising a nucleic acid molecule encoding a further gene product that results in death of a target cell or that augments or boosts an immune response.

54. The infectious agent of claim 53, 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 a reprogramming human somatic cells to pluripotency.

55. A pharmaceutical composition comprising the engineered immune cell of any of claims 1-35 or the infectious agent of any of claims 36-54 and a pharmaceutically acceptable carrier.

56. The pharmaceutical composition of claim 55 that is sterile.

57. A method of introducing an immunomodulatory protein into a subject, comprising administering the engineered cell of any one of claims 1-35, the infectious agent of any of claims 36-54 and a pharmaceutical composition of claim 55 or claim 56 to the subject.

58. A method of modulating an immune response in a subject, comprising administering the engineered immune cell of any one of claims 1-35, an infectious agent of any of claims 36-54 or a pharmaceutical composition of claim 55 or claim 56 to the subject.

59. The method of claim 58, wherein modulating the immune response treats a disease or disorder in the subject.

60. The method of claim 58 or claim 59, wherein the modulating the immune response comprises increasing the immune response.

61. The method of any of claim 59 or claim 60, wherein the disease or disorder is a cancer.

62. The method of claim 58 or claim 59, wherein the modulating the immune response comprises decreasing the immune response.

63. The method of claim 59 or claim 62, wherein the disease or disorder is an inflammatory disease or condition.

64. The method of any of claims 58-63, wherein the subject is human.

65. A composition for use in the treatment of a disease or disorder, wherein the composition comprises the engineered immune cell of any of claims 1-35 or the infectious agent of any of claims 36-54 and a pharmaceutically acceptable carrier.

66. Use of a composition for the manufacture of a medicament for the treatment of a disease or disorder, wherein the composition comprises the engineered immune cell of any of claims 1-35 or the infectious agent of any of claims 36-54 and a pharmaceutically acceptable carrier.

67. The composition of claim 65 or the use of claim 66, wherein the composition modulates an immune response.

68. The composition or use of claim 67, wherein the modulating the immune response comprises increasing the immune response.

69. The composition or use of any of claims 65-68, wherein the disease or disorder is a cancer.

70. The composition or use of claim 67, wherein the modulating the immune response comprises decreasing the immune response.

71. The composition or use of any of claims 65-68 and 70, wherein the disease or disorder is an inflammatory disease or condition.

72. The composition or use of any of claims 65-71, wherein the subject is human.

FIG. 1A

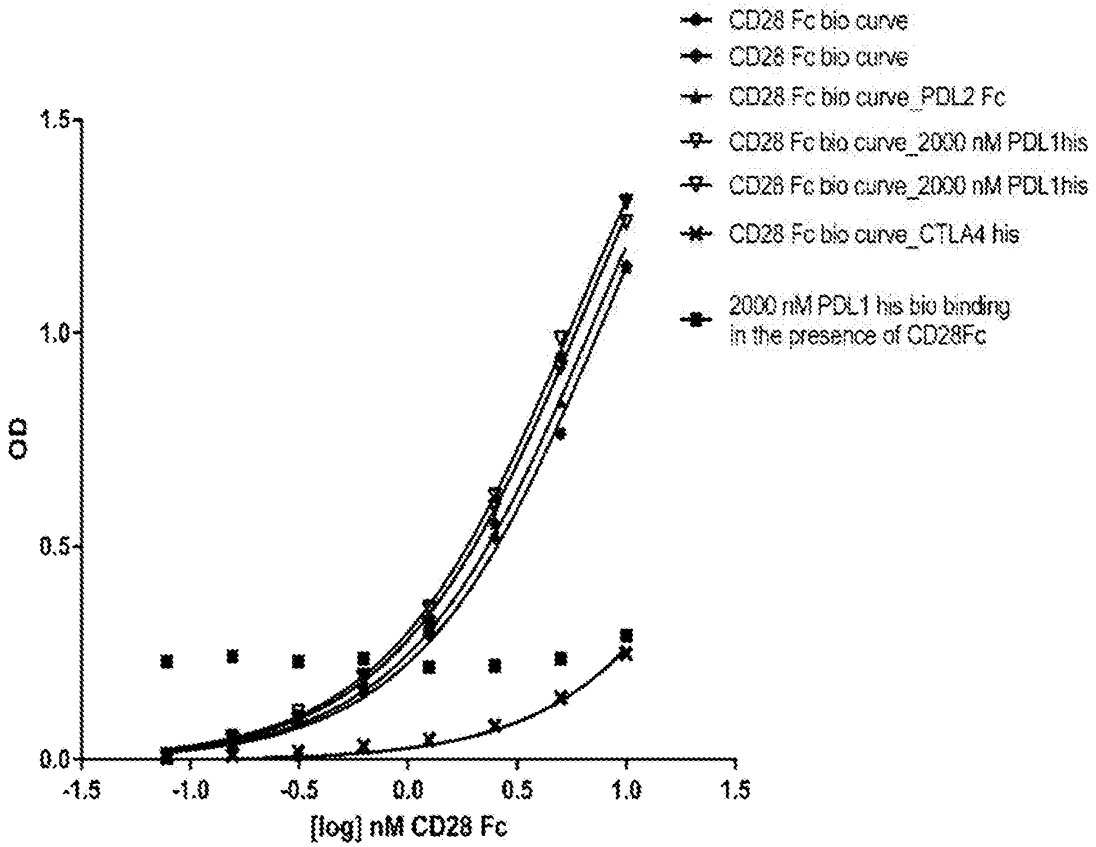

CD28 Fc bio curve
CD28 Fc bio curve
CD28 Fc bio curve_PDL2 Fc
CD28 Fc bio curve_2000 nM PDL1his
CD28 Fc bio curve_2000 nM PDL1his
CD28 Fc bio curve_CTLA4 his
2000 nM PDL1 his bio binding in the presence of CD28Fc
OD
1.5
1.0
0.5
0.0
-1.5
-1.0
-0.5
0.0
0.5
1.0
1.5
[log] nM CD28 Fc

FIG. 1B

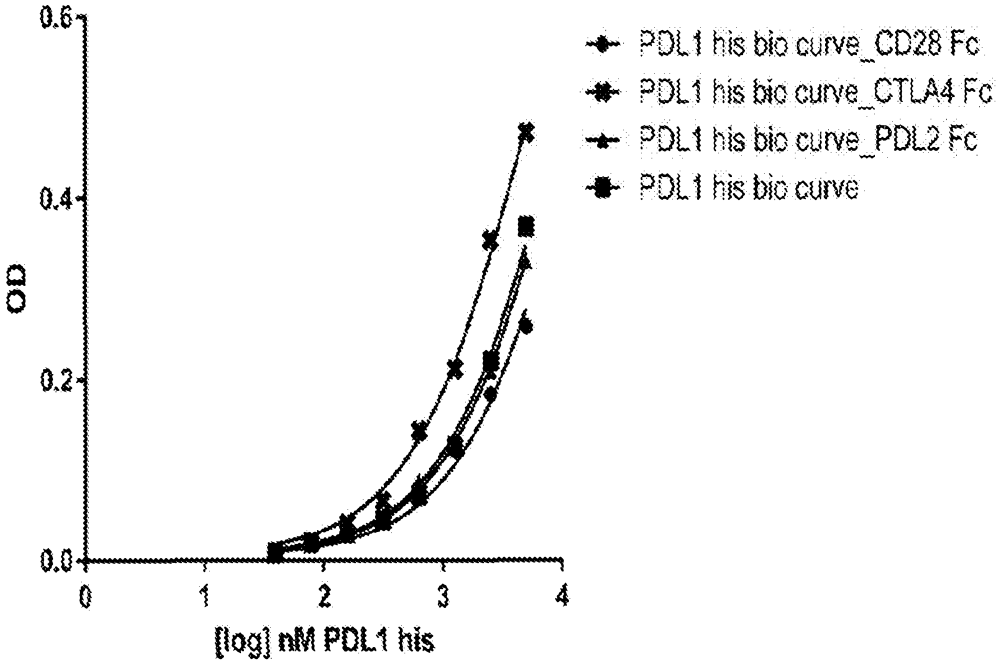
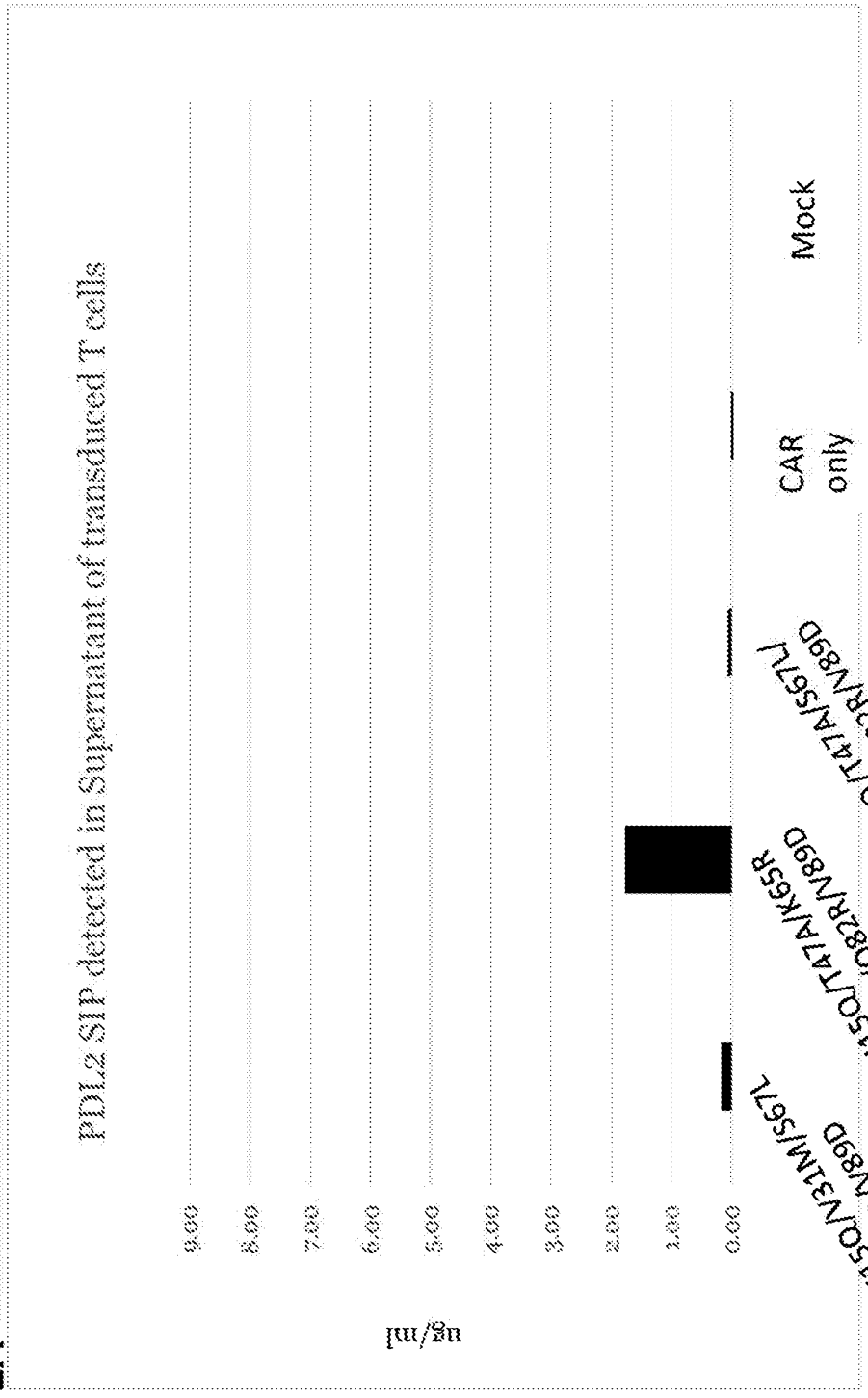

0.6
0.4
0.2
0.0
OD
0
1
2
3
4
[log] nM PDL1 his
PDL1 his bio curve_CD28 Fc
PDL1 his bio curve_CTLA4 Fc
PDL1 his bio curve_PDL2 Fc
PDL1 his bio curve

FIG. 2A


PDL2 SIP detected in Supernatant of transduced T cells
ug/ml
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
H15O/V31M/S67L /Q82R/N89D
H15O/T47A/K65R /S67L/Q82R/N89D
H15O/T47A/S67L R76G/Q82R/N89D
CAR only
Mock

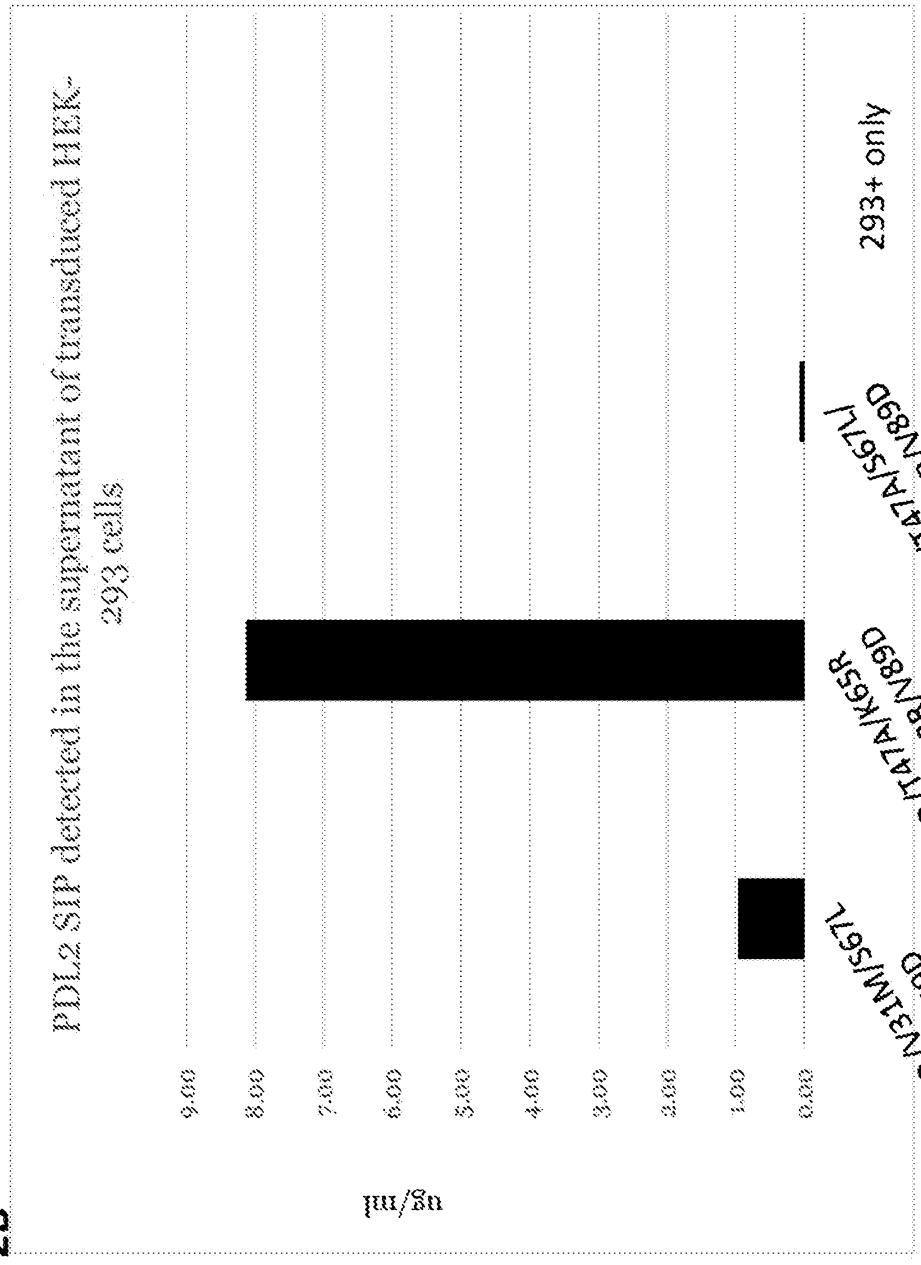

PDL2 SIP detected in the supernatant of transduced HEK-293 cells
ug/ml
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
293+ only
H150/R76G/Q82R/N89D
H150/T47A/S67L
H150/T47A/K65R/S67L/Q82R/N89D
H150/V31M/S67L/Q82R/N89D

FIG. 2B

FIG. 3A

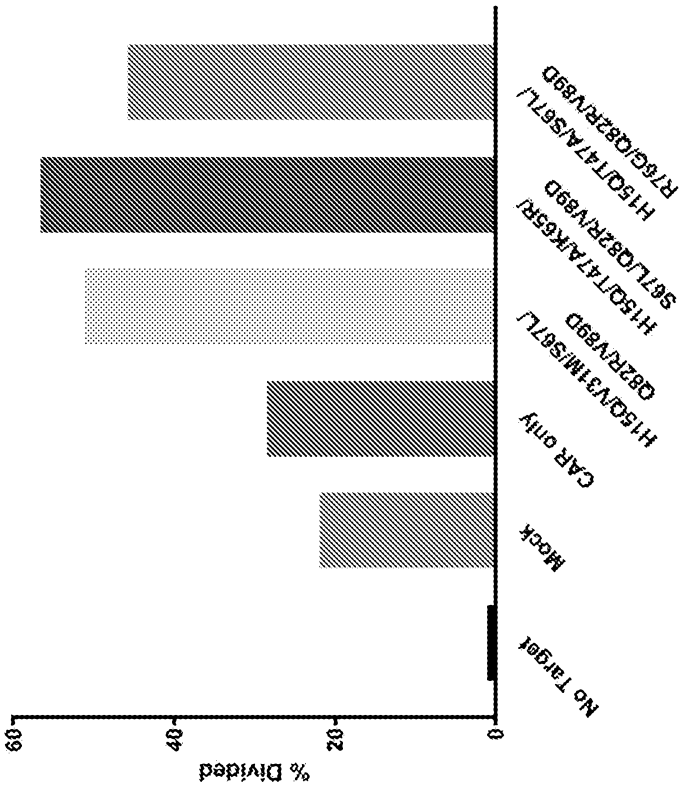
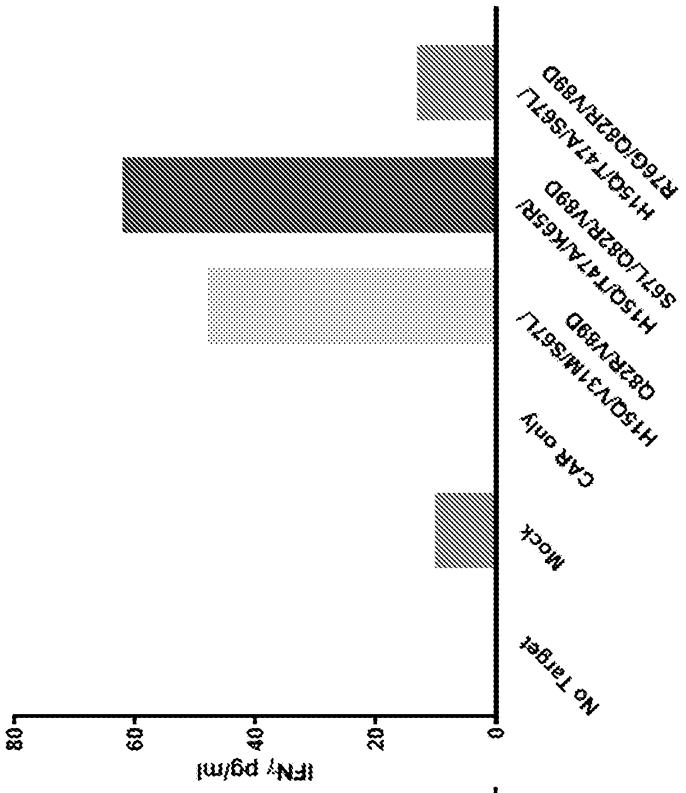

Proliferation of Transduced T cells on Day 5
% Divided
60
40
20
0
No Target
Mock
CAR only
H15Q/V31M/S67L/ Q82R/V89D
H15Q/T47A/K65R/ S67L/Q82R/V89D
H15Q/T47A/S67L/ R76G/Q82R/V89D

FIG. 3B


IFNγ dectected in the supernatant on Day 5
IFNγ pg/ml
80
60
40
20
0
No Target
Mock
CAR only
H15Q/V31M/S67L/ Q82R/V89D
H15Q/T47A/K65R/ S67L/Q82R/V89D
H15Q/T47A/S67L/ R76G/Q82R/V89D

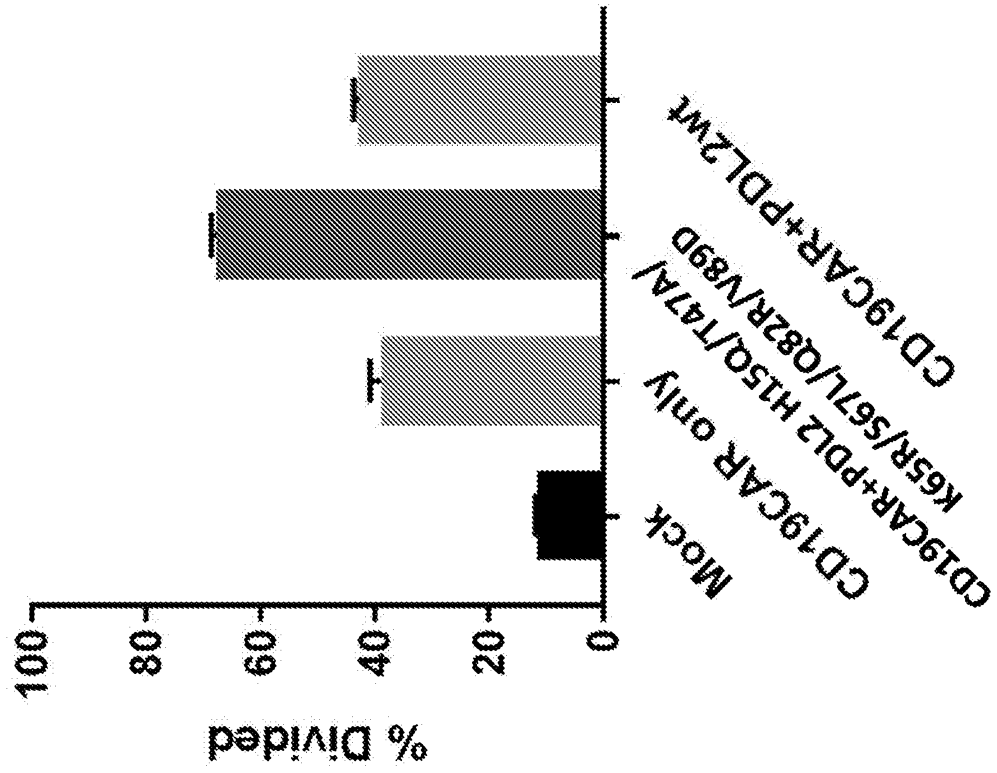

% Divided
100
80
60
40
20
0
Mock
CD19CAR only
CD19CAR+PDL2 H15Q/T47A/K65R/S67L/Q82R/V89D
CD19CAR+PDL2wt

FIG. 3C

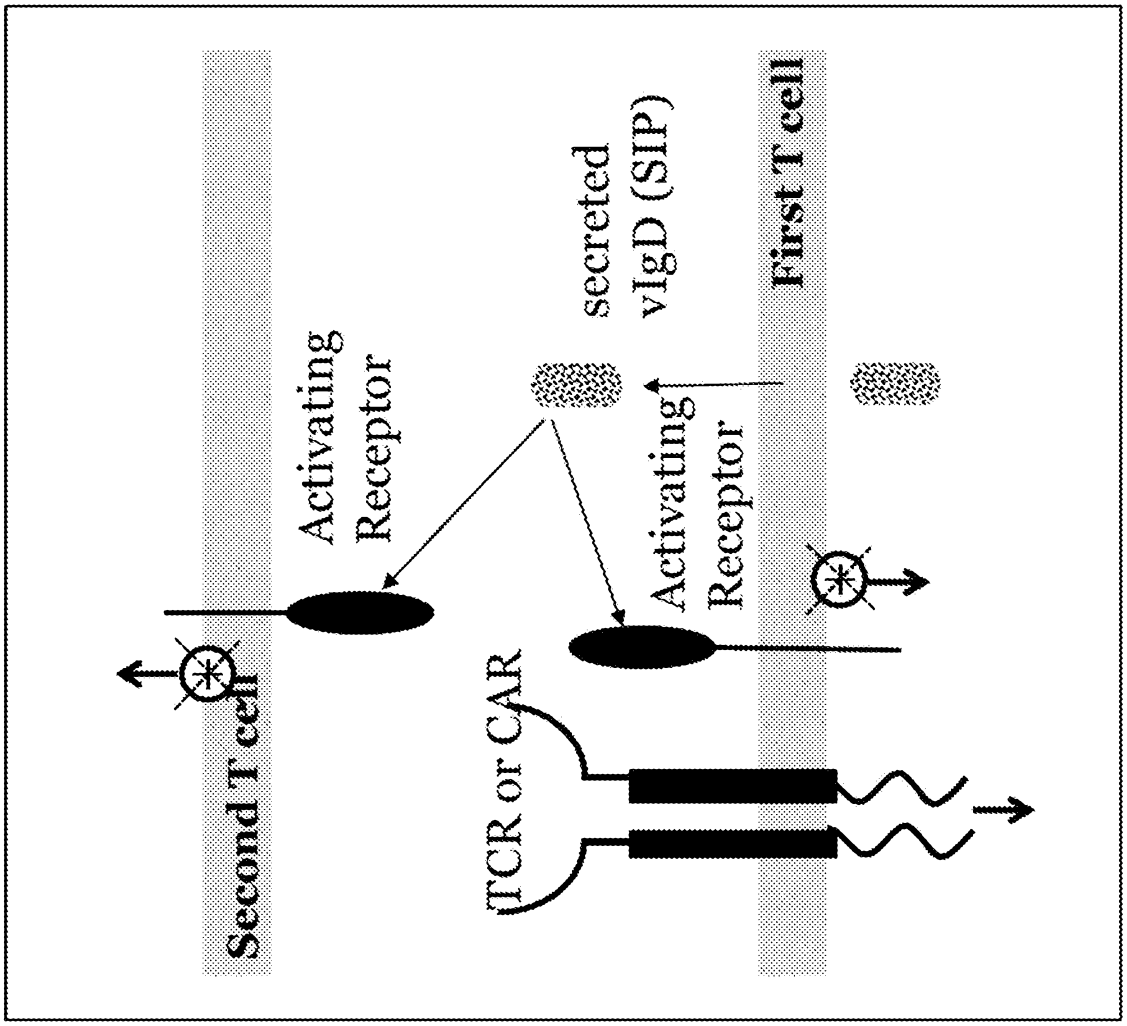

Second T cell
Activating Receptor
secreted vIgD (SIP)
First T cell
Activating Receptor
TCR or CAR

FIG. 4A

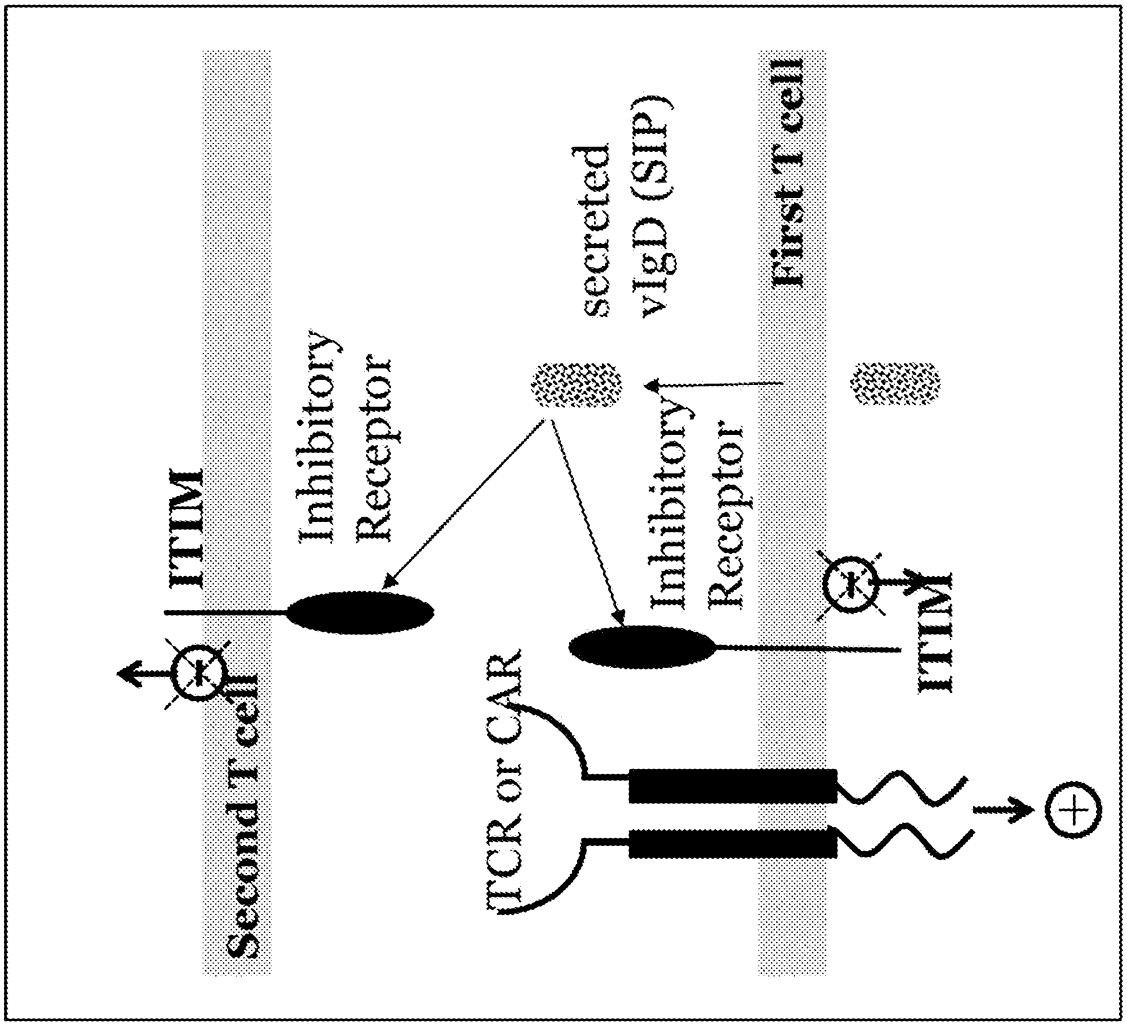

ITIM
Inhibitory Receptor
Second T cell
secreted vIgD (SIP)
Inhibitory Receptor
First T cell
ITIM
TCR or CAR

FIG. 4B

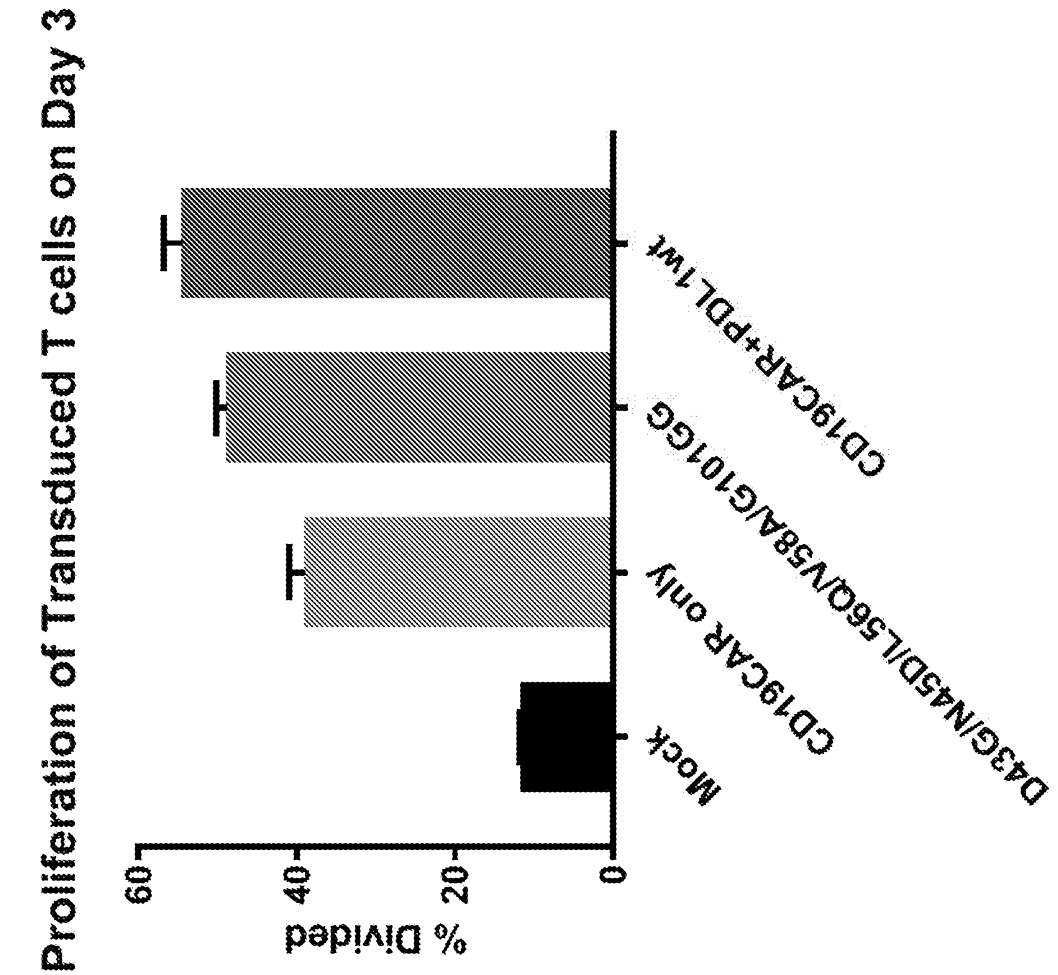

Proliferation of Transduced T cells on Day 3
% Divided
0
20
40
60
Mock
CD19CAR only
D43G/N45D/L56Q/V58A/G101GG
CD19CAR+PDL1wt

FIG. 5

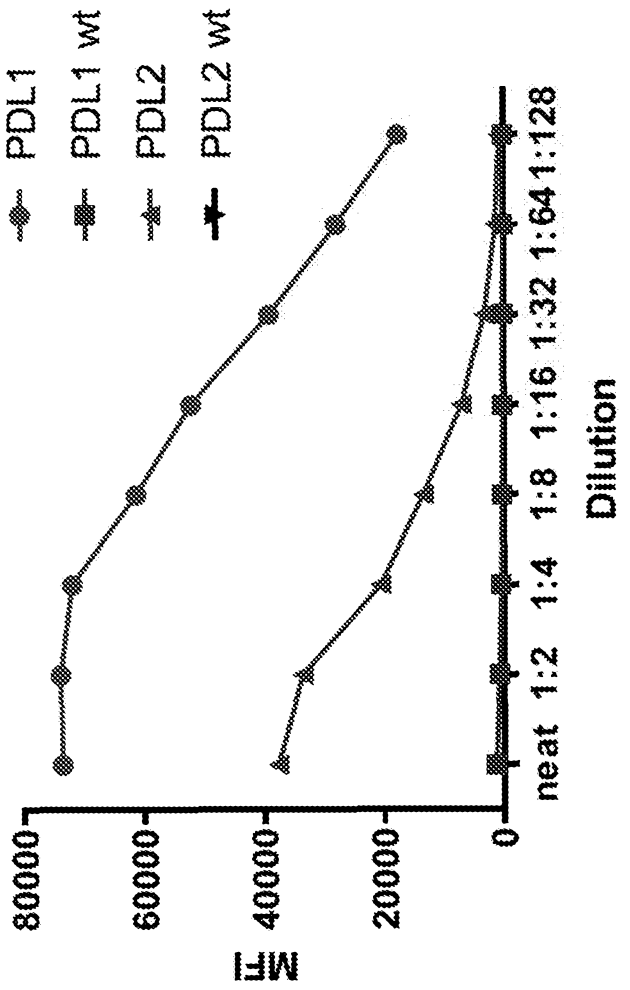

SIP transduced to 293c17
PDL1
PDL1 wt
PDL2
PDL2 wt
MFI
80000
60000
40000
20000
0
neat
1:2
1:4
1:8
1:16
1:32
1:64
1:128
Dilution

FIG. 6

SEQUENCE LISTING

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SWANSON, Ryan
KORNACKER, Michael

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50 55 60

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        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
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Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
        195                 200                 205

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    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

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50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
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Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
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Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
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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

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                165                 170                 175

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            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

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        275                 280                 285

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        35                  40                  45

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    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

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            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

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                165                 170                 175
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        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
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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
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> ICOSLG(B7RP1, CD275, ICOSL, B7-H2)

<400> 5

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
```

<210> 6
<211> 534

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD276(B7-H3)

<400> 6

```
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


<210>  7
<211>  282
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  VTCN1(B7-H4)
```

<400> 7

```
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
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD28

<400> 8

```
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

```
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>
<221>  MISC_FEATURE
<223>  CD274 (PD-L1, B7-H1) ECD

<400>  30

Phe Thr Val Thr Val Pro 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

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> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v1 ECD

<400> 55

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 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> 56
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v2 ECD

<400> 56

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 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 Ala 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> 57
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v3 ECD

<400> 57

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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ala Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 58
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v4 ECD

<400> 58

Val Ile His Met 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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 59
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v5 ECD

<400> 59

```
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 Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Ala 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> 60
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v6 ECD

<400> 60

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Leu 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 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 Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 61
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v7 ECD

<400> 61

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 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 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 Ala 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> 62
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v8 ECD

<400> 62

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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Gly Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 63
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v9 ECD

<400> 63

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 Gly 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 64
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v10 ECD

<400> 64

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 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 Gly 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Ala 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> 65
<211> 208

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v11 ECD

<400> 65

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

Ala 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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Thr Cys
115 120 125

Ser Ala 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> 66
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v12 ECD

<400> 66

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 Asn Glu Lys Asp Gly 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 Ala 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> 67
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v13 ECD

<400> 67

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 Ser 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 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 Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 68
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v14 ECD

<400> 68

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 Ser 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 Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Ala 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>  69
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v15 ECD

<400>  69

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 Glu 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 Thr 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 Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Ala Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

Gly Glu Glu Leu Asn Ala Ile Thr 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> 70
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v16 ECD

<400> 70

```
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 Gly 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 Phe Pro Thr Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Ala 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> 71
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v17 ECD

<400> 71

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 Glu Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Ser 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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 72
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v18 ECD

<400> 72

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 Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Pro 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>  73
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v19 ECD

<400>  73

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 Glu 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 Ala 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> 74
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v20 ECD

<400> 74

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 Gly 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> 75
<211> 208
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v21 ECD

<400> 75

```
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 Val 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 Gly 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Ala 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> 76
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v22 ECD

<400> 76

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 Met 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 Gly 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 Ser 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> 77
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v23 ECD

<400> 77

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 Thr 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 Gly 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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Asn Ala Ile Thr 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> 78
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v24 ECD

<400> 78

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 His 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 Gly 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 Gly Lys Asp Gly 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 Ala 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>  79
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v25 ECD

<400>  79

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 Glu Lys Lys Met Val Leu Gly 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 Phe Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 80
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v26 ECD

<400> 80

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 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 Ala 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> 81
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v27 ECD

<400> 81

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 His 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 Gly Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Ala Pro Ser
100 105 110

Ile Ser Asp Leu 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> 82
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v28 ECD

<400> 82

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 His 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 Gly 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

```
Ser Ala 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>  83
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v29 ECD

<400>  83

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 Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Ser 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> 84
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v30 ECD

<400> 84

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 Thr 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 Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Ser 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>  85
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v31 ECD

<400>  85
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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 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 Phe Pro Ala Pro Ser
            100                 105                 110


Ile Ser Asp Phe Glu Ile Pro Ser Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125


Ser Ala 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
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<210> 86
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v32 ECD

<400> 86

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 Val Val Leu Asp Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Gly 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 Gly Glu Gly Thr Tyr
65 70 75 80

Glu Cys Ala Val Leu Lys Tyr Glu Glu 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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>  87
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v33 ECD

<400>  87

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 Ala 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 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 Pro 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> 88
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v34 ECD

<400> 88

Val Ile His Val Thr Lys Glu Val Lys Glu Val Val Thr Leu Phe 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 Glu Lys Lys Met Val Leu Gly 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 Ala Ser Gly Gly Phe Pro Glu Leu His Leu Ser Trp Leu Glu Asn
130 135 140

Gly Glu Glu Leu Asn Ala Ile Thr 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> 89
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v35 ECD

<400> 89

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 Phe Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Gly Lys Asp Gly 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 Ser Ser Asn Ile Arg Arg Ile Ile Cys
115 120 125

Ser Ala 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> 90
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v36 ECD

<400> 90

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 Gly Pro 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 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 Ser 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
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<210> 91
<211> 208

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v37 ECD

<400> 91

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 Gly Leu Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Leu Pro Thr Pro Ser
100 105 110

Ile Ser Asp Phe Glu Ile Pro Ser 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> 92
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v38 ECD

<400> 92

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 Asp Ile Leu Trp
20 25 30

His Lys Glu Gly Lys Ile Val Leu Ala Met Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu 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>  93
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v39 ECD

<400>  93

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 Asp Ile Leu Trp
            20                  25                  30


His Lys Glu Gly Lys Ile Val Leu Ala Met Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu 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 Ser
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> 94
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v40 ECD

<400> 94

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 Asp Ile Leu Trp
20 25 30

His Lys Glu Gly Lys Ile Val Leu Ala Thr Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65                  70                  75                  80


Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu 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 Ser 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>  95
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v41 ECD

<400>  95

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 Gly Leu Ala Gln Thr Asp Ile Leu Trp
            20   25   30

His Lys Glu Gly Lys Ile Val Leu Ala Met Arg Ser Gly Asp Thr Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu 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

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu Arg
                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 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 Ser 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> 96
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v42 ECD

<400> 96

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 Asp Ile Leu Trp
            20   25   30

His Lys Glu Gly Lys Ile Val Leu Ala Met Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu 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 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> 97
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v43 ECD

<400> 97

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 Val Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Gln 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

Arg Cys Val Val Ile Lys Tyr Glu Arg Leu Glu Asn Gln Gly 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> 98
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v44 ECD

<400> 98

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 Ile 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 Gly 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> 99
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v45 ECD

<400> 99

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 Arg Lys Gly Tyr Arg 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 Ser 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

Ser 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> 100
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v46 ECD

<400> 100

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 Arg Lys Gly Tyr Arg 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> 101
<211> 208
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v47 ECD

<400> 101

```
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 Gly Gln Ile Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu 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


Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu His
                85                  90                  95


Leu Ala Gly 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 Ala 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> 102
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v48 ECD

<400> 102

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 Asp Arg Lys Gly Tyr Arg 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> 103
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v49 ECD

<400> 103

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 Gly Gln Ile Val Met 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> 104
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v50 ECD

<400> 104

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 Gly 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>  105
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v51 ECD

<400>  105

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 His Ile His Trp
            20                  25                  30
```

```
Gln Lys Glu Lys Lys Met Val Leu Gly 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 Asn Gly Glu Asn Gly Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Ser 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> 106
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v52 ECD

<400> 106

Val Ile His Val Thr Lys Glu Val Lys Glu Val Thr Thr Leu Ser Cys
1 5 10 15

Gly Leu 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 Val Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Lys 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 Ser 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 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> 107
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v53 ECD

<400> 107

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 Val Ile Phe Trp
20 25 30

Gln Lys Glu Gly Lys Leu Val Leu Thr Met Gln 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

Arg Cys Ile Val Ile Lys Tyr Glu Arg Leu Glu Asn Gln Gly 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> 108
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v54 ECD

<400> 108

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 Pro Ala Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Glu 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>  109
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v1 ECD

<400>  109

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 Ser 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>  110
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v2 ECD

<400>  110

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 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> 111
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v3 ECD

<400> 111

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 Asp 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> 112
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v4 ECD

<400> 112

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 Tyr 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 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 Leu 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 Pro 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>  113
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v5 ECD

<400>  113
```

```
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 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> 114
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v6 ECD

<400> 114

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 Ser 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 Cys Pro Arg Pro Asn Val Cys 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>  115
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v7 ECD

<400>  115

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 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 Arg 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>  116
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v8 ECD
```

<400> 116

```
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 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 Asp 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

Ala Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
225 230 235

<210> 117
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v9 ECD

<400> 117

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 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 Arg 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

Ala Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
225 230 235

<210> 118
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v10 ECD

<400> 118

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 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 Arg 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>  119
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> ICOSL v11 ECD

<400> 119

```
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 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 Gly 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> 120
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v12 ECD

<400> 120

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 Tyr 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>  121
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v13 ECD

<400>  121

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 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 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> 122
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v14 ECD

<400> 122

```
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 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 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>  123
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v15 ECD

<400>  123

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 Ser 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 Gly Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn
    130   135   140

Gly Tyr Pro Arg Pro Asn Val Cys 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> 124
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v16 ECD

<400> 124

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 Ser 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 Cys 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> 125
<211> 238

<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v17 ECD

<400> 125

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 Ser 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 Arg 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> 126
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v18 ECD

<400> 126

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 Tyr 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 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 Cys 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>  127
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v19 ECD

<400>  127

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 Tyr 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 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

Pro 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 Arg 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> 128
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v20 ECD

<400> 128

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 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

Pro 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 Arg 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> 129
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v21 ECD

<400> 129

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 Ser 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


Glu 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>  130
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v22 ECD

<400>  130

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 Ala 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> 131
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v23 ECD

<400> 131

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 Asp Ser Pro 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> 132
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v24 ECD

<400> 132

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 Lys 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 Pro
        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>  133
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v25 ECD

<400>  133

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 Ser 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 His 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> 134
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v26 ECD

<400> 134

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 Asp 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 Ala 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>  135
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v27 ECD

<400>  135

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 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 Thr 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> 136
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v28 ECD

<400> 136

```
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 Ser 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 Pro
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> 137
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v29 ECD

<400> 137

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 Ser 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 His 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 Ser 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>  138
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v30 ECD

<400>  138

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 Ser 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 Gln 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 Pro 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> 139
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v31 ECD

<400> 139

```
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 Ser 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 Gly 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> 140
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v32 ECD

<400> 140

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 Asp 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 His 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>  141
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v33 ECD

<400>  141

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 Ser 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 Asp Cys Phe
                85                  90                  95


Val Phe Ser Arg 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>  142
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v34 ECD
```

<400> 142

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 Ser 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 Asp Cys Phe
85 90 95

Val Phe Ser Arg Ser Leu Glu Phe Gln Glu Val Leu Ser Val Glu Val
100 105 110

Thr Leu His Val Ala Ala Asn Ser 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> 143
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v1 ECD

<400> 143

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> 144
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v2 ECD

<400> 144

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> 145
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v3 ECD

<400> 145

```
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>  146
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NKp30 v4 ECD

<400>  146

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>  147
<211>  117
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  NKp30 v5 ECD

<400>  147

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> 148
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v1 ECD

<400> 148

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> 149
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v2 ECD

<400> 149

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> 150
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v3 ECD

<400> 150

```
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> 151
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 v4 ECD

<400> 151

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>  152
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 WT IgV

<400>  152

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> 153
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v1 IgV

<400> 153

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
100

<210> 154
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v4 IgV

<400> 154

Val Ile His Met 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
            100

<210> 155
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v6 IgV

<400> 155

Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1   5   10   15

Gly His Asn Leu 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 Ser Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  156
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v7 IgV

<400>  156

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 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
            100
```

<210> 157
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v9 IgV

<400> 157

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 Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 158
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v10 IgV

<400> 158

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 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 Gly Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 159
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v11 IgV

<400> 159

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

Ala Cys Val Val Leu Lys Tyr Glu Lys Asp Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 160
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v12 IgV

<400> 160

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 Asn Glu Lys Asp Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 161
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v13 IgV

<400> 161

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 Ser 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 Lys His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 162
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v14 IgV

<400> 162

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 Ser 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
            100


<210>  163
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v15 IgV

<400>  163

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 Glu 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 Thr 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
            100

<210> 164
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v16 IgV

<400> 164

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 Gly 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
            100

<210> 165
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v17 IgV

<400> 165

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 Glu Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Ser 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
100

<210> 166
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v19 IgV

<400> 166

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 Glu Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 167
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v21 IgV

<400> 167

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 Val 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 Gly Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 168
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v22 IgV

<400> 168

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 Met 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 Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 169
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v23 IgV

<400> 169

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 Thr 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 Gly 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
            100
```

<210> 170
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v24 IgV

<400> 170

```
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 His 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 Gly 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 Gly Lys Asp Gly Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  171
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v25 IgV

<400>  171

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 Glu Lys Lys Met Val Leu Gly 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
            100


<210>  172
<211>  101
```

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v26 IgV

<400> 172

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 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> 173
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v27 IgV

<400> 173

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 His 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 Gly Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  174
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v28 IgV

<400>  174

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 His 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 Gly 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> 175
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v30 IgV

<400> 175

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 Thr 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
100

<210> 176
<211> 101
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v32 IgV

<400> 176

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 Val Val Leu Asp Met Ile Ser Gly Asp Met Asn
35 40 45

Ile Gly 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 Gly Glu Gly Thr Tyr
65 70 75 80

Glu Cys Ala Val Leu Lys Tyr Glu Glu Asp Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 177
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v33 IgV

<400> 177

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 Ala 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 Ala Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  178
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v34 IgV

<400>  178

Val Ile His Val Thr Lys Glu Val Lys Glu Val Val Thr Leu Phe 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 Glu Lys Lys Met Val Leu Gly 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> 179
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v35 IgV

<400> 179

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 Phe Val Ile Arg Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Gly Lys Asp Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 180
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v36 IgV

<400> 180

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 Gly Pro 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 Ala Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 181
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v37 IgV

<400> 181

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 Gly Leu Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 182
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v38 IgV

<400> 182

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 Asp Ile Leu Trp
20 25 30

His Lys Glu Gly Lys Ile Val Leu Ala Met Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 183
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v40 IgV

<400> 183

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 Asp Ile Leu Trp
20 25 30

His Lys Glu Gly Lys Ile Val Leu Ala Thr Arg 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 Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 184
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v41 IgV

<400> 184

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 Gly Leu Ala Gln Thr Asp Ile Leu Trp
            20   25   30

His Lys Glu Gly Lys Ile Val Leu Ala Met Arg Ser Gly Asp Thr Asn
        35   40   45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu 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

Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu Arg
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 185
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v43 IgV

<400> 185

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 Val Ile Tyr Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Gln 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

Arg Cys Val Val Ile Lys Tyr Glu Arg Leu Glu Asn Gln Gly Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 186
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v44 IgV

<400> 186

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 Ile 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 Gly Phe Lys Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 187
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD80 v45 IgV

<400> 187

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 Arg Lys Gly Tyr Arg Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 188
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v47 IgV

<400> 188

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 Gly Gln Ile Val Leu Thr Met Met Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu 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


Val Cys Val Val Arg Lys Tyr Glu Asn Asp Thr Pro Val Leu Glu His
                85                  90                  95


Leu Ala Gly Val Thr
            100


<210>  189
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v48 IgV

<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 Asp Arg Lys Gly Tyr Arg Arg Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 190
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v49 IgV

<400> 190

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 Gly Gln Ile Val Met 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> 191
<211> 101
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v50 IgV

<400> 191

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 Gly 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> 192
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v51 IgV

<400> 192

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 His Ile His Trp
            20   25   30

Gln Lys Glu Lys Lys Met Val Leu Gly 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 Asn Gly Glu Asn Gly Phe Lys Arg Glu His
                85                  90                  95


Leu Ala Glu Val Thr
            100


<210>  193
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v52 IgV

<400>  193

Val Ile His Val Thr Lys Glu Val Lys Glu Val Thr Thr Leu Ser Cys
1               5                   10                  15


Gly Leu 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 Val Ser Gly Asp Met Asn
        35                  40                  45


Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Leu Asp Ile Thr Asn Asn
    50                  55                  60


Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Lys 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> 194
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v53 IgV

<400> 194

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 Val Ile Phe Trp
20 25 30

Gln Lys Glu Gly Lys Leu Val Leu Thr Met Gln 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

Arg Cys Ile Val Ile Lys Tyr Glu Arg Leu Glu Asn Gln Gly Glu His
85 90 95

Leu Ala Glu Val Thr
100

<210> 195
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v54 IgV

<400> 195

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 Pro Ala Pro Arg Pro Ser Asp Glu Gly Thr Tyr
65   70   75   80

Glu Cys Val Val Leu Glu Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85   90   95

Leu Ala Glu Val Thr
            100

<210> 196
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL WT IgV

<400> 196

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
100 105 110

<210> 197
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v1 IgV

<400> 197

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 Ser 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
100 105 110

<210> 198
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v2 IgV

<400> 198

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 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
100 105 110

<210> 199
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v3 IgV

<400> 199

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 Asp 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
            100                 105                 110


<210>  200
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v4 IgV

<400>  200

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 Tyr 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 Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu
100 105 110

<210> 201
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v5 IgV

<400> 201

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
100 105 110

<210> 202
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v10 IgV

<400> 202

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 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 Arg Phe His Cys Leu
                85   90   95

Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu
            100   105   110

<210> 203
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v11 IgV

<400> 203

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 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 Gly Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu
            100                 105                 110


<210>  204
<211>  111
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  ICOSL v12 IgV

<400>  204

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 Tyr 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
100 105 110

<210> 205
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v13 IgV

<400> 205

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 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 Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu
100 105 110

<210> 206
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> ICOSL v14 IgV

<400> 206

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 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
            100   105   110

<210> 207
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v22 IgV

<400> 207

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 Ala 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
            100                 105                 110
```

<210> 208
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v23 IgV

<400> 208

```
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 Asp Ser Pro 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
100 105 110

<210> 209
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v24 IgV

<400> 209

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 Lys 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
100 105 110

<210> 210
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> ICOSL v28 IgV

<400> 210

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 Ser 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 Pro
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
100 105 110

<210> 211
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v30 IgV

<400> 211

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 Ser 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 Gln 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
            100   105   110

<210> 212
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v33 IgV

<400> 212

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 Ser 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 Asp Cys Phe
                85   90   95

Val Phe Ser Arg Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu
            100   105   110

<210> 213
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v34 IgV

<400> 213

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 Ser 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 Asp Cys Phe
85 90 95

Val Phe Ser Arg Ser Leu Glu Phe Gln Glu Val Leu Ser Val Glu
100 105 110

<210> 214
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 WT IgC-like

<400> 214

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>  215
<211>  108
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  NKp30 v1 IgC-like

<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 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>  216
<211>  108
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  NKp30 v2 IgC-like

<400>  216

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> 217
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> NKp30 v3 IgC-like

<400> 217

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> 218
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v4 IgC-like

<400> 218

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> 219
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v5 IgC-like

<400> 219

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> 220
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 WT IgV

<400> 220

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
1 5 10 15

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
20 25 30

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
35 40 45

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
50 55 60

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
65 70 75 80

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
85 90 95

Glu Leu Ser

<210> 221
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD86 v1 IgV

<400> 221

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
1 5 10 15

Ser Leu Ser Glu Leu Val Val Phe Trp His Asp Gln Glu Asn Leu Val
20 25 30

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
35 40 45

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
50 55 60

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
65 70 75 80

Leu His Lys Lys Pro Thr Gly Met Ile Arg Ile His His Met Asn Ser
85 90 95

Glu Leu Ser

<210> 222
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD86 v2 IgV

<400> 222

```
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
1               5                   10                  15


Ser Leu Ser Glu Leu Val Val Phe Trp His Asp Gln Glu Asn Leu Val
            20                  25                  30


Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
        35                  40                  45


Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
    50                  55                  60


Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
65                  70                  75                  80


His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
                85                  90                  95


Glu Leu Ser



<210>  223
<211>  99
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD86 v3 IgV

<400>  223

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
1               5                   10                  15


Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
            20                  25                  30


Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
        35                  40                  45
```

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
    50   55   60

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
65   70   75   80

Leu His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
                85   90   95

Glu Leu Ser

<210> 224
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD86 v4 IgV

<400> 224

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
1   5   10   15

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
            20   25   30

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
        35   40   45

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
    50   55   60

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
65   70   75   80

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His His Met Asn Ser
                85   90   95

Glu Leu Ser

<210> 225
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> VH signal peptide

<400> 225

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
1 5 10 15

Val Ser Ala

<210> 226
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> IgG1 Fc

<400> 226

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>  227
<211>  235
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
```

<223> IgG2 Fc

<400> 227

```
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> 228
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> IgV-IgV linker

<400> 228

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 229
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> IgV-Fc linker 1

<400> 229

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 230
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IgV-Fc linker 2

<400> 230

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala
1   5   10

<210> 231
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT linker 1

<400> 231

Lys Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro
1   5   10   15

<210> 232
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT linker 2

<400> 232

Thr Thr Lys Gln Glu His Phe Pro Asp Asn
1   5   10

<210> 233
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL WT linker 1

<400> 233

Val Thr Leu His Val Ala Ala Asn Phe Ser Val
1   5   10

<210> 234
<211> 29
<212> PRT
<213> Artificial Sequence

<220>

<223> ICOSL WT linker 2

<400> 234

Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Thr
1   5   10   15

Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
            20   25

<210> 235
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 WT linker 1

<400> 235

Val Glu Lys Glu His Pro Gln Leu Gly
1   5

<210> 236
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 WT linker 1

<400> 236

Ala Pro Leu Lys Ile Gln Ala Tyr Phe
1   5

<210> 237
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 WT linker 2

<400> 237

Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
1   5   10   15

Thr Glu

<210> 238
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> CD86 WT linker 3

<400> 238

Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro
1 5 10 15

Pro Pro Asp His Ile Pro
20

<210> 239
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v35 ECD

<400> 239

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 Ser 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 Glu 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>  240
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ICOSL v35 IgV

<400>  240
```

```
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 Ser 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 Glu Phe Gln Glu Val Leu Ser Val Glu
            100                 105                 110


<210>  241
<211>  116
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  CD155 IgV

<400>  241

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> 242
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 ECD

<400> 242

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> 243
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 ECD

<400> 243

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> 244
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v3 ECD

<400> 244

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> 245
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v4 ECD

<400> 245

```
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> 246
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v5 ECD

<400> 246

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> 247
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v6 ECD

<400> 247

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> 248
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v7 ECD

<400> 248

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> 249
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v8 ECD

<400> 249

```
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> 250
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 ECD

<400> 250

```
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> 251
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v10 ECD

<400> 251

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> 252
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v11 ECD

<400> 252

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> 253
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 ECD

<400> 253

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> 254
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v13 ECD

<400> 254

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> 255
<211> 323
<212> PRT
<213> Artificial Sequence

<220>

<223> CD155 v14 ECD

<400> 255

```
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>  256
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v15 ECD

<400>  256

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> 257
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v16 ECD

<400> 257

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> 258
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v17 ECD

<400> 258

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> 259
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v18 ECD

<400> 259

```
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> 260
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v19 ECD

<400> 260

```
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>  261
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v20 ECD

<400>  261

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> 262
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v21 ECD

<400> 262

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> 263
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 ECD

<400> 263

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> 264
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 IgV

<400> 264

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> 265
<211> 116

<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 IgV

<400> 265

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> 266
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v3 IgV

<400> 266

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>  267
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v4 IgV

<400>  267

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> 268
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v5 IgV

<400> 268

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>  269
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v6 IgV

<400>  269

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> 270
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v7 IgV

<400> 270

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> 271
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v8 IgV

<400> 271

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> 272
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 IgV

<400> 272

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>  273
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v10 IgV

<400>  273

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> 274
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v11 IgV

<400> 274

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> 275
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 IgV

<400> 275

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> 276
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v13 IgV

<400> 276

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> 277
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v14 IgV

<400> 277

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> 278
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v15 IgV

<400> 278

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> 279
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v16 IgV

<400> 279

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> 280
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v17 IgV

<400> 280

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> 281
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> CD155 v18 IgV

<400> 281

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> 282
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v19 IgV

<400> 282

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>  283
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v20 IgV

<400>  283

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> 284
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v21 IgV

<400> 284

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> 285
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 IgV

<400> 285

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> 286
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD112 IgV

<400> 286

Gln Asp Val Arg Val Gln Val 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> 287
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v1 ECD

<400> 287

Gln Asp Val Arg Val Gln Val 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>  288
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v2 ECD

<400>  288

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> 289
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v3 ECD

<400> 289

Gln Asp Val Arg Val Gln Val 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> 290
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v4 ECD

<400> 290

Gln Asp Val Arg Val Gln Val 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> 291
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v5 ECD

<400> 291

Gln Asp Val Arg Val Gln Val 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> 292
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v6 ECD

<400> 292

```
Gln Asp Val Arg Val Gln 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>  293
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v7 ECD

<400>  293

Gln Asp Val Arg Val Gln Val 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>  294
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v8 ECD

<400>  294

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> 295
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 ECD

<400> 295

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> 296
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 ECD

<400> 296

Gln Asp Val Arg Val Gln Val 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> 297
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 ECD

<400> 297

```
Gln Asp Val Arg Val Gln Val 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>  298
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v12 ECD

<400>  298

Gln Asp Val Arg Val Gln Val 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> 299
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v13 ECD

<400> 299

Gln Asp Val Arg Val Gln Val 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>  300
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v14 ECD

<400>  300

Gln Asp Val Arg Val Gln Val 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 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> 301
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v15 ECD

<400> 301

Gln Asp Val Arg Val Gln Val 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> 302
<211> 329
<212> PRT
<213> Artificial Sequence

<220>

<223> CD112 v16 ECD

<400> 302

```
Gln Asp Val Arg Val Gln Val 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


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>  303
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v17 ECD

<400>  303

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> 304
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v18 ECD

<400> 304

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> 305
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v19 ECD

<400> 305

Gln Asp Val Arg Val Gln Val 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> 306
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v20 ECD

<400> 306

Gln Asp Val Arg Val Gln 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> 307
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v21 ECD

<400> 307

```
Gln Asp Val Arg Val Gln Val 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>  308
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v22 ECD

<400>  308

Gln Asp Val Arg Val Gln Val 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> 309
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v23 ECD

<400> 309

Gln Asp Val Arg Val Gln Val 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>  310
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v24 ECD

<400>  310

Gln Asp Val Arg Val Gln 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> 311
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 ECD

<400> 311

Gln Asp Val Arg Val Gln Val 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> 312
<211> 329

<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v26 ECD

<400> 312

Gln Asp Val Arg Val Gln Val 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>  313
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v27 ECD

<400>  313

Gln Asp Val Arg Val Gln Val 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>  314
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v28 ECD

<400>  314

Gln Asp Val Arg Val Gln Val 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>  315
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v29 ECD

<400>  315

Gln Asp Val Arg Val Gln Val 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>  316
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v30 ECD

<400>  316

Gln Asp Val Arg Val Gln Val 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> 317
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v31 ECD

<400> 317

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>  318
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v32 ECD

<400>  318
```

```
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> 319
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v33 ECD

<400> 319

Gln Asp Val Arg Val Gln Val 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> 320
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 ECD

<400> 320

Gln Asp Val Arg Val Gln Val 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> 321
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 ECD

<400> 321

Gln Asp Val Arg Val Gln Val 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> 322
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 ECD

<400> 322

Gln Asp Val 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> 323
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 ECD

<400> 323

Gln Asp Val Arg Val Gln Val 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> 324
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v38 ECD

<400> 324

```
Gln Asp Val Arg Val Gln 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> 325
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v39 ECD

<400> 325

Gln Asp Val Arg Val Gln Val 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 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> 326
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v40 ECD

<400> 326

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 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> 327
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v41 ECD

<400> 327

Gln Asp Val Arg Val Gln Val 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> 328
<211> 329
<212> PRT
<213> Artificial Sequence

<220>

<223> CD112 v42 ECD

<400> 328

```
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


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>  329
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v43 ECD

<400>  329

Gln Asp Val Arg Val Gln Val 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>  330
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v44 ECD

<400>  330

Gln Asp Val Arg Val Gln 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> 331
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v45 ECD

<400> 331

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> 332
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v46 ECD

<400> 332

Gln Asp Val Arg Val Gln Val 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 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>  333
<211>  329
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> CD112 v47 ECD

<400> 333

```
Gln Asp Val Arg Val Gln Val 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>  334
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v1 IgV

<400>  334

Gln Asp Val Arg Val Gln Val 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> 335
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v2 IgV

<400> 335

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> 336
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v3 IgV

<400> 336

Gln Asp Val Arg Val Gln Val 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> 337
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v4 IgV

<400> 337

Gln Asp Val Arg Val Gln Val 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> 338
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v5 IgV

<400> 338

Gln Asp Val Arg Val Gln Val 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> 339
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v6 IgV

<400> 339

Gln Asp Val Arg Val Gln 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>  340
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v7 IgV

<400>  340

Gln Asp Val Arg Val Gln Val 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> 341
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v8 IgV

<400> 341

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> 342
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 IgV

<400> 342

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> 343
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 IgV

<400> 343

Gln Asp Val Arg Val Gln Val 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> 344
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 IgV

<400> 344

Gln Asp Val Arg Val Gln Val 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> 345
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v12 IgV

<400> 345

Gln Asp Val Arg Val Gln Val 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

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Gln Asn Val Ala Ala Phe His Pro Lys 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>  346
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v13 IgV

<400>  346

Gln Asp Val Arg Val Gln Val 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 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> 347
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v14 IgV

<400> 347

Gln Asp Val Arg Val Gln Val 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> 348
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v15 IgV

<400> 348

Gln Asp Val Arg Val Gln Val 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> 349
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v16 IgV

<400> 349

Gln Asp Val Arg Val Gln Val 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> 350
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v17 IgV

<400> 350

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> 351
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v18 IgV

<400> 351

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> 352
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v19 IgV

<400> 352

Gln Asp Val Arg Val Gln Val 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> 353
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v20 IgV

<400> 353

Gln Asp Val Arg Val Gln 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> 354
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> CD112 v21 IgV

<400> 354

Gln Asp Val Arg Val Gln Val 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> 355
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v22 IgV

<400> 355

Gln Asp Val Arg Val Gln Val 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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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>  356
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v23 IgV

<400>  356

Gln Asp Val Arg Val Gln Val 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> 357
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v24 IgV

<400> 357

Gln Asp Val Arg Val Gln 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> 358
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 IgV

<400> 358

Gln Asp Val Arg Val Gln Val 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> 359
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v26 IgV

<400> 359

Gln Asp Val Arg Val Gln Val 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> 360
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v27 IgV

<400> 360

Gln Asp Val Arg Val Gln Val 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> 361
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v28 IgV

<400> 361

Gln Asp Val Arg Val Gln Val 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> 362
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v29 IgV

<400> 362

Gln Asp Val Arg Val Gln Val 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> 363
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v30 IgV

<400> 363

Gln Asp Val Arg Val Gln Val 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> 364
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v31 IgV

<400> 364

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> 365
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v32 IgV

<400> 365

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>  366
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v33 IgV

<400>  366

Gln Asp Val Arg Val Gln Val 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> 367
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 IgV

<400> 367

Gln Asp Val Arg Val Gln Val 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> 368
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 IgV

<400> 368

Gln Asp Val Arg Val Gln Val 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> 369
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 IgV

<400> 369

Gln Asp Val 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> 370
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 IgV

<400> 370

```
Gln Asp Val Arg Val Gln Val 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>  371
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v38 IgV

<400>  371

Gln Asp Val Arg Val Gln 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
        115                 120                 125


<210>  372
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v39 IgV

<400>  372

Gln Asp Val Arg Val Gln Val 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> 373
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v40 IgV

<400> 373

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> 374
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v41 IgV

<400> 374

Gln Asp Val Arg Val Gln Val 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> 375
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v42 IgV

<400> 375

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> 376
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v43 IgV

<400> 376

Gln Asp Val Arg Val Gln Val 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> 377
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v44 IgV

<400> 377

Gln Asp Val Arg Val Gln 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> 378
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v45 IgV

<400> 378

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> 379
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v46 IgV

<400> 379

Gln Asp Val Arg Val Gln Val 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> 380
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> CD112 v47 IgV

<400> 380

Gln Asp Val Arg Val Gln Val 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> 381
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD80(B7-1)

<400> 381

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> 382
<211> 306
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD86(B7-2)

<400> 382

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> 383
<211> 272
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD274 (PD-L1, B7-H1)

<400> 383

```
Phe Thr Val Thr Val Pro 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>  384
<211>  254
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature PDCD1LG2(PD-L2, CD273)

<400>  384

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>  385
<211>  284
<212>  PRT
<213>  Homo sapiens
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<220>
<221> MISC_FEATURE
<223> Mature ICOSLG(B7RP1, CD275, ICOSL, B7-H2)

<400> 385

```
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>  386
<211>  506
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD276(B7-H3)

<400>  386

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>  387
<211>  258
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature VTCN1(B7-H4)

<400>  387

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>  388
<211>  202
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature CD28

<400>  388
```

```
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> 389
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CTLA4

<400> 389

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>  390
<211>  268
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature PDCD1(PD-1)

<400>  390

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>  391
<211>  179
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature ICOS

<400>  391

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> 392
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> Mature BTLA(CD272)

<400> 392

```
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> 393
<211> 433
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD4

<400> 393

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> 394
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD8A(CD8-alpha)

<400> 394

```
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> 395
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD8B(CD8-beta)

<400> 395

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>  396
<211>  497
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature LAG3

<400>  396

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> 397
<211> 280
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature HAVCR2(TIM-3)

<400> 397

```
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> 398
<211> 492
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CEACAM1

<400> 398

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> 399
<211> 222
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature TIGIT

<400> 399

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 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> 400
<211> 397
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature PVR(CD155)

<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 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>  401
<211>  507
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature PVRL2(CD112)

<400>  401

Gln Asp Val Arg Val Gln Val 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> 402
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD226

<400> 402

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> 403
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD2

<400> 403

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>  404
<211>  154
<212>  PRT
<213>  Homo sapiens
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<220>
<221> MISC_FEATURE
<223> Mature CD160

<400> 404

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> 405
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD200

<400> 405

```
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> 406
<211> 297
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature CD200R1(CD200R)

<400> 406

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> 407
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Mature NC R3 (NKp30)

<400> 407

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>  408
<211>  414
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  VSIG8

<400>  408

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>  409
<211>  393
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Mature VSIG8

<400>  409

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> 410
<211> 242
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> VSIG8 ECD

<400> 410

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> 411
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD33 Signal Peptide

<400> 411

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

<210> 412
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> IgGkappa light chain

<400> 412

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> 413
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> HSA signal peptide

<400> 413

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 414
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig kappa light chain

<400> 414

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> 415
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Human azurocidin preprotein signal sequence

<400> 415

Met Thr Arg Leu Thr Val Leu Ala Leu Leu Ala Gly Leu Leu Ala Ser
1 5 10 15

Ser Arg Ala

<210> 416
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 416

Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
1   5   10   15

Val Gln Cys

<210> 417
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 417

Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1   5   10   15

Val Gln Cys

<210> 418
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 418

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1   5   10   15

Val Leu Ser

<210> 419
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 419

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 420
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 420

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
1 5 10 15

Val Gln Ser

<210> 421
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 421

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys

<210> 422
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> IgG heavy chain signal peptide

<400> 422

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Phe Arg Gly
1   5   10   15

Val Gln Cys

<210> 423
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG heavy chain signal peptide

<400> 423

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> 424
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG Kappa light chain signal sequence

<400> 424

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> 425
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG Kappa light chain signal sequence

<400> 425

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> 426
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Gaussia luciferase

<400> 426

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1   5   10   15

Ala

<210> 427
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Human albumin

<400> 427

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1   5   10   15

Tyr Ser

<210> 428
<211> 18

<212> PRT
<213> Artificial Sequence

<220>
<223> Human chymotrypsinogen

<400> 428

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1   5   10   15

Phe Gly

<210> 429
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Human interleukin-2

<400> 429

Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val
1   5   10

<210> 430
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human trypsinogen-2

<400> 430

Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala
1   5   10   15

<210> 431
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 ECD

<400> 431

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> 432
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 ECD

<400> 432

```
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> 433
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v124 ECD

<400> 433

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>  434
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v125 ECD

<400>  434

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> 435
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v126 ECD

<400> 435

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>  436
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v127 ECD

<400>  436
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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 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> 437
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 ECD

<400> 437

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>  438
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v130 ECD

<400>  438

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> 439
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v131 ECD

<400> 439

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>  440
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v132 ECD

<400>  440

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>  441
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v133 ECD

<400>  441

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> 442
<211> 208

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v134 ECD

<400> 442

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> 443
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v135 ECD

<400> 443

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>  444
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v136 ECD

<400>  444

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> 445
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v137 ECD

<400> 445

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>  446
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v138 ECD

<400>  446

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> 447
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v139 ECD

<400> 447

```
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> 448
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v140 ECD

<400> 448

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> 449
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v141 ECD

<220>
<221> VARIANT
<222> (27)..(27)
<223> X is a stop codon

<400> 449

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 Xaa 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> 450
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 ECD

<400> 450

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> 451
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 ECD

<220>

<221> VARIANT
<222> (27)..(27)
<223> X is a stop codon

<400> 451

```
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 Xaa 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>  452
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v144 ECD

<400>  452

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> 453
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v145 ECD

<400> 453

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>  454
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v146 ECD

<400>  454

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> 455
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 ECD

<400> 455

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> 456
<211> 208
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v148 ECD

<400> 456

```
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>  457
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v149 ECD

<400>  457

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> 458
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 ECD

<400> 458

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> 459
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v151 ECD

<400> 459

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>  460
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v152 ECD

<400>  460

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> 461
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v153 ECD

<400> 461

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> 462
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v154 ECD

<400> 462

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> 463
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v155 ECD

<400> 463

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>  464
<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>  464

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>  465
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v157 ECD

<400>  465

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> 466
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v158 ECD

<400> 466

```
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>  467
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v159 ECD

<400>  467

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> 468
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 ECD

<400> 468

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>  469
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v161 ECD

<400>  469

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>  470
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v162 ECD

<400>  470

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> 471
<211> 208
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v163 ECD

<400> 471

```
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> 472
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v164 ECD

<400> 472

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> 473
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 ECD

<400> 473

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> 474
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 ECD

<400> 474

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>  475
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v167 ECD

<400>  475

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> 476
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v168 ECD

<400> 476

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> 477
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 ECD

<400> 477

```
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> 478
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 ECD

<400> 478

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>  479
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v171 ECD

<400>  479

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> 480
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v172 ECD

<400> 480

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>  481
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v173 ECD

<400>  481
```

```
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> 482
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v174 ECD

<400> 482

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> 483
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v175 ECD

<400> 483

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> 484
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v176 ECD

<400> 484

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>  485
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v177 ECD

<400>  485

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> 486
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v178 ECD

<400> 486

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> 487
<211> 208

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v179 ECD

<400> 487

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> 488
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v180 ECD

<400> 488

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>  489
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v181 ECD

<400>  489

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> 490
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v182 ECD

<400> 490

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>  491
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v183 ECD

<400>  491

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> 492
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v184 ECD

<400> 492

```
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> 493
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v185 ECD

<400> 493

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> 494
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 ECD

<400> 494

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>  495
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v187 ECD

<400>  495

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> 496
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 ECD

<400> 496

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>  497
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> CD80 v189 ECD

<400> 497

```
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>  498
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v190 ECD

<400>  498

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> 499
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v191 ECD

<400> 499

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> 500
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v192 ECD

<400> 500

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>  501
<211>  208
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v193 ECD

<400>  501

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> 502
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v194 ECD

<400> 502

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> 503
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 ECD

<400> 503

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> 504
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT IgV

<400> 504

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> 505
<211> 101

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 IgV

<400> 505

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> 506
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 IgV

<400> 506

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>  507
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v124 IgV

<400>  507

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> 508
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v125 IgV

<400> 508

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> 509
<211> 101
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v126 IgV

<400> 509

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> 510
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v127 IgV

<400> 510

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> 511
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 IgV

<400> 511

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> 512
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v130 IgV

<400> 512

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> 513
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v131 IgV

<400> 513

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> 514
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v132 IgV

<400> 514

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>  515
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v133 IgV

<400>  515

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> 516
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v134 IgV

<400> 516

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> 517
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v135 IgV

<400> 517

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> 518
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v136 IgV

<400> 518

```
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> 519
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v137 IgV

<400> 519

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> 520
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v138 IgV

<400> 520

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> 521
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v139 IgV

<400> 521

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> 522
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v140 IgV

<400> 522

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> 523
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v141 IgV

<220>
<221> VARIANT
<222> (27)..(27)
<223> X = is a stop codon

<400> 523

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 Xaa 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> 524
<211> 101

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 IgV

<400> 524

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> 525
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 IgV

<220>
<221> VARIANT
<222> (27)..(27)
<223> X is a stop codon

<400> 525

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 Xaa 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> 526
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v144 IgV

<400> 526

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>  527
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v145 IgV

<400>  527

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> 528
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v146 IgV

<400> 528

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> 529
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 IgV

<400> 529

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> 530
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v148 IgV

<400> 530

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> 531
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v149 IgV

<400> 531

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> 532
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 IgV

<400> 532

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> 533
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v151 IgV

<400> 533

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> 534
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v152 IgV

<400> 534

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> 535
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v153 IgV

<400> 535

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> 536
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v154 IgV

<400> 536

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> 537
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v155 IgV

<400> 537

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> 538
<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> 538

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> 539
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v157 IgV

<400> 539

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> 540
<211> 101
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v158 IgV

<400> 540

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> 541
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v159 IgV

<400> 541

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> 542
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 IgV

<400> 542

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> 543
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v161 IgV

<400> 543

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> 544
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v162 IgV

<400> 544

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> 545
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v163 IgV

<400> 545

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>  546
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v164 IgV

<400>  546

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> 547
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 IgV

<400> 547

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> 548
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 IgV

<400> 548

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>  549
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v167 IgV

<400>  549

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> 550
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v168 IgV

<400> 550

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> 551
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 IgV

<400> 551

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> 552
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 IgV

<400> 552

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>  553
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v171 IgV

<400>  553

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> 554
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v172 IgV

<400> 554

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> 555
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v173 IgV

<400> 555

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> 556
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v174 IgV

<400> 556

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>  557
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v175 IgV

<400>  557

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> 558
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v176 IgV

<400> 558

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> 559
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v177 IgV

<400> 559

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>  560
<211>  101
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v178 IgV

<400>  560

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> 561
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v179 IgV

<400> 561

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> 562
<211> 101

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v180 IgV

<400> 562

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> 563
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v181 IgV

<400> 563

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> 564
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v182 IgV

<400> 564

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> 565
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v183 IgV

<400> 565

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> 566
<211> 101
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v184 IgV

<400> 566

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> 567
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v185 IgV

<400> 567

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> 568
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 IgV

<400> 568

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> 569
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v187 IgV

<400> 569

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> 570
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 IgV

<400> 570

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> 571
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v189 IgV

<400> 571

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> 572
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v190 IgV

<400> 572

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> 573
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v191 IgV

<400> 573

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> 574
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v192 IgV

<400> 574

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> 575
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v193 IgV

<400> 575

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> 576
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v194 IgV

<400> 576

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> 577
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 IgV

<400> 577

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> 578
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 WT IgV

<400> 578

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> 579
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v122 IgV

<400> 579

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> 580
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v123 IgV

<400> 580

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> 581
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v124 IgV

<400> 581

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> 582
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v125 IgV

<400> 582

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> 583
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v126 IgV

<400> 583

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> 584
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v127 IgV

<400> 584

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> 585
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v128 IgV

<400> 585

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>  586
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v130 IgV

<400>  586

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> 587
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v131 IgV

<400> 587

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> 588
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v132 IgV

<400> 588

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> 589
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v133 IgV

<400> 589

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>  590
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v134 IgV

<400>  590

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
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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> 591
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v135 IgV

<400> 591

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> 592
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> CD80 v136 IgV

<400> 592

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> 593
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v137 IgV

<400> 593

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> 594
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v138 IgV

<400> 594

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> 595
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v139 IgV

<400> 595

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> 596
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v140 IgV

<400> 596

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> 597
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v141 IgV

<220>
<221> VARIANT
<222> (27)..(27)
<223> X = is a stop codon

<400> 597

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 Xaa 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> 598
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v142 IgV

<400> 598

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> 599
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v143 IgV

<220>
<221> VARIANT
<222> (27)..(27)
<223> X is a stop codon

<400> 599

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 Xaa 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> 600
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v144 IgV

<400> 600

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> 601
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v145 IgV

<400> 601

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> 602
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v146 IgV

<400> 602

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> 603
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v147 IgV

<400> 603

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> 604
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v148 IgV

<400> 604

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> 605
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v149 IgV

<400> 605

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> 606
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v150 IgV

<400> 606

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> 607
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v151 IgV

<400> 607

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> 608
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v152 IgV

<400> 608

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> 609
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v153 IgV

<400> 609

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> 610
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v154 IgV

<400> 610

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
100 105

<210> 611

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v155 IgV

<400> 611

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> 612
<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> 612

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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 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>  613
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v157 IgV

<400>  613

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
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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> 614
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v158 IgV

<400> 614

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> 615
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v159 IgV

<400> 615

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> 616
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v160 IgV

<400> 616

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 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>  617
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v161 IgV

<400>  617

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> 618
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v162 IgV

<400> 618

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> 619
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v163 IgV

<400> 619

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> 620
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v164 IgV

<400> 620

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> 621
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v165 IgV

<400> 621

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> 622
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v166 IgV

<400> 622

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> 623
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v167 IgV

<400> 623

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> 624
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v168 IgV

<400> 624

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> 625
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v169 IgV

<400> 625

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> 626
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v170 IgV

<400> 626

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> 627
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v171 IgV

<400> 627

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>  628
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v172 IgV

<400>  628

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> 629
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v173 IgV

<400> 629

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

<210> 630

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v174 IgV

<400> 630

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> 631
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v175 IgV

<400> 631

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> 632
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v176 IgV

<400> 632

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>  633
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v177 IgV

<400>  633

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>  634
<211>  107
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> CD80 v178 IgV

<400> 634

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> 635
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v179 IgV

<400> 635

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> 636
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v180 IgV

<400> 636

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> 637
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v181 IgV

<400> 637

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> 638
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v182 IgV

<400> 638

```
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>  639
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v183 IgV

<400>  639

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> 640
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v184 IgV

<400> 640

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> 641
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v185 IgV

<400> 641

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> 642
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v186 IgV

<400> 642

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>  643
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v187 IgV

<400>  643

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> 644
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v188 IgV

<400> 644

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> 645
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> CD80 v189 IgV

<400> 645

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> 646
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v190 IgV

<400> 646

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>  647
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD80 v191 IgV

<400>  647

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> 648
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v192 IgV

<400> 648

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> 649
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v193 IgV

<400> 649

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> 650
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v194 IgV

<400> 650

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> 651
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80 v195 IgV

<400> 651

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> 652
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD155 IgV wildtype

<400> 652

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> 653
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v1 IgV

<400> 653

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> 654
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v2 IgV

<400> 654

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> 655
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v3 IgV

<400> 655

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> 656
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v4 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 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> 657
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v5 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 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> 658
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v6 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 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> 659
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v7 IgV

<400> 659

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> 660
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v8 IgV

<400> 660

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> 661
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v9 IgV

<400> 661

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> 662
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v10 IgV

<400> 662

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> 663

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v11 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 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> 664
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v12 IgV

<400> 664

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> 665
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v14 IgV

<400> 665

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> 666
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v15 IgV

<400> 666

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> 667
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v16 IgV

<400> 667

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> 668
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v17 IgV

<400> 668

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> 669
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v18 IgV

<400> 669

```
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>  670
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v19 IgV

<400>  670

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> 671
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v20 IgV

<400> 671

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>  672
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v21 IgV

<400>  672

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> 673
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v22 IgV

<400> 673

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> 674
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 ECD

<400> 674

```
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> 675
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 ECD

<400> 675

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> 676
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 ECD

<400> 676

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> 677
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v26 ECD

<400> 677

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> 678
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v27 ECD

<400> 678

```
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> 679
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 ECD

<400> 679

```
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> 680
<211> 323
<212> PRT
<213> Artificial Seqeunce

<220>
<223> CD155 v39 ECD

<400> 680

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> 681
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v30 ECD

<400> 681

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> 682
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 ECD

<400> 682

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> 683
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 ECD

<400> 683

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> 684
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v33 ECD

<400> 684

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> 685
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v34 ECD

<400> 685

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> 686
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 ECD

<400> 686

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> 687
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v36 ECD

<400> 687

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> 688
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 ECD

<400> 688

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> 689

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v38 ECD

<400> 689

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> 690
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v39 ECD

<400> 690

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> 691
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v40 ECD

<400> 691

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> 692
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v41 ECD

<400> 692

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> 693
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 ECD

<400> 693

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> 694
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 ECD

<400> 694

```
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> 695
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 ECD

<400> 695

```
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> 696
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v45 ECD

<400> 696

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> 697
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v46 ECD

<400> 697

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> 698
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v47 ECD

<400> 698

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> 699
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v48 ECD

<400> 699

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>  700
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v49 ECD
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<400> 700

```
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> 701
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 ECD

<400> 701

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> 702
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 ECD

<400> 702

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> 703
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v52 ECD

<400> 703

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> 704
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v53 ECD

<400> 704

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> 705
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v54 ECD

<400> 705

```
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> 706
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 ECD

<400> 706

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> 707
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v56 ECD

<400> 707

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> 708
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 ECD

<400> 708

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> 709
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v58 ECD

<400> 709

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>  710
<211>  323
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> CD155 v59 ECD

<400> 710

```
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> 711
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v60 ECD

<400> 711

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> 712
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 ECD

<400> 712

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> 713
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 ECD

<400> 713

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> 714
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 ECD

<400> 714

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> 715

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 ECD

<400> 715

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> 716
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v65 ECD

<400> 716

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> 717
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v66 ECD

<400> 717

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> 718
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v67 ECD

<400> 718

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> 719
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 ECD

<400> 719

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> 720
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v69 ECD

<400> 720

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> 721
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v70 ECD

<400> 721

```
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> 722
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v71 ECD

<400> 722

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> 723
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v72 ECD

<400> 723

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> 724
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v73 ECD

<400> 724

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> 725
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v74 ECD

<400> 725

```
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>  726
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v75 ECD
```

<400> 726

```
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> 727
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 ECD

<400> 727

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> 728
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 ECD

<400> 728

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> 729
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v78 ECD

<400> 729

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> 730
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v79 ECD

<400> 730

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> 731
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 ECD

<400> 731

```
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>  732
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v81 ECD

<400>  732

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> 733
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v82 ECD

<400> 733

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> 734
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 ECD

<400> 734

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> 735
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 ECD

<400> 735

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

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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> 736
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v85 ECD

<400> 736

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> 737
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v86 ECD

<400> 737

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> 738
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 ECD

<400> 738

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> 739
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 ECD

<400> 739

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

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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> 740
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 ECD

<400> 740

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> 741

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 ECD

<400> 741

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> 742
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v91 ECD

<400> 742

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> 743
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v92 ECD

<400> 743

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
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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> 744
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 744

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> 745
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 745

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

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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> 746
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 ECD

<400> 746

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> 747
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 ECD

<400> 747

```
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> 748
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v97 ECD

<400> 748

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> 749
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v98 ECD

<400> 749

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> 750
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v99 ECD

<400> 750

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> 751
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v100 ECD

<400> 751

```
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>  752
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v101 ECD
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<400> 752

```
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> 753
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 ECD

<400> 753

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> 754
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 ECD

<400> 754

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> 755
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v104 ECD

<400> 755

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> 756
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v105 ECD

<400> 756

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> 757
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 ECD

<400> 757

```
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> 758
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v107 ECD

<400> 758

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> 759
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v108 ECD

<400> 759

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> 760
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 ECD

<400> 760

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> 761
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 ECD

<400> 761

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> 762
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v111 ECD

<400> 762

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> 763
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v112 ECD

<400> 763

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> 764
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 ECD

<400> 764

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> 765
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v114 ECD

<400> 765

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> 766
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 ECD

<400> 766

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> 767

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 ECD

<400> 767

```
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> 768
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v117 ECD

<400> 768

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> 769
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v118 ECD

<400> 769

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> 770
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v119 ECD

<400> 770

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> 771
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 IgV

<400> 771

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> 772
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 IgV

<400> 772

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> 773
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 IgV

<400> 773

```
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>  774
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v26 IgV

<400>  774

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> 775
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v27 IgV

<400> 775

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> 776
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 IgV

<400> 776

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> 777
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v29 IgV

<400> 777

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> 778
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v30 IgV

<400> 778

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> 779
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 IgV

<400> 779

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> 780
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 IgV

<400> 780

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> 781
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v33 IgV

<400> 781

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> 782
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v34 IgV

<400> 782

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> 783
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 IgV

<400> 783

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> 784
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v36 IgV

<400> 784

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> 785
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 IgV

<400> 785

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

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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>  786
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v38 IgV

<400>  786

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


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> 787
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v39 IgV

<400> 787

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
100 105 110

Asp Ile Trp Leu
115

<210> 788
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v40 IgV

<400> 788

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> 789
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v41 IgV

<400> 789

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> 790
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 IgV

<400> 790

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> 791
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 IgV

<400> 791

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> 792
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 IgV

<400> 792

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> 793

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v45 IgV

<400> 793

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> 794
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v46 IgV

<400> 794

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> 795
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v47 IgV

<400> 795

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> 796
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v48 IgV

<400> 796

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> 797
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v49 IgV

<400> 797

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> 798
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 IgV

<400> 798

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> 799
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 IgV

<400> 799

```
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>  800
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v52 IgV

<400>  800

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> 801
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v53 IgV

<400> 801

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>  802
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v54 IgV

<400>  802

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> 803
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 IgV

<400> 803

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> 804
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v56 IgV

<400> 804

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> 805
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 IgV

<400> 805

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>  806
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v58 IgV

<400>  806

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> 807
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v59 IgV

<400> 807

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> 808
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v60 IgV

<400> 808

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> 809
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 IgV

<400> 809

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> 810
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 IgV

<400> 810

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> 811
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 IgV

<400> 811

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> 812
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 IgV

<400> 812

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

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> 813
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v65 IgV

<400> 813

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> 814
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v66 IgV

<400> 814

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> 815
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v67 IgV

<400> 815

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> 816
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 IgV

<400> 816

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> 817
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v69 IgV

<400> 817

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

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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>  818
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v70 IgV

<400>  818

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>  819
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<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v71 IgV

<400> 819

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> 820
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v72 IgV

<400> 820

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> 821
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v73 IgV

<400> 821

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> 822
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v74 IgV

<400> 822

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> 823
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v75 IgV

<400> 823

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> 824
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 IgV

<400> 824

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> 825
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 IgV

<400> 825

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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 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>  826
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v78 IgV

<400>  826

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> 827
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v79 IgV

<400> 827

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> 828
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 IgV

<400> 828

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> 829
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v81 IgV

<400> 829

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> 830
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v82 IgV

<400> 830

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> 831
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 IgV

<400> 831

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> 832
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 IgV

<400> 832

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> 833
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v85 IgV

<400> 833

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> 834
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v86 IgV

<400> 834

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> 835
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 IgV

<400> 835

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> 836
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 IgV

<400> 836

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> 837
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 IgV

<400> 837

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> 838
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 IgV

<400> 838

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> 839
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v91 IgV

<400> 839

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> 840
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v92 IgV

<400> 840

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> 841
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v93 IgV

<400> 841

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> 842
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 IgV

<400> 842

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> 843
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v95 IgV

<400> 843

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> 844
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 IgV

<400> 844

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> 845

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v97 IgV

<400> 845

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> 846
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v98 IgV

<400> 846

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> 847
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v99 IgV

<400> 847

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> 848
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v100 IgV

<400> 848

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> 849
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v101 IgV

<400> 849

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> 850
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 IgV

<400> 850

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> 851
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 IgV

<400> 851

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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>  852
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v104 IgV

<400>  852

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> 853
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v105 IgV

<400> 853

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> 854
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 IgV

<400> 854

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> 855
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v107 IgV

<400> 855

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> 856
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v108 IgV

<400> 856

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> 857
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 IgV

<400> 857

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> 858
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 IgV

<400> 858

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> 859
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v111 IgV

<400> 859

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> 860
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v112 IgV

<400> 860

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> 861
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 IgV

<400> 861

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> 862
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v114 IgV

<400> 862

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> 863
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 IgV

<400> 863

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> 864
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 IgV

<400> 864

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> 865
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v117 IgV

<400> 865

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> 866
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v118 IgV

<400> 866

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> 867
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v119 IgV

<400> 867

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> 868
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v23 IgV

<400> 868

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> 869
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v24 IgV

<400> 869

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> 870
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v25 IgV

<400> 870

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> 871

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v26 IgV

<400> 871

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> 872
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v27 IgV

<400> 872

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> 873
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v28 IgV

<400> 873

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>  874
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v29 IgV

<400>  874

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
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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> 875
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v30 IgV

<400> 875

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> 876
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v31 IgV

<400> 876

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> 877
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v32 IgV

<400> 877

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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 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>  878
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v33 IgV

<400>  878

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> 879
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v34 IgV

<400> 879

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> 880
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v35 IgV

<400> 880

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> 881
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v36 IgV

<400> 881

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> 882
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v37 IgV

<400> 882

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> 883
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v38 IgV

<400> 883

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>  884
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v39 IgV

<400>  884

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> 885
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v40 IgV

<400> 885

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> 886
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v41 IgV

<400> 886

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> 887
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v42 IgV

<400> 887

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> 888
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v43 IgV

<400> 888

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> 889
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v44 IgV

<400> 889

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>  890
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v45 IgV

<400>  890

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
115 120

<210> 891
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v46 IgV

<400> 891

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> 892
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v47 IgV

<400> 892

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> 893
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v48 IgV

<400> 893

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> 894
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v49 IgV

<400> 894

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> 895
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v50 IgV

<400> 895

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> 896
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v51 IgV

<400> 896

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> 897

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v52 IgV

<400> 897

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> 898
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v53 IgV

<400> 898

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> 899
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v54 IgV

<400> 899

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> 900
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v55 IgV

<400> 900

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> 901
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v56 IgV

<400> 901

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> 902
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v57 IgV

<400> 902

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> 903
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v58 IgV

<400> 903

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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 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>  904
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v59 IgV

<400>  904

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> 905
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v60 IgV

<400> 905

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> 906
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v61 IgV

<400> 906

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> 907
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v62 IgV

<400> 907

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> 908
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v63 IgV

<400> 908

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> 909
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v64 IgV

<400> 909

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

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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>  910
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v65 IgV

<400>  910

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> 911
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v66 IgV

<400> 911

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> 912
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v67 IgV

<400> 912

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> 913
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v68 IgV

<400> 913

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> 914
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v69 IgV

<400> 914

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> 915
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v70 IgV

<400> 915

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>  916
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v71 IgV

<400>  916

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
115 120

<210> 917
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v72 IgV

<400> 917

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> 918
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v73 IgV

<400> 918

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> 919
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v74 IgV

<400> 919

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> 920
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v75 IgV

<400> 920

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> 921
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v76 IgV

<400> 921

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> 922
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v77 IgV

<400> 922

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> 923

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v78 IgV

<400> 923

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> 924
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v79 IgV

<400> 924

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> 925
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v80 IgV

<400> 925

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> 926
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v81 IgV

<400> 926

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> 927
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v82 IgV

<400> 927

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> 928
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v83 IgV

<400> 928

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> 929
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v84 IgV

<400> 929

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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 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>  930
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v85 IgV

<400>  930

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> 931
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v86 IgV

<400> 931

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> 932
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v87 IgV

<400> 932

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> 933
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v88 IgV

<400> 933

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> 934
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v89 IgV

<400> 934

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> 935
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v90 IgV

<400> 935

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>  936
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v91 IgV

<400>  936

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> 937
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v92 IgV

<400> 937

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> 938
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v93 IgV

<400> 938

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> 939
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v94 IgV

<400> 939

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> 940
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v95 IgV

<400> 940

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> 941
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v96 IgV

<400> 941

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>  942
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v97 IgV

<400>  942

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> 943
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v98 IgV

<400> 943

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> 944
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v99 IgV

<400> 944

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> 945
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v100 IgV

<400> 945

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> 946
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v101 IgV

<400> 946

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> 947
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v102 IgV

<400> 947

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> 948
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v103 IgV

<400> 948

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> 949

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v104 IgV

<400> 949

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> 950
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v105 IgV

<400> 950

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> 951
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v106 IgV

<400> 951

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> 952
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v107 IgV

<400> 952

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> 953
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v108 IgV

<400> 953

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> 954
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v109 IgV

<400> 954

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> 955
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v110 IgV

<400> 955

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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 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>  956
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v111 IgV

<400>  956

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> 957
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v112 IgV

<400> 957

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> 958
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v113 IgV

<400> 958

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> 959
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v114 IgV

<400> 959

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> 960
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v115 IgV

<400> 960

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> 961
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v116 IgV

<400> 961

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>  962
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v117 IgV

<400>  962

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> 963
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v118 IgV

<400> 963

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> 964
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v119 IgV

<400> 964

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> 965
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD112 IgV Wildtype

<400> 965

Gln Asp Val Arg Val Gln Val 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> 966
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v1 IgV

<400> 966

Gln Asp Val Arg Val Gln Val 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> 967
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v2 IgV

<400> 967

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> 968
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v3 IgV

<400> 968

Gln Asp Val Arg Val Gln Val 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> 969
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v4 IgV

<400> 969

Gln Asp Val Arg Val Gln Val 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> 970

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v5 IgV

<400> 970

Gln Asp Val Arg Val Gln Val 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> 971
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v6 IgV

<400> 971

Gln Asp Val Arg Val Gln 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> 972
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v7 IgV

<400> 972

Gln Asp Val Arg Val Gln Val 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> 973
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v8 IgV

<400> 973

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> 974
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v9 IgV

<400> 974

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> 975
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v10 IgV

<400> 975

Gln Asp Val Arg Val Gln Val 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> 976
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v11 IgV

<400> 976

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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 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>  977
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v12 IgV

<400>  977

Gln Asp Val Arg Val Gln Val 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> 978
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v13 IgV

<400> 978

Gln Asp Val Arg Val Gln Val 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> 979
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v14 IgV

<400> 979

Gln Asp Val Arg Val Gln Val 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> 980
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v15 IgV

<400> 980

Gln Asp Val Arg Val Gln Val 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> 981
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v16 IgV

<400> 981

Gln Asp Val Arg Val Gln Val 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> 982
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v17 IgV

<400> 982

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>  983
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v18 IgV

<400>  983

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> 984
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v19 IgV

<400> 984

Gln Asp Val Arg Val Gln Val 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> 985
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v20 IgV

<400> 985

Gln Asp Val Arg Val Gln 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> 986
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v21 IgV

<400> 986

Gln Asp Val Arg Val Gln Val 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> 987
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v22 IgV

<400> 987

Gln Asp Val Arg Val Gln Val 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> 988
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v23 IgV

<400> 988

Gln Asp Val Arg Val Gln Val 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

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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>  989
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v24 IgV

<400>  989

Gln Asp Val Arg Val Gln 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> 990
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v25 IgV

<400> 990

Gln Asp Val Arg Val Gln Val 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> 991
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v26 IgV

<400> 991

Gln Asp Val Arg Val Gln Val 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> 992
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v27 IgV

<400> 992

Gln Asp Val Arg Val Gln Val 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> 993
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v28 IgV

<400> 993

Gln Asp Val Arg Val Gln Val 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> 994
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v29 IgV

<400> 994

Gln Asp Val Arg Val Gln Val 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> 995
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v30 IgV

<400> 995

Gln Asp Val Arg Val Gln Val 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> 996

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v31 IgV

<400> 996

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> 997
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v32 IgV

<400> 997

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> 998
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v33 IgV

<400> 998

Gln Asp Val Arg Val Gln Val 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> 999
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v34 IgV

<400> 999

Gln Asp Val Arg Val Gln Val 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> 1000
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v35 IgV

<400> 1000

Gln Asp Val Arg Val Gln Val 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> 1001
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v36 IgV

<400> 1001

Gln Asp Val 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> 1002
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v37 gV

<400> 1002

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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 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>  1003
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v38 gV

<400>  1003

Gln Asp Val Arg Val Gln 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> 1004
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v39 gV

<400> 1004

Gln Asp Val Arg Val Gln Val 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> 1005
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v40 gV

<400> 1005

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> 1006
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v41 gV

<400> 1006

Gln Asp Val Arg Val Gln Val 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> 1007
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v42 gV

<400> 1007

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> 1008
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v43 gV

<400> 1008

Gln Asp Val Arg Val Gln Val 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> 1009
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v44 gV

<400> 1009

Gln Asp Val Arg Val Gln 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> 1010
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v45 IgV

<400> 1010

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> 1011
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v46 IgV

<400> 1011

Gln Asp Val Arg Val Gln Val 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> 1012
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v47 IgV

<400> 1012

Gln Asp Val Arg Val Gln Val 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> 1013
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v48 ECD

<400> 1013

Gln Asp Val Arg Val Gln Val 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 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> 1014
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v49 ECD

<400> 1014

Gln Asp Val Arg Val Gln Val 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> 1015
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v50 ECD

<400> 1015

Gln Asp Val Arg Val Gln Val 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 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> 1016
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v51 ECD

<400> 1016

Gln Asp Val Arg Val Gln Val 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> 1017
<211> 329
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v52 ECD

<400> 1017

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

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> 1018
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v53 ECD

<400> 1018

Gln Asp Val Arg Val Gln Val 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> 1019
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v54 ECD

<400> 1019

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> 1020
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v55 ECD

<400> 1020

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> 1021
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v56 ECD

<400> 1021

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> 1022

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v57 ECD

<400> 1022

Gln Asp Val Arg Val Gln Val 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>  1023
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v58 ECD

<400>  1023

Gln Asp Val Arg Val Gln Val 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> 1024
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 ECD

<400> 1024

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> 1025
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v60 ECD

<400> 1025

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> 1026
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 ECD

<400> 1026

Gln Asp Val Arg Val Gln Val 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> 1027
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v62 ECD

<400> 1027

Gln Asp Val Arg Val Gln Val 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> 1028
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v63 ECD

<400> 1028

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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 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
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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>  1029
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v64 ECD

<400>  1029

Gln Asp Val Arg Val Gln Val 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> 1030
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v65 ECD

<400> 1030

Gln Asp Val Arg Val Gln Val 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

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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 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> 1031
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v66 ECD

<400> 1031

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> 1032
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v67 ECD

<400> 1032

Gln Asp Val Arg Val Gln Val 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> 1033
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v68 ECD

<400> 1033

Gln Asp Val Arg Val Gln Val 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> 1034
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v69 ECD

<400> 1034

Gln Asp Val Arg Val Gln Val 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> 1035
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 ECD

<400> 1035

Gln Asp Val Arg Val Gln Val 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> 1036
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v71 ECD

<400> 1036

Gln Asp Val Arg Val Gln Val 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> 1037
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 ECD

<400> 1037

Gln Asp Val Arg Val Gln Val 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> 1038
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 ECD

<400> 1038

```
Gln Asp Val Arg Val Gln Val 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>  1039
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v74 ECD

<400>  1039

Gln Asp Val Arg Val Gln Val 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

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> 1040
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v75 ECD

<400> 1040

Gln Asp Val Arg Val Gln Val 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
```

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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>  1041
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v76 ECD

<400>  1041

Gln Asp Val Arg Val Gln Val 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> 1042
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v77 ECD

<400> 1042

Gln Asp Val Arg Val Gln Val 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> 1043
<211> 329
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v78 ECD

<400> 1043

```
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

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> 1044
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v79 ECD

<400> 1044

Gln Asp Val Arg Val Gln Val 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> 1045
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v80 ECD

<400> 1045

Gln Asp Val Arg Val Gln Val 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> 1046
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v81 ECD

<400> 1046

Gln Asp Val Arg Val Gln Val 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> 1047
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v82 ECD

<400> 1047

Gln Asp Val Arg Val Gln Val 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> 1048

<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v83 ECD

<400> 1048

Gln Asp Val Arg Val Gln Val 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>  1049
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v84 ECD

<400>  1049

Gln Asp Val Arg Val Gln Val 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> 1050
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 ECD

<400> 1050

Gln Asp Val Arg Val Gln Val 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> 1051
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v86 ECD

<400> 1051

Gln Asp Val Arg Val Gln Val 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> 1052
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 ECD

<400> 1052

Gln Asp Val Arg Val Gln Val 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> 1053
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v88 ECD

<400> 1053

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> 1054
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v48 IgV

<400> 1054

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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 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>  1055
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v49 IgV

<400>  1055

Gln Asp Val Arg Val Gln Val 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> 1056
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v50 IgV

<400> 1056

Gln Asp Val Arg Val Gln Val 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>  1057
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v51 IgV

<400>  1057

Gln Asp Val Arg Val Gln Val 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> 1058
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v52 IgV

<400> 1058

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> 1059
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v53 IgV

<400> 1059

Gln Asp Val Arg Val Gln Val 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> 1060
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v54 IgV

<400> 1060

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>  1061
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v55 IgV

<400>  1061

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> 1062
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v56 IgV

<400> 1062

Gln Asp Val Arg Val Gln Val 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> 1063
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v57 IgV

<400> 1063

Gln Asp Val Arg Val Gln Val 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> 1064
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v58 IgV

<400> 1064

Gln Asp Val Arg Val Gln Val 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> 1065
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 IgV

<400> 1065

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> 1066
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v60 IgV

<400> 1066

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> 1067
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 IgV

<400> 1067

Gln Asp Val Arg Val Gln Val 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> 1068
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v62 IgV

<400> 1068

Gln Asp Val Arg Val Gln Val 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> 1069
<211> 125
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v63 IgV

<400> 1069

Gln Asp Val Arg Val Gln Val 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> 1070
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v64 IgV

<400> 1070

Gln Asp Val Arg Val Gln Val 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> 1071
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v65 IgV

<400> 1071

Gln Asp Val Arg Val Gln Val 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> 1072
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v66 IgV

<400> 1072

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> 1073
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v67 IgV

<400> 1073

Gln Asp Val Arg Val Gln Val 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> 1074

<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v68 IgV

<400> 1074

Gln Asp Val Arg Val Gln Val 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> 1075
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v69 IgV

<400> 1075

Gln Asp Val Arg Val Gln Val 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> 1076
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 IgV

<400> 1076

Gln Asp Val Arg Val Gln Val 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> 1077
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v71 IgV

<400> 1077

Gln Asp Val Arg Val Gln Val 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> 1078
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 IgV

<400> 1078

Gln Asp Val Arg Val Gln Val 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> 1079
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 IgV

<400> 1079

Gln Asp Val Arg Val Gln Val 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> 1080
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v74 IgV

<400> 1080

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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 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>  1081
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v75 IgV

<400>  1081

Gln Asp Val Arg Val Gln Val 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> 1082
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v76 IgV

<400> 1082

Gln Asp Val Arg Val Gln Val 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

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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 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>  1083
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v77 IgV

<400>  1083

Gln Asp Val Arg Val Gln Val 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
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115 120 125

<210> 1084
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v78 IgV

<400> 1084

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> 1085
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v79 IgV

<400> 1085

Gln Asp Val Arg Val Gln Val 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> 1086
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v80 IgV

<400> 1086

Gln Asp Val Arg Val Gln Val 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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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>  1087
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v81 IgV

<400>  1087

Gln Asp Val Arg Val Gln Val 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> 1088
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v82 IgV

<400> 1088

Gln Asp Val Arg Val Gln Val 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> 1089
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v83 IgV

<400> 1089

Gln Asp Val Arg Val Gln Val 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> 1090
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v84 IgV

<400> 1090

Gln Asp Val Arg Val Gln Val 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> 1091
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 IgV

<400> 1091

Gln Asp Val Arg Val Gln Val 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> 1092
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v86 IgV

<400> 1092

Gln Asp Val Arg Val Gln Val 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> 1093
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 IgV

<400> 1093

Gln Asp Val Arg Val Gln Val 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> 1094
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v88 IgV

<400> 1094

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> 1095
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v48 IgV

<400> 1095

Gln Asp Val Arg Val Gln Val 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> 1096
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v49 IgV

<400> 1096

Gln Asp Val Arg Val Gln Val 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> 1097
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v50 IgV

<400> 1097

Gln Asp Val Arg Val Gln Val 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> 1098
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v51 IgV

<400> 1098

Gln Asp Val Arg Val Gln Val 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> 1099
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v52 IgV

<400> 1099

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> 1100

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v53 IgV

<400> 1100

Gln Asp Val Arg Val Gln Val 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> 1101
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v54 IgV

<400> 1101

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> 1102
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v55 IgV

<400> 1102

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> 1103
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v56 IgV

<400> 1103

Gln Asp Val Arg Val Gln Val 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> 1104
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v57 IgV

<400> 1104

Gln Asp Val Arg Val Gln Val 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> 1105
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v58 IgV

<400> 1105

Gln Asp Val Arg Val Gln Val 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> 1106
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v59 IgV

<400> 1106

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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 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>  1107
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v60 IgV

<400>  1107

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> 1108
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v61 IgV

<400> 1108

Gln Asp Val Arg Val Gln Val 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>  1109
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v62 IgV

<400>  1109

Gln Asp Val Arg Val Gln Val 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
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115 120 125

<210> 1110
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v63 IgV

<400> 1110

Gln Asp Val Arg Val Gln Val 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> 1111
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v64 IgV

<400> 1111

Gln Asp Val Arg Val Gln Val 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> 1112
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v65 IgV

<400> 1112

Gln Asp Val Arg Val Gln Val 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> 1113
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v66 IgV

<400> 1113

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> 1114
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v67 IgV

<400> 1114

Gln Asp Val Arg Val Gln Val 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> 1115
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v68 IgV

<400> 1115

Gln Asp Val Arg Val Gln Val 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> 1116
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v69 IgV

<400> 1116

Gln Asp Val Arg Val Gln Val 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> 1117
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v70 IgV

<400> 1117

Gln Asp Val Arg Val Gln Val 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> 1118
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v71 IgV

<400> 1118

Gln Asp Val Arg Val Gln Val 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> 1119
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v72 IgV

<400> 1119

Gln Asp Val Arg Val Gln Val 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> 1120
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v73 IgV

<400> 1120

Gln Asp Val Arg Val Gln Val 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> 1121
<211> 127
<212> PRT

<213> Artificial Sequence

<220>
<223> CD112 v74 IgV

<400> 1121

Gln Asp Val Arg Val Gln Val 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> 1122
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v75 IgV

<400> 1122

Gln Asp Val Arg Val Gln Val 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> 1123
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v76 IgV

<400> 1123

Gln Asp Val Arg Val Gln Val 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> 1124
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v77 IgV

<400> 1124

Gln Asp Val Arg Val Gln Val 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> 1125
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v78 IgV

<400> 1125

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> 1126

<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v79 IgV

<400> 1126

Gln Asp Val Arg Val Gln Val 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> 1127
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v80 IgV

<400> 1127

Gln Asp Val Arg Val Gln Val 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> 1128
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v81 IgV

<400> 1128

Gln Asp Val Arg Val Gln Val 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>  1129
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v82 IgV

<400>  1129

Gln Asp Val Arg Val Gln Val 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> 1130
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v83 IgV

<400> 1130

Gln Asp Val Arg Val Gln Val 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> 1131
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v84 IgV

<400> 1131

Gln Asp Val Arg Val Gln Val 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> 1132
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v85 IgV

<400> 1132

```
Gln Asp Val Arg Val Gln Val 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>  1133
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v86 IgV

<400>  1133

Gln Asp Val Arg Val Gln Val 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> 1134
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> CD112 v87 IgV

<400> 1134

Gln Asp Val Arg Val Gln Val 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>  1135
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD112 v88 IgV

<400>  1135

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> 1136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV

<400> 1136

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> 1137
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v1

<400> 1137

Phe Thr Val Thr Val Pro 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> 1138
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v2

<400> 1138

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>  1139
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v3

<400>  1139

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> 1140
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v4

<400> 1140

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>  1141
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v5
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<400> 1141

```
Phe Thr Val Thr Val Pro 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> 1142
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v6

<400> 1142

Phe Thr Val Thr Val Pro 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>  1143
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v7

<400>  1143

Phe Thr Val Thr Val Pro 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> 1144
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v8

<400> 1144

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> 1145
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v9

<400> 1145

Phe Thr Val Thr Val Pro 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> 1146
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v10

<400> 1146

Phe Thr Val Thr Val Pro 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>  1147
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v11

<400>  1147

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> 1148
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v12

<400> 1148

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
    210                 215                 220
```

<210> 1149
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v13

<400> 1149

```
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> 1150
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v14

<400> 1150

Phe Thr Val Thr Val Pro 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>  1151
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v15

<400>  1151

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
210 215 220

<210> 1152
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v16

<400> 1152

```
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> 1153
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v17

<400> 1153

Phe Thr Val Thr Val Pro 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> 1154
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v18

<400> 1154

Phe Thr Val Thr Val Pro 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>  1155
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v19

<400>  1155

Phe Thr Val Thr Val Pro 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

<210> 1156
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v20

<400> 1156

```
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> 1157
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v21

<400> 1157

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> 1158
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v22

<400> 1158

Phe Thr Val Thr Val Pro 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> 1159
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v23

<400> 1159

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
210 215 220

<210> 1160

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v24

<400> 1160

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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 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> 1161
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v25

<400> 1161

Phe Thr Val Thr Val Pro 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> 1162
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v26

<400> 1162

Phe Thr Val Thr Val Pro 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>  1163
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v27

<400>  1163

Phe Thr Val Thr Val Pro 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> 1164
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v28

<400> 1164

Phe Thr Val Thr Val Pro 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>  1165
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v29

<400>  1165

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> 1166
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v30

<400> 1166

Phe Thr Val Thr Val Pro 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>  1167
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v31
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<400> 1167

```
Phe Thr Val Thr Val Pro 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> 1168
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v32

<400> 1168

Phe Thr Val Thr Val Pro 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>  1169
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v33

<400>  1169

Phe Thr Val Thr Val Pro 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> 1170
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v34

<400> 1170

Phe Thr Val Thr Val Pro 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
    210                 215                 220
```

<210> 1171
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v35

<400> 1171

```
Phe Thr Val Thr Val Pro 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> 1172
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v36

<400> 1172

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>  1173
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>   PD-L1 ECD v37

<400>  1173

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> 1174
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v38

<400> 1174

Phe Thr Val Thr Val Pro 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
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<210> 1175
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v39

<400> 1175

```
Phe Thr Val Thr Val Pro 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> 1176
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v40

<400> 1176

Phe Thr Val Thr Val Pro 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> 1177
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v41

<400> 1177

Phe Thr Val Thr Val Pro 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> 1178
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v42

<400> 1178

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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 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> 1179
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v43

<400> 1179

Phe Thr Val Thr Val Pro 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> 1180
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v44

<400> 1180

Phe Thr Val Thr Val Pro 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>  1181
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v45

<400>  1181

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
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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> 1182
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v46

<400> 1182

```
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> 1183
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v47

<400> 1183

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> 1184
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v48

<400> 1184

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> 1185
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v49

<400> 1185

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> 1186

<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v50

<400> 1186

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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 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> 1187
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v51

<400> 1187

Phe Thr Val Thr Val Pro 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> 1188
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v52

<400> 1188

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>  1189
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v53

<400>  1189

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 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> 1190
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v54

<400> 1190

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> 1191
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v55

<400> 1191

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> 1192
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v56

<400> 1192

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>  1193
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v57
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<400> 1193

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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 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> 1194
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v58

<400> 1194

Phe Thr 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>  1195
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v59

<400>  1195

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> 1196
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v60

<400> 1196

Phe Thr Val Thr Val Pro 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> 1197
<211> 220
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 ECD v61

<400> 1197

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> 1198
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v62

<400> 1198

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>  1199
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v63

<400>  1199

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> 1200
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v64

<400> 1200

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> 1201
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v65

<400> 1201

Phe Thr 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
210 215 220

<210> 1202
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v1

<400> 1202

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> 1203
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v2

<400> 1203

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> 1204
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v3

<400> 1204

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> 1205
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v4

<400> 1205

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

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> 1206
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v5

<400> 1206

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
100 105

<210> 1207
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v6

<400> 1207

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> 1208
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v7

<400> 1208

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> 1209
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v8

<400> 1209

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 Val Lys Val
100 105

<210> 1210
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v9

<400> 1210

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> 1211
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v10

<400> 1211

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> 1212
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v11

<400> 1212

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> 1213
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v12

<400> 1213

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> 1214
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v13

<400> 1214

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> 1215
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v14

<400> 1215

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> 1216
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v15

<400> 1216

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> 1217
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v16

<400> 1217

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> 1218

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v17

<400> 1218

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> 1219
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v18

<400> 1219

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> 1220
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v19

<400> 1220

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> 1221
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v20

<400> 1221

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> 1222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v21

<400> 1222

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> 1223
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v22

<400> 1223

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> 1224
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v23

<400> 1224

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> 1225
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v24

<400> 1225

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> 1226
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v25

<400> 1226

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> 1227
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v26

<400> 1227

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> 1228
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v27

<400> 1228

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> 1229
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v28

<400> 1229

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> 1230
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v29

<400> 1230

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> 1231
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v30

<400> 1231

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> 1232
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v31

<400> 1232

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
100 105

<210> 1233
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v32

<400> 1233

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> 1234
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v33

<400> 1234

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> 1235
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v34

<400> 1235

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> 1236
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v35

<400> 1236

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> 1237
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v36

<400> 1237

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> 1238
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v37

<400> 1238

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> 1239
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v38

<400> 1239

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> 1240
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v39

<400> 1240

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> 1241
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v40

<400> 1241

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> 1242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v41

<400> 1242

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 Lys Arg Ile Thr Val Lys Val
100 105

<210> 1243
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v42

<400> 1243

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> 1244

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v43

<400> 1244

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> 1245
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v44

<400> 1245

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> 1246
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v45

<400> 1246

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> 1247
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v46

<400> 1247

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> 1248
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v47

<400> 1248

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> 1249
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v48

<400> 1249

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 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> 1250
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v49

<400> 1250

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> 1251
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v50

<400> 1251

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> 1252
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v51

<400> 1252

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> 1253
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v52

<400> 1253

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> 1254
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v53

<400> 1254

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> 1255
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v54

<400> 1255

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> 1256
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v55

<400> 1256

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> 1257
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v56

<400> 1257

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> 1258
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v57

<400> 1258

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
100 105

<210> 1259
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v58

<400> 1259

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> 1260
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v59

<400> 1260

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> 1261
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v60

<400> 1261

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> 1262
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v61

<400> 1262

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> 1263
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v62

<400> 1263

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> 1264
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v63

<400> 1264

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> 1265
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v64

<400> 1265

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> 1266
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v65

<400> 1266

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> 1267
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v1

<400> 1267

Phe Thr Val Thr Val Pro 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> 1268
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v2

<400> 1268

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> 1269
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v3

<400> 1269

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> 1270
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v4

<400> 1270

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> 1271
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v5

<400> 1271

Phe Thr Val Thr Val Pro 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> 1272
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v6

<400> 1272

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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 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>  1273
<211>  114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v7

<400>  1273

Phe Thr Val Thr Val Pro 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> 1274
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v8

<400> 1274

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> 1275
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v9

<400> 1275

Phe Thr Val Thr Val Pro 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> 1276
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v10

<400> 1276

Phe Thr Val Thr Val Pro 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> 1277
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v11

<400> 1277

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> 1278
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v12

<400> 1278

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> 1279
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v13

<400> 1279

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> 1280
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v14

<400> 1280

Phe Thr Val Thr Val Pro 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> 1281
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v15

<400> 1281

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> 1282
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v16

<400> 1282

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> 1283
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v17

<400> 1283

Phe Thr Val Thr Val Pro 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> 1284
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v18

<400> 1284

Phe Thr Val Thr Val Pro 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> 1285
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v19

<400> 1285

Phe Thr Val Thr Val Pro 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> 1286
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v20

<400> 1286

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> 1287
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v21

<400> 1287

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> 1288
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v22

<400> 1288

Phe Thr Val Thr Val Pro 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> 1289
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v23

<400> 1289

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> 1290
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v24

<400> 1290

Phe Thr Val Thr Val Pro 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> 1291
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v25

<400> 1291

Phe Thr Val Thr Val Pro 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> 1292

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v26

<400> 1292

Phe Thr Val Thr Val Pro 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> 1293
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v27

<400> 1293

Phe Thr Val Thr Val Pro 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> 1294
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v28

<400> 1294

Phe Thr Val Thr Val Pro 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> 1295
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v29

<400> 1295

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> 1296
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v30

<400> 1296

Phe Thr Val Thr Val Pro 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> 1297
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v31

<400> 1297

Phe Thr Val Thr Val Pro 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> 1298
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v32

<400> 1298

```
Phe Thr Val Thr Val Pro 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>  1299
<211>  114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v33

<400>  1299

Phe Thr Val Thr Val Pro 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> 1300
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v34

<400> 1300

Phe Thr Val Thr Val Pro 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> 1301
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v35

<400> 1301

Phe Thr Val Thr Val Pro 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> 1302
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v36

<400> 1302

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> 1303
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v37

<400> 1303

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> 1304
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v38

<400> 1304

Phe Thr Val Thr Val Pro 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> 1305
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v39

<400> 1305

Phe Thr Val Thr Val Pro 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> 1306
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v40

<400> 1306

Phe Thr Val Thr Val Pro 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> 1307
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v41

<400> 1307

Phe Thr Val Thr Val Pro 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> 1308
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v42

<400> 1308

Phe Thr Val Thr Val Pro 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> 1309
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v43

<400> 1309

Phe Thr Val Thr Val Pro 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> 1310
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v44

<400> 1310

Phe Thr Val Thr Val Pro 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> 1311
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v45

<400> 1311

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> 1312
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v46

<400> 1312

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> 1313
<211> 114
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L1 IgV v47

<400> 1313

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> 1314
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v48

<400> 1314

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> 1315
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v49

<400> 1315

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> 1316
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v50

<400> 1316

Phe Thr Val Thr Val Pro 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> 1317
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v51

<400> 1317

Phe Thr Val Thr Val Pro 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> 1318

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v52

<400> 1318

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> 1319
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v53

<400> 1319

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> 1320
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v54

<400> 1320

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> 1321
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v55

<400> 1321

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> 1322
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v56

<400> 1322

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> 1323
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v57

<400> 1323

Phe Thr Val Thr Val Pro 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> 1324
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v58

<400> 1324

```
Phe Thr 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>  1325
<211>  114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v59

<400>  1325

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> 1326
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v60

<400> 1326

Phe Thr Val Thr Val Pro 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> 1327
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v61

<400> 1327

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> 1328
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v62

<400> 1328

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> 1329
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v63

<400> 1329

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> 1330
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v64

<400> 1330

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> 1331
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v65

<400> 1331

Phe Thr 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> 1332
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> PD-L1 IgV wildtype

<400> 1332

Phe Thr Val Thr Val Pro 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> 1333
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV

<400> 1333

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> 1334
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v1

<400> 1334

```
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> 1335
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v2

<400> 1335

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> 1336
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v3

<400> 1336

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> 1337
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v4

<400> 1337

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>  1338
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v5

<400>  1338

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> 1339
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v6

<400> 1339

```
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> 1340
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v7

<400> 1340

```
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> 1341
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v8

<400> 1341

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> 1342
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v9

<400> 1342

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> 1343
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v10

<400> 1343

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> 1344
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v11

<400> 1344

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> 1345

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v12

<400> 1345

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> 1346
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v13

<400> 1346

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> 1347
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v14

<400> 1347

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>  1348
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v15

<400>  1348

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> 1349
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v16

<400> 1349

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> 1350
<211> 201
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 ECD v17

<400> 1350

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> 1351
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v18

<400> 1351

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>  1352
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v19

<400>  1352

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> 1353
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v20

<400> 1353

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>  1354
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v21

<400>  1354

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> 1355
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v22

<400> 1355

```
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> 1356
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v23

<400> 1356

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> 1357
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v24

<400> 1357

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> 1358
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v25

<400> 1358

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> 1359
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v26

<400> 1359

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>  1360
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v27
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<400> 1360

```
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> 1361
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v28

<400> 1361

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> 1362
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v29

<400> 1362

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> 1363
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v30

<400> 1363

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>  1364
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v31

<400>  1364

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> 1365
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v32

<400> 1365

```
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> 1366
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v33

<400> 1366

```
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> 1367
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v34

<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 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> 1368
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v35

<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 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> 1369
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v36

<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 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> 1370
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v37

<400> 1370

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> 1371

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v38

<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 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>  1372
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v39

<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 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> 1373
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v40

<400> 1373

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> 1374
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v41

<400> 1374

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> 1375
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v42

<400> 1375

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> 1376
<211> 201
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 ECD v43

<400> 1376

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> 1377
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v44

<400> 1377

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>  1378
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v45

<400>  1378

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> 1379
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v46

<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 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>  1380
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v47

<400>  1380

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> 1381
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v48

<400> 1381

```
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>  1382
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v49

<400>  1382

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> 1383
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v50

<400> 1383

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> 1384
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v51

<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 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> 1385
<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> 1385

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> 1386

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v53

<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 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> 1387
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v54

<400> 1387

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> 1388
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v55

<400> 1388

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> 1389
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v56

<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 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> 1390
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v57

<400> 1390

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> 1391
<211> 201
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 ECD v58

<400> 1391

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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> 1392
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v59

<400> 1392

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> 1393
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> PD-L2 IgV wildtype

<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 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> 1394
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v61

<400> 1394

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> 1395
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v62

<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 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> 1396
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v63

<400> 1396

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> 1397
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v64

<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 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>  1398
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 ECD v65
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<400> 1398

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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
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195 200

<210> 1399
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v66

<400> 1399

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> 1400
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v67

<400> 1400

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 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> 1401
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v68

<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 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> 1402
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v69

<400> 1402

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> 1403
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v70

<400> 1403

```
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> 1404
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v71

<400> 1404

```
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> 1405
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v72

<400> 1405

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> 1406
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v73

<400> 1406

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

<210> 1407
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v74

<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 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> 1408
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v75

<400> 1408

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> 1409

<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v76

<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 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> 1410
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 ECD v77

<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 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> 1411
<211> 98
<212> PRT
<213> Artificial Seqeunce

<220>
<223> PD-L2 IgV v1

<400> 1411

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> 1412
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v2

<400> 1412

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> 1413
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v3

<400> 1413

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> 1414
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v4

<400> 1414

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> 1415
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v5

<400> 1415

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> 1416
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v6

<400> 1416

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> 1417
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v7

<400> 1417

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> 1418
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v8

<400> 1418

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> 1419
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v9

<400> 1419

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> 1420
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v10

<400> 1420

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> 1421
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v11

<400> 1421

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> 1422
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v12

<400> 1422

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> 1423
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v13

<400> 1423

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> 1424
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v14

<400> 1424

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> 1425
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v15

<400> 1425

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> 1426
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v16

<400> 1426

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> 1427
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v17

<400> 1427

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> 1428
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v18

<400> 1428

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> 1429
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v19

<400> 1429

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> 1430
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v20

<400> 1430

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> 1431

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v21

<400> 1431

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> 1432
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v22

<400> 1432

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> 1433
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v23

<400> 1433

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> 1434
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v24

<400> 1434

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> 1435
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v25

<400> 1435

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> 1436
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v26

<400> 1436

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> 1437
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v27

<400> 1437

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> 1438
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v28

<400> 1438

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> 1439
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v29

<400> 1439

```
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>  1440
<211>  98
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L2 IgV v30

<400>  1440

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> 1441
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v31

<400> 1441

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> 1442
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v32

<400> 1442

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> 1443
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v33

<400> 1443

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> 1444
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v34

<400> 1444

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> 1445
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v35

<400> 1445

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> 1446
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v36

<400> 1446

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> 1447
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v37

<400> 1447

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> 1448
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v38

<400> 1448

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> 1449
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v39

<400> 1449

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> 1450
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v40

<400> 1450

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> 1451
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v41

<400> 1451

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> 1452
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v42

<400> 1452

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> 1453
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v43

<400> 1453

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> 1454
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v44

<400> 1454

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> 1455
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v45

<400> 1455

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> 1456
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v46

<400> 1456

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> 1457

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v47

<400> 1457

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> 1458
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v48

<400> 1458

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> 1459
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v49

<400> 1459

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> 1460
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v50

<400> 1460

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> 1461
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v51

<400> 1461

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> 1462
<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> 1462

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> 1463
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v53

<400> 1463

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> 1464
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v54

<400> 1464

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> 1465
<211> 98
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v55

<400> 1465

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> 1466
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v56

<400> 1466

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> 1467
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v57

<400> 1467

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> 1468
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v58

<400> 1468

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> 1469
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v60

<400> 1469

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> 1470
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v61

<400> 1470

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> 1471
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v62

<400> 1471

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> 1472
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v63

<400> 1472

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> 1473
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v64

<400> 1473

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> 1474
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v65

<400> 1474

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> 1475
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v66

<400> 1475

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> 1476

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v67

<400> 1476

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> 1477
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v68

<400> 1477

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> 1478
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v69

<400> 1478

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> 1479
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v70

<400> 1479

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> 1480
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v71

<400> 1480

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> 1481
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v72

<400> 1481

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> 1482
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v73

<400> 1482

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> 1483
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v74

<400> 1483

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> 1484
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v75

<400> 1484

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> 1485
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v76

<400> 1485

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> 1486
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v77

<400> 1486

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> 1487
<211> 102
<212> PRT
<213> Artificial Seqeunce

<220>
<223> PD-L2 IgV v1

<400> 1487

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> 1488
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v2

<400> 1488

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> 1489
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v3

<400> 1489

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> 1490
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v4

<400> 1490

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> 1491
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v5

<400> 1491

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> 1492
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v6

<400> 1492

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> 1493
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v7

<400> 1493

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> 1494
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v8

<400> 1494

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> 1495
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v9

<400> 1495

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> 1496
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v10

<400> 1496

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> 1497
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v11

<400> 1497

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> 1498
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v12

<400> 1498

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> 1499
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v13

<400> 1499

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> 1500
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v14

<400> 1500

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> 1501
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v15

<400> 1501

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> 1502

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v16

<400> 1502

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> 1503
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v17

<400> 1503

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> 1504
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v18

<400> 1504

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> 1505
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v19

<400> 1505

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> 1506
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v20

<400> 1506

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> 1507
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v21

<400> 1507

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> 1508
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v22

<400> 1508

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> 1509
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v23

<400> 1509

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> 1510
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v24

<400> 1510

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> 1511
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v25

<400> 1511

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> 1512
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v26

<400> 1512

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> 1513
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v27

<400> 1513

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> 1514
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v28

<400> 1514

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> 1515
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v29

<400> 1515

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> 1516
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v30

<400> 1516

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> 1517
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v31

<400> 1517

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> 1518
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v32

<400> 1518

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> 1519
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v33

<400> 1519

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> 1520
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v34

<400> 1520

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> 1521
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v35

<400> 1521

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> 1522
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v36

<400> 1522

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> 1523
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v37

<400> 1523

```
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> 1524
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v38

<400> 1524

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> 1525
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v39

<400> 1525

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> 1526
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v40

<400> 1526

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> 1527
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v41

<400> 1527

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> 1528

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v42

<400> 1528

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> 1529
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v43

<400> 1529

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> 1530
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v44

<400> 1530

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> 1531
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v45

<400> 1531

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> 1532
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v46

<400> 1532

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> 1533
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v47

<400> 1533

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> 1534
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v48

<400> 1534

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> 1535
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v49

<400> 1535

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> 1536
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v50

<400> 1536

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> 1537
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v51

<400> 1537

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> 1538
<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> 1538

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> 1539
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v53

<400> 1539

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> 1540
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v54

<400> 1540

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> 1541
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v55

<400> 1541

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> 1542
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v56

<400> 1542

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> 1543
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v57

<400> 1543

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> 1544
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v58

<400> 1544

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> 1545
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v60

<400> 1545

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> 1546
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v61

<400> 1546

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> 1547

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v62

<400> 1547

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> 1548
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v63

<400> 1548

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> 1549
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v64

<400> 1549

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> 1550
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v65

<400> 1550

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> 1551
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v66

<400> 1551

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> 1552
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v67

<400> 1552

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> 1553
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v68

<400> 1553

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> 1554
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v69

<400> 1554

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> 1555
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v70

<400> 1555

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> 1556
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v71

<400> 1556

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> 1557
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v72

<400> 1557

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> 1558
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v73

<400> 1558

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> 1559
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v74

<400> 1559

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> 1560
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v75

<400> 1560

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> 1561
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 IgV v76

<400> 1561

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> 1562
<211> 102
<212> PRT

<213> Artificial Sequence

<220>
<223> PD-L2 IgV v77

<400> 1562

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> 1563
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v89 ECD

<400> 1563

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 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 Thr Ser Ile Asn Gly
    130                 135                 140

Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser Leu
145                 150                 155                 160

Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg Gly
                165                 170                 175

Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser Val
            180                 185                 190

Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu Thr
        195                 200                 205

Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Ala
    210                 215                 220

Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
225                 230                 235
```

<210> 1564
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> ICOSL v85 ECD

<400> 1564

```
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 Ser Ser Pro 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> 1565
<211> 111
<212> PRT
<213> ARtificial Sequence

<220>
<223> ICOSL v85 IgV

<400> 1565

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 Ser Ser Pro 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
100 105 110

<210> 1566
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> NKp30 v1 IgC-like (long)

<400> 1566

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> 1567
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 Signal Peptide

<400> 1567

Met Ile Phe Leu Leu Leu Met Leu Ser Leu Glu Leu Gln Leu His Gln
1   5   10   15

Ile Ala Ala

<210> 1568
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Avitag

<400> 1568

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
1   5   10   15

<210> 1569
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 1569

His His His His His His
1   5

<210> 1570
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Wildtype PD-L2 SIP

<400> 1570

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
115 120

<210> 1571
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 v49 SIP

<400> 1571

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 Gln Gly Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser
35 40 45

His Met 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 Leu Phe His Ile Pro Gln Val Gln Val Arg Asp
                85   90   95

Glu Gly Gln Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr
            100   105   110

Lys Tyr Leu Thr Leu Lys Val Lys Ala
        115   120

<210> 1572
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 v62 SIP

<400> 1572

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 Gln 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 Ala Ser Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu
65   70   75   80

Pro Leu Gly Arg Ala Leu Phe His Ile Pro Gln Val Gln Val Arg Asp

85 90 95

Glu Gly Gln Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr
100 105 110

Lys Tyr Leu Thr Leu Lys Val Lys Ala
115 120

<210> 1573
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L2 v76 SIP

<400> 1573

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 Gln 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 Ala Ser Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu
65 70 75 80

Pro Leu Gly Lys Ala Leu Phe His Ile Pro Gln Val Gln Val Gly Asp
85 90 95

Glu Gly Gln Tyr Arg Cys Ile Ile Ile Tyr Gly Asp Ala Trp Asp Tyr
100 105 110

Lys Tyr Leu Thr Leu Lys Val Lys Ala Gly Leu Asn Asp Ile Phe Glu
115 120 125

Ala Gln Lys Ile Glu Trp His Glu His His His His His His
130 135 140

<210> 1574
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8-derived hinge and transmembrane domain

<400> 1574

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> 1575
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3zeta intracellular signaling domain

<400> 1575

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> 1576
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD19 scFv

<400> 1576

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> 1577
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD19 scFv

<400> 1577

```
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> 1578
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8-derived hinge and transmembrane domain

<400> 1578

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> 1579
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB-derived costimulatory domain

<400> 1579

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> 1580
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1580

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> 1581
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1581

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> 1582
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28-derived costimulatory domain

<400> 1582

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> 1583
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 ECD

<400> 1583

Gln Asp Val Arg Val Gln Val 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> 1584
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 ECD

<400> 1584

Gln Asp Val Arg Val Gln Val 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> 1585
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v91 ECD

<400> 1585

Gln Asp Val Arg Val Gln Val 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> 1586
<211> 329
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v92 ECD

<400> 1586

```
Gln Asp Val Arg Val Gln Val 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> 1587
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 ECD

<400> 1587

Gln Asp Val Arg Val Gln Val 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> 1588
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v94 ECD

<400> 1588

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> 1589
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v95 ECD

<400> 1589

Gln Asp Val Arg Val Gln Val 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> 1590
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v96 ECD

<400> 1590

Gln Asp Val Arg Val Gln Val 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> 1591

<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v97 ECD

<400> 1591

Gln Asp Val Arg Val Gln Val 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>  1592
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v98 ECD

<400>  1592

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> 1593
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v99 ECD

<400> 1593

Gln Asp Val Arg Val Gln Val 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> 1594
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 ECD

<400> 1594

Gln Asp Val Arg Val Gln Val 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> 1595
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v101 ECD

<400> 1595

Gln Asp Val Arg Val Gln Val 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> 1596
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 ECD

<400> 1596

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> 1597
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 ECD

<400> 1597

```
Gln Asp Val Arg Val Gln Val 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>  1598
<211>  329
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v104 ECD

<400>  1598

Gln Asp Val Arg Val Gln Val 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> 1599
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v105 ECD

<400> 1599

Gln Asp Val Arg Val Gln Val 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

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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 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> 1600
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v106 ECD

<400> 1600

Gln Asp Val Arg Val Gln Val 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

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> 1601
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v107 ECD

<400> 1601

Gln Asp Val Arg Val Gln Val 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> 1602
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v108 ECD

<400> 1602

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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 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> 1603
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v109 ECD

<400> 1603

Gln Asp Val Arg Val Gln Val 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> 1604
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 ECD

<400> 1604

Gln Asp Val Arg Val Gln Val 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> 1605
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v111 ECD

<400> 1605

Gln Asp Val Arg Val Gln Val 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> 1606
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v112 ECD

<400> 1606

Gln Asp Val Arg Val Gln Val 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> 1607
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 IgV

<400> 1607

Gln Asp Val Arg Val Gln Val 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> 1608
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 IgV

<400> 1608

Gln Asp Val Arg Val Gln Val 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> 1609
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v91 IgV

<400> 1609

Gln Asp Val Arg Val Gln Val 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>  1610
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v92 IgV

<400>  1610

Gln Asp Val Arg Val Gln Val 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> 1611
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 IgV

<400> 1611

Gln Asp Val Arg Val Gln Val 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> 1612
<211> 125
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v94 IgV

<400> 1612

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> 1613
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v95 IgV

<400> 1613

Gln Asp Val Arg Val Gln Val 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> 1614
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v96 IgV

<400> 1614

Gln Asp Val Arg Val Gln Val 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> 1615
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v97 IgV

<400> 1615

Gln Asp Val Arg Val Gln Val 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> 1616
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v98 IgV

<400> 1616

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> 1617

<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v99 IgV

<400> 1617

Gln Asp Val Arg Val Gln Val 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> 1618
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1618

Gln Asp Val Arg Val Gln Val 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> 1619
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v101 IgV

<400> 1619

Gln Asp Val Arg Val Gln Val 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> 1620
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 IgV

<400> 1620

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> 1621
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 IgV

<400> 1621

Gln Asp Val Arg Val Gln Val 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> 1622
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v104 IgV

<400> 1622

Gln Asp Val Arg Val Gln Val 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> 1623
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v105 IgV

<400> 1623

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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 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>  1624
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v106 IgV

<400>  1624

Gln Asp Val Arg Val Gln Val 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> 1625
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v107 IgV

<400> 1625

Gln Asp Val Arg Val Gln Val 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> 1626
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v108 IgV

<400> 1626

Gln Asp Val Arg Val Gln Val 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> 1627
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v109 IgV

<400> 1627

Gln Asp Val Arg Val Gln Val 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> 1628
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1628

Gln Asp Val Arg Val Gln Val 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> 1629
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v111 IgV

<400> 1629

Gln Asp Val Arg Val Gln Val 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>  1630
<211>  125
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v112 IgV

<400>  1630

Gln Asp Val Arg Val Gln Val 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
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65 70 75 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> 1631
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v89 IgV

<400> 1631

Gln Asp Val Arg Val Gln Val 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> 1632
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v90 IgV

<400> 1632

Gln Asp Val Arg Val Gln Val 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> 1633
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v91 IgV

<400> 1633

Gln Asp Val Arg Val Gln Val 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> 1634
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v92 IgV

<400> 1634

Gln Asp Val Arg Val Gln Val 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> 1635
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v93 IgV

<400> 1635

Gln Asp Val Arg Val Gln Val 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> 1636
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v94 IgV

<400> 1636

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> 1637
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v95 IgV

<400> 1637

Gln Asp Val Arg Val Gln Val 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> 1638
<211> 127
<212> PRT

<213> Artificial sequence

<220>
<223> CD112 v96 IgV

<400> 1638

Gln Asp Val Arg Val Gln Val 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> 1639
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v97 IgV

<400> 1639

Gln Asp Val Arg Val Gln Val 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> 1640
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v98 IgV

<400> 1640

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> 1641
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v99 IgV

<400> 1641

Gln Asp Val Arg Val Gln Val 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> 1642
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v100 IgV

<400> 1642

Gln Asp Val Arg Val Gln Val 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> 1643

<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v101 IgV

<400> 1643

Gln Asp Val Arg Val Gln Val 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> 1644
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v102 IgV

<400> 1644

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> 1645
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v103 IgV

<400> 1645

Gln Asp Val Arg Val Gln Val 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> 1646
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v104 IgV

<400> 1646

Gln Asp Val Arg Val Gln Val 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> 1647
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v105 IgV

<400> 1647

Gln Asp Val Arg Val Gln Val 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> 1648
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v106 IgV

<400> 1648

Gln Asp Val Arg Val Gln Val 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> 1649
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v107 IgV

<400> 1649

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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 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>  1650
<211>  127
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v109 IgV

<400>  1650

Gln Asp Val Arg Val Gln Val 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> 1651
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v109 IgV

<400> 1651

Gln Asp Val Arg Val Gln Val 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>  1652
<211>  127
<212>  PRT
<213>  Artificial sequence

<220>
<223>  CD112 v100 IgV

<400>  1652

Gln Asp Val Arg Val Gln Val 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
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115 120 125

<210> 1653
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v111 IgV

<400> 1653

Gln Asp Val Arg Val Gln Val 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> 1654
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> CD112 v112 IgV

<400> 1654

Gln Asp Val Arg Val Gln Val 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> 1655
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 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 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> 1656
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v121 IgV

<400> 1656

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> 1657
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 IgV

<400> 1657

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> 1658
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 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 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> 1659
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v124 IgV

<400> 1659

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> 1660
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v125 IgV

<400> 1660

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> 1661
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 IgV

<400> 1661

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>  1662
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v127 IgV

<400>  1662

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> 1663
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 IgV

<400> 1663

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> 1664
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v129 IgV

<400> 1664

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> 1665
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v130 IgV

<400> 1665

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> 1666
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v131 IgV

<400> 1666

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> 1667
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v132 IgV

<400> 1667

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> 1668
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v133 IgV

<400> 1668

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> 1669

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v134 IgV

<400> 1669

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> 1670
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v135 IgV

<400> 1670

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> 1671
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 IgV

<400> 1671

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> 1672
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 IgV

<400> 1672

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> 1673
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v138 IgV

<400> 1673

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> 1674
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 IgV

<400> 1674

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> 1675
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 IgV

<400> 1675

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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>  1676
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v141 IgV

<400>  1676

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> 1677
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 IgV

<400> 1677

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> 1678
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 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 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> 1679
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v121 IgV

<400> 1679

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> 1680
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 IgV

<400> 1680

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> 1681
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 IgV

<400> 1681

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> 1682
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v124 IgV

<400> 1682

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> 1683
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v125 IgV

<400> 1683

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> 1684
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 IgV

<400> 1684

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> 1685
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v127 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 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> 1686
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 IgV

<400> 1686

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> 1687
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v129 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 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> 1688
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v130 IgV

<400> 1688

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> 1689
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v131 IgV

<400> 1689

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> 1690
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v132 IgV

<400> 1690

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> 1691
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v133 IgV

<400> 1691

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> 1692
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v134 IgV

<400> 1692

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> 1693
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v135 IgV

<400> 1693

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> 1694
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 IgV

<400> 1694

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> 1695

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 IgV

<400> 1695

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> 1696
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v138 IgV

<400> 1696

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> 1697
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 IgV

<400> 1697

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> 1698
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 IgV

<400> 1698

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> 1699
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v141 IgV

<400> 1699

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> 1700
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 IgV

<400> 1700

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> 1701
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v120 ECD

<400> 1701

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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 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
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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> 1702
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v121 ECD

<400> 1702

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> 1703
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v122 ECD

<400> 1703

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

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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> 1704
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v123 ECD

<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

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> 1705
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v124 ECD

<400> 1705

```
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>  1706
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v125 ECD
```

<400> 1706

```
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> 1707
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v126 ECD

<400> 1707

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> 1708
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v127 ECD

<400> 1708

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> 1709
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v128 ECD

<400> 1709

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> 1710
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v129 ECD

<400> 1710

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> 1711
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v130 ECD

<400> 1711

```
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>  1712
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v131 ECD

<400>  1712

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> 1713
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v132 ECD

<400> 1713

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> 1714
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v133 ECD

<400> 1714

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> 1715
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v134 ECD

<400> 1715

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> 1716
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v135 ECD

<400> 1716

```
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
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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> 1717
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v136 ECD

<400> 1717

Trp Pro Pro Pro Gly Thr Gly Asp Ile Ile Val Gln Ala Pro Thr Gln
1 5 10 15

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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> 1718
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v137 ECD

<400> 1718

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> 1719
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v138 ECD

<400> 1719

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

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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> 1720
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v139 ECD

<400> 1720

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> 1721

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v140 ECD

<400> 1721

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

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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>  1722
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v141 ECD

<400>  1722

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> 1723
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v142 ECD

<400> 1723

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
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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>  1724
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v143 ECD

<400>  1724

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> 1725
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v143 IgV

<400> 1725

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> 1726
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v143 IgV

<400> 1726

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> 1727
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 ECD

<400> 1727

```
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> 1728
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v145 ECD

<400> 1728

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> 1729
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v146 ECD

<400> 1729

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> 1730
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v147 ECD

<400> 1730

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> 1731
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v148 ECD

<400> 1731

```
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>  1732
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v149 ECD
```

<400> 1732

```
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> 1733
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v150 ECD

<400> 1733

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> 1734
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v151 ECD

<400> 1734

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> 1735
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v152 ECD

<400> 1735

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> 1736
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v153 ECD

<400> 1736

```
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> 1737
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v154 ECD

<400> 1737

```
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>  1738
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v155 ECD

<400>  1738

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> 1739
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 ECD

<400> 1739

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> 1740
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v157 ECD

<400> 1740

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> 1741
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 ECD

<400> 1741

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> 1742
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v159 ECD

<400> 1742

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> 1743
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v160 ECD

<400> 1743

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> 1744
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 ECD

<400> 1744

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> 1745
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v162 ECD

<400> 1745

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> 1746
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v163 ECD

<400> 1746

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> 1747

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 ECD

<400> 1747

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>  1748
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v165 ECD

<400>  1748

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> 1749
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v166 ECD

<400> 1749

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> 1750
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 ECD

<400> 1750

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> 1751
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v168 ECD

<400> 1751

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> 1752
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 ECD

<400> 1752

```
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> 1753
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 ECD

<400> 1753

```
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>  1754
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v171 ECD

<400>  1754

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> 1755
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v172 ECD

<400> 1755

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> 1756
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v173 ECD

<400> 1756

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> 1757
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v174 ECD

<400> 1757

```
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>  1758
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v175 ECD
```

<400> 1758

```
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> 1759
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 ECD

<400> 1759

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> 1760
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v177 ECD

<400> 1760

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> 1761
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 ECD

<400> 1761

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> 1762
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 ECD

<400> 1762

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> 1763
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v180 ECD

<400> 1763

```
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>  1764
<211>  323
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v181 ECD

<400>  1764

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> 1765
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v182 ECD

<400> 1765

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> 1766
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v183 ECD

<400> 1766

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> 1767
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v184 ECD

<400> 1767

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> 1768
<211> 323
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v185 ECD

<400> 1768

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> 1769
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v186 ECD

<400> 1769

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> 1770
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 ECD

<400> 1770

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> 1771
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v188 ECD

<400> 1771

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> 1772
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v189 ECD

<400> 1772

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> 1773

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 IgV

<400> 1773

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> 1774
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v145 IgV

<400> 1774

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> 1775
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v146 IgV

<400> 1775

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>  1776
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v147 IgV

<400>  1776

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> 1777
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v148 IgV

<400> 1777

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> 1778
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v149 IgV

<400> 1778

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> 1779
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v150 IgV

<400> 1779

```
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>  1780
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v151 IgV

<400>  1780

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> 1781
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v152 IgV

<400> 1781

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>  1782
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v153 IgV

<400>  1782

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> 1783
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v154 IgV

<400> 1783

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> 1784
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v155 IgV

<400> 1784

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> 1785
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 IgV

<400> 1785

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> 1786
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v157 IgV

<400> 1786

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> 1787
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 IgV

<400> 1787

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> 1788
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v159 IgV

<400> 1788

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> 1789
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v160 IgV

<400> 1789

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> 1790
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 IgV

<400> 1790

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> 1791
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v162 IgV

<400> 1791

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> 1792
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v163 IgV

<400> 1792

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> 1793
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 IgV

<400> 1793

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> 1794
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v165 IgV

<400> 1794

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> 1795
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v166 IgV

<400> 1795

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> 1796
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 IgV

<400> 1796

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> 1797
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v168 IgV

<400> 1797

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> 1798
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 IgV

<400> 1798

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> 1799

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 IgV

<400> 1799

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> 1800
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v171 IgV

<400> 1800

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> 1801
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v172 IgV

<400> 1801

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>  1802
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v173 IgV

<400>  1802

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
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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> 1803
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v174 IgV

<400> 1803

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> 1804
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v175 IgV

<400> 1804

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> 1805
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 IgV

<400> 1805

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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>  1806
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v177 IgV

<400>  1806

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> 1807
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 IgV

<400> 1807

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> 1808
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 IgV

<400> 1808

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> 1809
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v180 IgV

<400> 1809

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> 1810
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v181 IgV

<400> 1810

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> 1811
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v182 IgV

<400> 1811

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> 1812
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v183 IgV

<400> 1812

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> 1813
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v184 IgV

<400> 1813

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> 1814
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v185 IgV

<400> 1814

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> 1815
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v186 IgV

<400> 1815

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> 1816
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 IgV

<400> 1816

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> 1817
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v188 IgV

<400> 1817

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> 1818
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v189 IgV

<400> 1818

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> 1819
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v144 IgV

<400> 1819

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> 1820
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v145 IgV

<400> 1820

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> 1821
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v146 IgV

<400> 1821

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> 1822
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v147 IgV

<400> 1822

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> 1823
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v148 IgV

<400> 1823

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> 1824
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v149 IgV

<400> 1824

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> 1825

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v150 IgV

<400> 1825

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> 1826
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v151 IgV

<400> 1826

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> 1827
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v152 IgV

<400> 1827

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> 1828
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v153 IgV

<400> 1828

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> 1829
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v154 IgV

<400> 1829

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> 1830
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v155 IgV

<400> 1830

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> 1831
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v156 IgV

<400> 1831

```
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>  1832
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v157 IgV

<400>  1832

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> 1833
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v158 IgV

<400> 1833

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>  1834
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v159 IgV

<400>  1834

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> 1835
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v160 IgV

<400> 1835

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> 1836
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v161 IgV

<400> 1836

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> 1837
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v162 IgV

<400> 1837

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>  1838
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v163 IgV

<400>  1838

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> 1839
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v164 IgV

<400> 1839

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> 1840
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v165 IgV

<400> 1840

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> 1841
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v166 IgV

<400> 1841

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> 1842
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v167 IgV

<400> 1842

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> 1843
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v168 IgV

<400> 1843

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> 1844
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v169 IgV

<400> 1844

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> 1845
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v170 IgV

<400> 1845

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> 1846
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> CD155 v171 IgV

<400> 1846

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> 1847
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v172 IgV

<400> 1847

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> 1848
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v173 IgV

<400> 1848

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> 1849
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v174 IgV

<400> 1849

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> 1850
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v175 IgV

<400> 1850

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> 1851

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v176 IgV

<400> 1851

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> 1852
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v177 IgV

<400> 1852

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> 1853
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v178 IgV

<400> 1853

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> 1854
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v179 IgV

<400> 1854

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> 1855
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v180 IgV

<400> 1855

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> 1856
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v181 IgV

<400> 1856

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> 1857
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v182 IgV

<400> 1857

```
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>  1858
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v183 IgV

<400>  1858

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> 1859
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v184 IgV

<400> 1859

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>  1860
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v185 IgV

<400>  1860

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> 1861
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v186 IgV

<400> 1861

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> 1862
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v187 IgV

<400> 1862

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> 1863
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> CD155 v188 IgV

<400> 1863

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>  1864
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD155 v189 IgV

<400>  1864

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> 1865
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Stack Fc Lysine removed (homodimeric)

<400> 1865

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>  1866
<211>  231
<212>  PRT
<213>  artificial Sequence

<220>
<223>  Fc (C5S (C220S), R77C, (R292C),  N82G (N297G), V87C (V302C),
       L232del (K447del))

<400>  1866

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> 1867
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc with C220S/L234A/L235E/G237A/K447del

<400> 1867

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>  1868
<211>  230
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fc with C220S/E233P/L234V/L235A/G236del/S267K/K447del

<400>  1868

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>  1869
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Linker

<400>  1869

Gly Ser Gly Gly Gly Gly Ser
1               5


<210>  1870
<211>  5
```

<212> PRT
<213> Artificial Sequence

<220>
<223> 4GS Linker

<400> 1870

Gly Gly Gly Gly Ser
1   5

<210> 1871
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v66

<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 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>  1872
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV 66

<400>  1872

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> 1873
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v66

<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 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> 1874
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Wildtype PD-L1 ECD

<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 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>  1875
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v67

<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 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>  1876
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v68

<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 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>  1877
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> PD-L1 ECD v69

<400> 1877

```
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> 1878
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v70

<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 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> 1879
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v71

<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 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> 1880
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v72

<400> 1880

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> 1881
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v73

<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 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> 1882
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v74

<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 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> 1883
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v75

<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 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> 1884
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v76

<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 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> 1885
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v77

<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 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>  1886
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v78

<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 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>  1887
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v79

<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 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> 1888
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v80

<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 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> 1889
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v81

<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 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> 1890
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v82

<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 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> 1891
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v83

<400> 1891

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> 1892
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v84

<400> 1892

```
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> 1893
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v85

<400> 1893

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> 1894
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v86

<400> 1894

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>  1895
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v87

<400>  1895

Phe Thr Val Thr Val Pro 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> 1896
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v88

<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 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> 1897
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v89

<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 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> 1898
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v90

<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 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>  1899
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v91

<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 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> 1900
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v92

<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 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> 1901
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v93

<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 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> 1902
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v94

<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 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> 1903
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v95

<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 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> 1904
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v96

<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 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> 1905
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v97

<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 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> 1906
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v98

<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 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> 1907
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v99

<400> 1907

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>  1908
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v100

<400>  1908

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> 1909
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v101

<400> 1909

```
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>  1910
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v102

<400>  1910

Phe Thr Val Thr Val Pro 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> 1911
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v103

<400> 1911

```
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> 1912
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v104

<400> 1912

Phe Thr Val Thr Val Pro 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>  1913
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v105

<400>  1913

Phe Thr Val Thr Val Pro 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> 1914
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v106

<400> 1914

Phe Thr Val Thr Val Pro 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> 1915
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v107

<400> 1915

Phe Thr Val Thr Val Pro 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> 1916
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v108

<400> 1916

Phe Thr Val Thr Val Pro 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 Thr
    210                 215                 220


<210>  1917
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v109

<400>  1917

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> 1918
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v110

<400> 1918

```
Phe Thr Val Thr Val Pro 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> 1919
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v111

<400> 1919

Phe Thr Val Thr Val Pro 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> 1920
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v112

<400> 1920

Phe Thr Val Thr Val Pro 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>  1921
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v113

<400>  1921

Phe Thr Val Thr Val Pro 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> 1922
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v114

<400> 1922

```
Phe Thr Val Thr Val Pro 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> 1923
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v115

<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 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>  1924
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v116

<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 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>  1925
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v117

<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 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> 1926
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v118

<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 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>  1927
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v119

<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 Glu Asp Leu 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>  1928
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v120

<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 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> 1929
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v121

<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 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> 1930
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v122

<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 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> 1931
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v123

<400> 1931

Phe Thr Val Thr Val Pro 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>  1932
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v124

<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 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
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<210> 1933
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v125

<400> 1933

Phe Thr Val Thr Val Pro 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> 1934
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v126

<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 Pro Tyr Asn Lys Ile Asn Gln Arg 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> 1935
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v127

<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 Val Gln His Ser Ser Tyr Arg
    50                  55                  60
```

```
Gln Arg Ala Arg 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>  1936
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v128

<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 Gln Asp Ala Gly Val Tyr Arg Cys
                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> 1937
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v129

<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 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> 1938
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 1938

Phe Thr Val Thr Val Pro 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>  1939
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v131

<400>  1939

Phe Thr Val Thr Val Pro 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 Thr
    210                 215                 220
```

<210> 1940
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v132

<400> 1940

```
Phe Thr Val Thr Val Pro 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> 1941
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v133

<400> 1941

Phe Thr 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> 1942
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v134

<400> 1942

Phe Thr Val Thr Val Pro 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>  1943
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v135

<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 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> 1944
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v136

<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 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> 1945
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v137

<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 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> 1946
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v138

<400> 1946

Phe Thr Val Thr Val Pro 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>  1947
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v139

<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 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> 1948
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v140

<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 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
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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> 1949
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v141

<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 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>  1950
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v142

<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 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>  1951
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v143

<400>  1951
```

```
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> 1952
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v144

<400> 1952

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>  1953
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v145

<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 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> 1954
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v146

<400> 1954

Phe Thr 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> 1955
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v147

<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 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> 1956
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v148

<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 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>  1957
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v149

<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 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>  1958
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v150

<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 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> 1959
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v151

<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 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>  1960
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v152

<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 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>  1961
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v153

<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

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>  1962
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v154

<400>  1962

Phe Thr Val Thr Val Pro 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> 1963
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v155

<400> 1963

Phe Thr Val Thr Val Pro 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> 1964
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v156

<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

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>  1965
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v67

<400>  1965

Phe Thr Val Thr Val Pro 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
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```
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
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<210> 1966
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v68

<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 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> 1967
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v69

<400> 1967

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> 1968
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v70

<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

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>  1969
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v72

<400>  1969

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
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<210> 1970
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v73

<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 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> 1971
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v74

<400> 1971

Phe Thr Val Thr Val Pro 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> 1972
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v75

<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 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>  1973
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v76

<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

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> 1974
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v77

<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

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> 1975
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v78

<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

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>  1976
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v79

<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 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>  1977
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v80

<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 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> 1978
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v81

<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 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>  1979
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v82

<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 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>  1980
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v83

<400>  1980

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> 1981
<211> 220
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v84

<400> 1981

```
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
210 215 220

<210> 1982
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v85

<400> 1982

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
    210                 215                 220


<210>  1983
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v86

<400>  1983

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> 1984
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v87

<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

```
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
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<210> 1985
<211> 220

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v88

<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

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>  1986
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v89

<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


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>  1987
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v90

<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 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
    210                 215                 220


<210>  1988
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v91

<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 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
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<210> 1989
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v92

<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 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> 1990
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v93

<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 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>  1991
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v94

<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 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> 1992
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v95

<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 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> 1993
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v96

<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 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> 1994
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v97

<400> 1994

Phe Thr Val Thr Val Pro 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>  1995
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v98

<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 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> 1996
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v99

<400> 1996

```
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> 1997
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v100

<400> 1997

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> 1998
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v101

<400> 1998

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>  1999
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v102

<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

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> 2000
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v103

<400> 2000

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> 2001
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v104

<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 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>  2002
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v105

<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 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> 2003
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v106

<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 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> 2004
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v107

<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 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>  2005
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v108

<400>  2005

Phe Thr Val Thr Val Pro 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>  2006
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v109

<400>  2006

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>  2007
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> PD-L1 ECD v110

<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 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> 2008
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v111

<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 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>  2009
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v112

<400>  2009

Phe Thr Val Thr Val Pro 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> 2010
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v113

<400> 2010

Phe Thr Val Thr Val Pro 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> 2011
<211> 220

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v114

<400> 2011

Phe Thr Val Thr Val Pro 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>  2012
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v115

<400>  2012

Phe Thr Val Thr Val Pro 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> 2013
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v116

<400> 2013

```
Phe Thr Val Thr Val Pro 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>  2014
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v117

<400>  2014

Phe Thr Val Thr Val Pro 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> 2015
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v118

<400> 2015

```
Phe Thr Val Thr Val Pro 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> 2016
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v119

<400> 2016

Phe Thr Val Thr Val Pro 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>  2017
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v120

<400>  2017

Phe Thr Val Thr Val Pro 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
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<210> 2018
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v121

<400> 2018

Phe Thr Val Thr Val Pro 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> 2019
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v122

<400> 2019

Phe Thr Val Thr Val Pro 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> 2020
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v123

<400> 2020

Phe Thr Val Thr Val Pro 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>  2021
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v124

<400>  2021

Phe Thr Val Thr Val Pro 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> 2022
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v125

<400> 2022

```
Phe Thr Val Thr Val Pro 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> 2023
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v126

<400> 2023

Phe Thr Val Thr Val Pro 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> 2024
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v127

<400> 2024

Phe Thr Val Thr Val Pro 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>  2025
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v128

<400>  2025

Phe Thr Val Thr Val Pro 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> 2026
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v129

<400> 2026

Phe Thr Val Thr Val Pro 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> 2027
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 2027

Phe Thr Val Thr Val Pro 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> 2028
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v131

<400> 2028

Phe Thr Val Thr Val Pro 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>  2029
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v132

<400>  2029
```

```
Phe Thr Val Thr Val Pro 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> 2030
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v133

<400> 2030

Phe Thr 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>  2031
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v134

<400>  2031

Phe Thr Val Thr Val Pro 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>  2032
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v135

<400>  2032

Phe Thr Val Thr Val Pro 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>  2033
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> PD-L1 ECD v136

<400> 2033

```
Phe Thr Val Thr Val Pro 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> 2034
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v137

<400> 2034

Phe Thr Val Thr Val Pro 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>  2035
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v138

<400>  2035

Phe Thr Val Thr Val Pro 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> 2036
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v139

<400> 2036

Phe Thr Val Thr Val Pro 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> 2037
<211> 220

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v140

<400> 2037

Phe Thr Val Thr Val Pro 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>  2038
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v141

<400>  2038

Phe Thr Val Thr Val Pro 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> 2039
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v142

<400> 2039

```
Phe Thr Val Thr Val Pro 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>  2040
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v143

<400>  2040

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> 2041
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v144

<400> 2041

```
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> 2042
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v145

<400> 2042

Phe Thr Val Thr Val 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>  2043
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v146

<400>  2043

Phe Thr 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> 2044
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v147

<400> 2044

Phe Thr 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> 2045
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v148

<400> 2045

Phe Thr Val Thr Val Pro 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> 2046
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v149

<400> 2046

Phe Thr Val Thr Val Pro 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>  2047
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v150

<400>  2047

Phe Thr Val Thr Val Pro 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> 2048
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v151

<400> 2048

```
Phe Thr Val Thr Val Pro 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> 2049
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v152

<400> 2049

Phe Thr Val Thr Val Pro 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> 2050
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v153

<400> 2050

Phe Thr Val Thr Val Pro 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>  2051
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v154

<400>  2051

Phe Thr Val Thr Val Pro 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> 2052
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v155

<400> 2052

Phe Thr Val Thr Val Pro 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
210 215 220

<210> 2053
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v156

<400> 2053

Phe Thr Val Thr Val Pro 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

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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


<210>  2054
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v67

<400>  2054

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> 2055
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v75

<400> 2055

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> 2056
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v80

<400> 2056

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> 2057
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v81

<400> 2057

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>  2058
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 IgV v82

<400>  2058

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
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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> 2059
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v87

<400> 2059

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

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> 2060
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v94

<400> 2060

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
            100   105

<210> 2061
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v98

<400> 2061

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> 2062
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v100

<400> 2062

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> 2063
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v102

<400> 2063

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> 2064
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v103

<400> 2064

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> 2065
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v110

<400> 2065

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> 2066
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v118

<400> 2066

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> 2067
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v127

<400> 2067

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> 2068
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v152

<400> 2068

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> 2069
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v67

<400> 2069

Phe Thr Val Thr Val Pro 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> 2070
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v75

<400> 2070

Phe Thr Val Thr Val Pro 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> 2071
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v80

<400> 2071

Phe Thr Val Thr Val Pro 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> 2072
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v81

<400> 2072

Phe Thr Val Thr Val Pro 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> 2073
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v82

<400> 2073

Phe Thr Val Thr Val Pro 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> 2074
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v87

<400> 2074

Phe Thr Val Thr Val Pro 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> 2075
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v94

<400> 2075

Phe Thr Val Thr Val Pro 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> 2076
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v98

<400> 2076

Phe Thr Val Thr Val Pro 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> 2077
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v100

<400> 2077

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> 2078
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v102

<400> 2078

Phe Thr Val Thr Val Pro 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> 2079
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v103

<400> 2079

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> 2080
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v110

<400> 2080

Phe Thr Val Thr Val Pro 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> 2081
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v118

<400> 2081

Phe Thr Val Thr Val Pro 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> 2082
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v127

<400> 2082

Phe Thr Val Thr Val Pro 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> 2083
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 IgV v152

<400> 2083

Phe Thr Val Thr Val Pro 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> 2084
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc (C5S (C220S), R77C, (R292C), N82G (N297G), V87C (V302C))

<400> 2084

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> 2085
<211> 232

<212> PRT
<213> Artificial Sequence

<220>
<223> Fc with C220S/L234A/L235E/G237A

<400> 2085

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> 2086
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc with C220S/E233P/L234V/L235A/G236del/S267K

<400> 2086

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> 2087
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v1

<400> 2087

Phe Thr Val Thr Val Pro 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> 2088
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v2

<400> 2088

```
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> 2089
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v3

<400> 2089

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> 2090
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v4

<400> 2090

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>  2091
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v5

<400>  2091

Phe Thr Val Thr Val Pro 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> 2092
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v6

<400> 2092

Phe Thr Val Thr Val Pro 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> 2093
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v7

<400> 2093

Phe Thr Val Thr Val Pro 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> 2094
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v8

<400> 2094

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> 2095
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v9

<400> 2095

```
Phe Thr Val Thr Val Pro 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> 2096
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v10

<400> 2096

Phe Thr Val Thr Val Pro 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>  2097
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v11

<400>  2097

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>  2098
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v12

<400>  2098

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>  2099
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> PD-L1 ECD v13

<400> 2099

```
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> 2100
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v14

<400> 2100

Phe Thr Val Thr Val Pro 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>  2101
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v15

<400>  2101

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> 2102
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v16

<400> 2102

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
```

<210> 2103
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v17

<400> 2103

Phe Thr Val Thr Val Pro 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>  2104
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v18

<400>  2104

Phe Thr Val Thr Val Pro 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> 2105
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v19

<400> 2105

```
Phe Thr Val Thr Val Pro 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>  2106
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v20

<400>  2106

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> 2107
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v21

<400> 2107

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>  2108
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v22

<400>  2108

Phe Thr Val Thr Val Pro 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>  2109
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v23

<400>  2109

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> 2110
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v24

<400> 2110

Phe Thr Val Thr Val Pro 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> 2111
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v25

<400> 2111

Phe Thr Val Thr Val Pro 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> 2112
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v26

<400> 2112

Phe Thr Val Thr Val Pro 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>  2113
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v27

<400>  2113

Phe Thr Val Thr Val Pro 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> 2114
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v28

<400> 2114

```
Phe Thr Val Thr Val Pro 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> 2115
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v29

<400> 2115

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> 2116
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v30

<400> 2116

Phe Thr Val Thr Val Pro 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>  2117
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v31

<400>  2117

Phe Thr Val Thr Val Pro 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
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<210> 2118
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v32

<400> 2118

Phe Thr Val Thr Val Pro 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> 2119
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v33

<400> 2119

Phe Thr Val Thr Val Pro 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> 2120
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v34

<400> 2120

Phe Thr Val Thr Val Pro 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>  2121
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v35

<400>  2121
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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 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> 2122
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v36

<400> 2122

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>  2123
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>   PD-L1 ECD v37

<400>  2123

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>  2124
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v38

<400>  2124

Phe Thr Val Thr Val Pro 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>  2125
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> PD-L1 ECD v39

<400> 2125

```
Phe Thr Val Thr Val Pro 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> 2126
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v40

<400> 2126

Phe Thr Val Thr Val Pro 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>  2127
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v41

<400>  2127

Phe Thr Val Thr Val Pro 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> 2128
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v42

<400> 2128

Phe Thr Val Thr Val Pro 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> 2129
<211> 221

<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v43

<400> 2129

Phe Thr Val Thr Val Pro 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>  2130
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v44

<400>  2130

Phe Thr Val Thr Val Pro 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> 2131
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v45

<400> 2131

```
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>  2132
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v46

<400>  2132

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> 2133
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v47

<400> 2133

```
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> 2134
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v48

<400> 2134

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>  2135
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v49

<400>  2135

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
```

<210> 2136
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v50

<400> 2136

Phe Thr Val Thr Val Pro 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> 2137
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v51

<400> 2137

Phe Thr Val Thr Val Pro 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> 2138
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v52

<400> 2138

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>  2139
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v53

<400>  2139

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> 2140
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v54

<400> 2140

```
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> 2141
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v55

<400> 2141

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> 2142
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v56

<400> 2142

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> 2143
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v57

<400> 2143

```
Phe Thr Val Thr Val Pro 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> 2144
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v58

<400> 2144

```
Phe Thr 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> 2145
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v59

<400> 2145

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> 2146
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v60

<400> 2146

Phe Thr Val Thr Val Pro 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> 2147
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v61

<400> 2147

```
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> 2148
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v62

<400> 2148

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>  2149
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v63

<400>  2149

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>  2150
<211>  221
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PD-L1 ECD v64

<400>  2150

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> 2151
<211> 221
<212> PRT
<213> Artificial Sequence

<220>

<223> PD-L1 ECD v65

<400> 2151

```
Phe Thr 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> 2152
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 ECD v66

<400> 2152

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>  2153
<211>  232
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Stack Fc (homodimeric)

<400>  2153

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> 2154
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag tag

<400> 2154

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Asp Tyr Lys Asp Asp Asp Asp Lys
1               5
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<210> 2155
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Wildtype PD-L1 SIP

<400> 2155

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 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> 2156
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1 v60 SIP

<400> 2156

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> 2157
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal Peptide

<400> 2157

Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
1   5   10   15

Val Ser Ala

<210> 2158
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 hinge and transmembrane domain

<400> 2158

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> 2159
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-2

<400> 2159

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
```

<210> 2160
<211> 707
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-2

<400> 2160

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 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
705

<210> 2161
<211> 8708
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD19 chimeric antigen receptor CAR-2

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caacatgcct tacaaggaga gaaaaagcac cgtgcatgcc gattggtgga agtaaggtgg 120

tacgatcgtg ccttattagg aaggcaacag acgggtctga catggattgg acgaaccact 180

gaattgccgc attgcagaga tattgtattt aagtgcctag ctcgatacaa taaacgggtc 240

tctctggtta gaccagatct gagcctggga gctctctggc taactaggga acccactgct 300

taagcctcaa taaagcttgc cttgagtgct tcaagtagtg tgtgcccgtc tgttgtgtga 360

ctctggtaac tagagatccc tcagaccctt ttagtcagtg tggaaaatct ctagcagtgg 420

cgcccgaaca gggacttgaa agcgaaaggg aaaccagagg agctctctcg acgcaggact 480

cggcttgctg aagcgcgcac ggcaagaggc gaggggcggc gactggtgag tacgccaaaa 540

attttgacta gcggaggcta gaaggagaga gatgggtgcg agagcgtcag tattaagcgg 600

gggagaatta gatcgcgatg ggaaaaaatt cggttaaggc caggggaaa gaaaaaatat 660

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ctgttagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atcccttcag 780

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aaattttatc gatcacgaga ctagcctcga gaagcttgat atcgaattcc cacggggttg 1980

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atctgtggta agcagttcct gccccggctc agggccaaga acagatggtc cccagatgcg 2160

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tcgccctttg acgttggagt ccacgttctt taatagtgga ctcttgttcc aaactggaac 6360

aacactcaac cctatctcgg tctattcttt tgatttataa gggattttgc cgatttcggc 6420

ctattggtta aaaaatgagc tgatttaaca aaaatttaac gcgaatttta acaaaatatt 6480

aacgtttaca atttcccagg tggcactttt cggggaaatg tgcgcggaac ccctatttgt 6540

ttatttttct aaatacattc aaatatgtat ccgctcatga gacaataacc ctgataaatg 6600

cttcaataat attgaaaaag gaagagtatg agtattcaac atttccgtgt cgcccttatt 6660

ccctttttg cggcattttg ccttcctgtt tttgctcacc cagaaacgct ggtgaaagta 6720

aaagatgctg aagatcagtt gggtgcacga gtgggttaca tcgaactgga tctcaacagc 6780

ggtaagatcc ttgagagttt tcgccccgaa gaacgttttc caatgatgag cacttttaaa 6840

gttctgctat gtggcgcggt attatcccgt attgacgccg ggcaagagca actcggtcgc 6900

cgcatacact attctcagaa tgacttggtt gagtactcac cagtcacaga aaagcatctt 6960

acggatggca tgacagtaag agaattatgc agtgctgcca taaccatgag tgataacact 7020

gcggccaact tacttctgac aacgatcgga ggaccgaagg agctaaccgc ttttttgcac 7080

aacatggggg atcatgtaac tcgccttgat cgttgggaac cggagctgaa tgaagccata 7140

ccaaacgacg agcgtgacac cacgatgcct gtagcaatgg caacaacgtt gcgcaaacta 7200

ttaactggcg aactacttac tctagcttcc cggcaacaat taatagactg gatggaggcg 7260

gataaagttg caggaccact tctgcgctcg gcccttccgg ctggctggtt tattgctgat 7320

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gtttactcat atatacttta gattgattta aaacttcatt tttaatttaa aaggatctag 7560

gtgaagatcc tttttgataa tctcatgacc aaaatccctt aacgtgagtt ttcgttccac 7620

tgagcgtcag accccgtaga aaagatcaaa ggatcttctt gagatccttt ttttctgcgc 7680

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caagagctac caactctttt tccgaaggta actggcttca gcagagcgca gataccaaat 7800

actgtccttc tagtgtagcc gtagttaggc caccacttca agaactctgt agcaccgcct 7860

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gtaagcggca gggtcggaac aggagagcgc acgagggagc ttccaggggg aaacgcctgg 8160

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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

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gagctgca 8708

<210> 2162
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19 chimeric antigen receptor CAR-1

<400> 2162

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>  2163
<211>  706
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  antiCD19 chimeric antigen receptor CAR-1

<400>  2163

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> 2164
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Blue fluorescent protein

<400> 2164

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>  2165
<211>  18
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  T2A

<400>  2165

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1               5                   10                  15
```

Gly Pro

<210> 2166
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> antiCD19z chimeric antigen receptor

<400> 2166

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>  2167
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD8-derived signal sequence

<400>  2167

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>  2168
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD8-derived signal sequence

<400>  2168

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> 2169
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A protein

<400> 2169

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> 2170
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Blue fluorescent protein

<400> 2170

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>  2171
<211>  472
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  2nd Gen CAR

<400>  2171

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> 2172
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> 2nd Gen CAR

<400> 2172

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> 2173
<211> 471
<212> PRT
<213> Artificial Sequence

<220>

<223> 2nd Gen CAR with CD28-derived costimulatory domain

<400> 2173

```
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
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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> 2174
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD19 scFv

<400> 2174

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>  2175
<211>  1356
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  antiCD19 chimeric antigen receptor nucleotide

<400>  2175
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60
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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> 2176
<211> 63
<212> PRT
<213> Artificial Sequence

<220>

<223> T2A nucleotide

<400> 2176

Gly Gly Cys Ala Gly Thr Gly Gly Cys Gly Ala Gly Gly Gly Cys Ala
1 5 10 15

Gly Ala Gly Gly Ala Ala Gly Thr Cys Thr Gly Cys Thr Ala Ala Cys
20 25 30

Ala Thr Gly Cys Gly Gly Thr Gly Ala Cys Gly Thr Cys Gly Ala Gly
35 40 45

Gly Ala Gly Ala Ala Thr Cys Cys Thr Gly Gly Cys Cys Cys Ala
50 55 60

<210> 2177
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A Protein

<400> 2177

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> 2178
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A protein

<400> 2178

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> 2179
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> eGFP

<400> 2179

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

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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>  2180
<211>  237
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Green fluorescent protein

<400>  2180

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
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```
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
```