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(54) SWITCH RECEPTORS USING IL-9
SIGNALING DOMAINS

(71) Applicants: **Parker Institute for Cancer
Immunotherapy**, San Francisco, CA
(US); **The Board of Trustees of the
Leland Stanford Junior University**,
Stanford, CA (US)

(72) Inventors: **John CONNOLLY**, Red Oak, TX
(US); **Sean PARKER**, San Francisco,
CA (US); **Kenan Christopher
GARCIA**, San Francisco, CA (US)

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(2006.01)

(52) **U.S. Cl.**

CPC

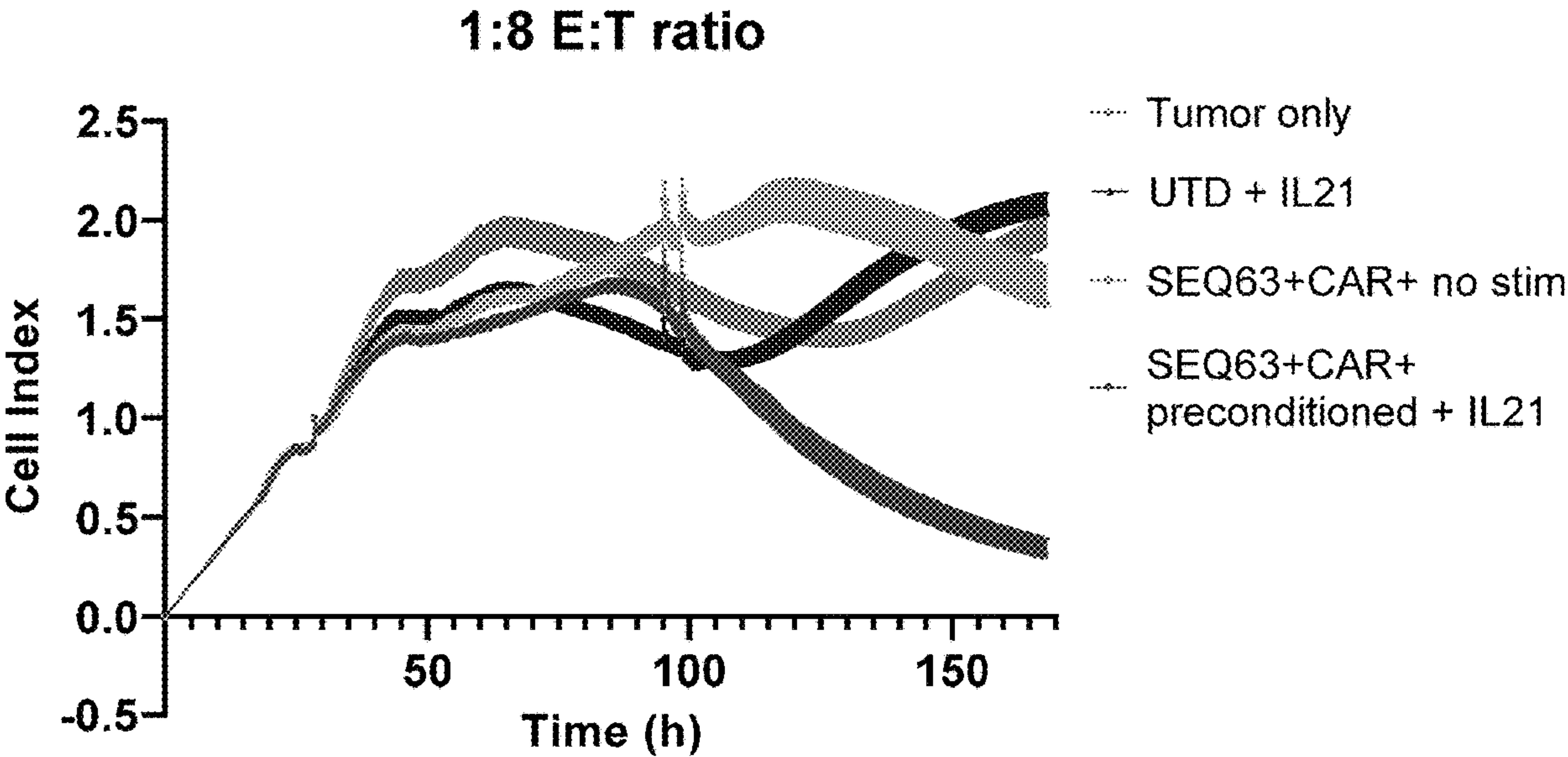
C07K 14/7155 (2013.01); *C12N 5/0634*
(2013.01); *C12N 15/85* (2013.01); *C07K*
2319/03 (2013.01)

(57)

ABSTRACT

The present disclosure generally relates to, inter alia, a class of chimeric switch receptors containing an endodomain of an IL-9 receptor, engineered to modulate transcriptional regulation in a ligand-dependent manner. The disclosure also provides compositions and methods useful for producing such receptors, nucleic acids encoding same, host cells genetically modified with the nucleic acids, as well as methods for modulating gene expression, modulating an activity of a cell, and/or for the treatment of various health conditions or diseases.

Specification includes a Sequence Listing.



Sequence ID	Ligand-binding domain	Transmembrane domain	Intracellular domain	Linker	pSTAT type	No Ligand Stimulation (gMFI)	Ligand Stimulated (gMFI)	Fold increase in gMFI
SEQ63+CAR+	IL21R	IL9R	IL9R	N/A	pSTAT1	620	1478	2.38
					pSTAT3	345	1831	5.31
					pSTAT5	700	870	1.24
SEQ66	IL15Ra	IL9R	IL9R	N/A	pSTAT1	491	917	1.87
					pSTAT3	330	594	1.80
					pSTAT5	669	2283	3.41
SEQ72+CAR+	IL4Ra	IL9R	IL9R	N/A	pSTAT1	471	770	1.63
					pSTAT3	243	444	1.83
					pSTAT5	536	660	1.23
SEQ153+CAR+	IL10Ra	IL9R	IL9R	G _i S	pSTAT1	261	1900	7.28
					pSTAT3	78	1569	20.12
					pSTAT5	284	663	2.33

FIG. 1

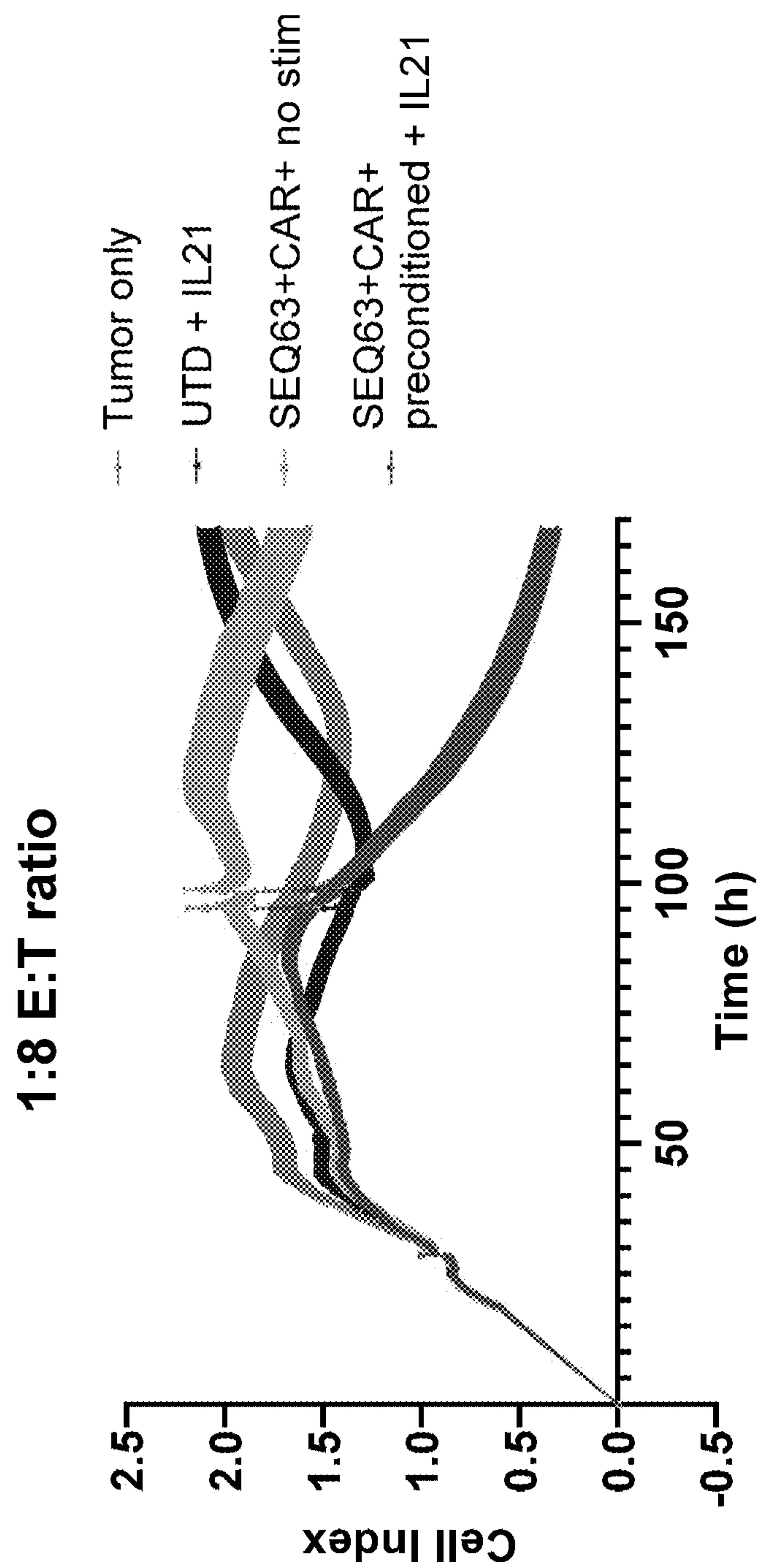


FIG. 2

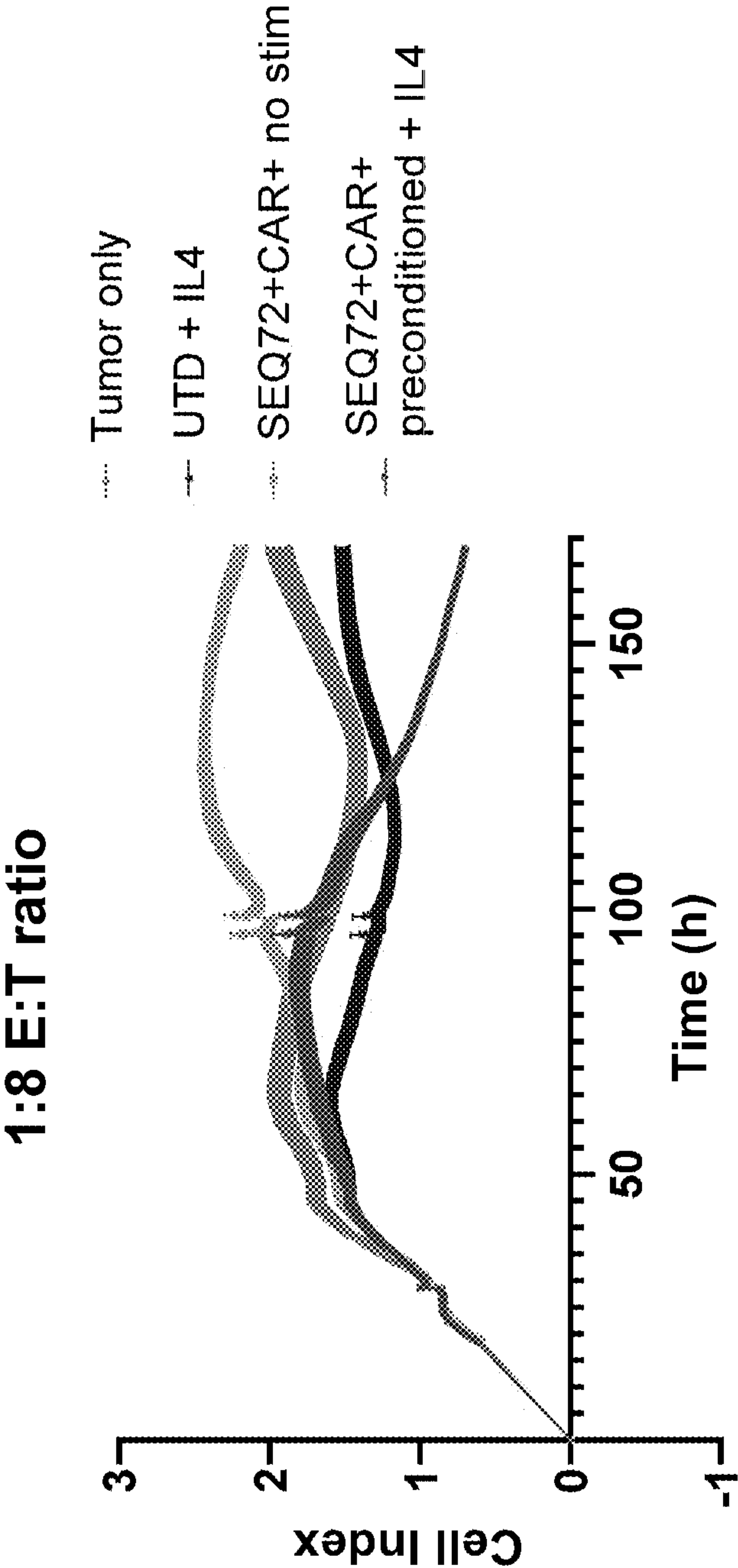


FIG. 3

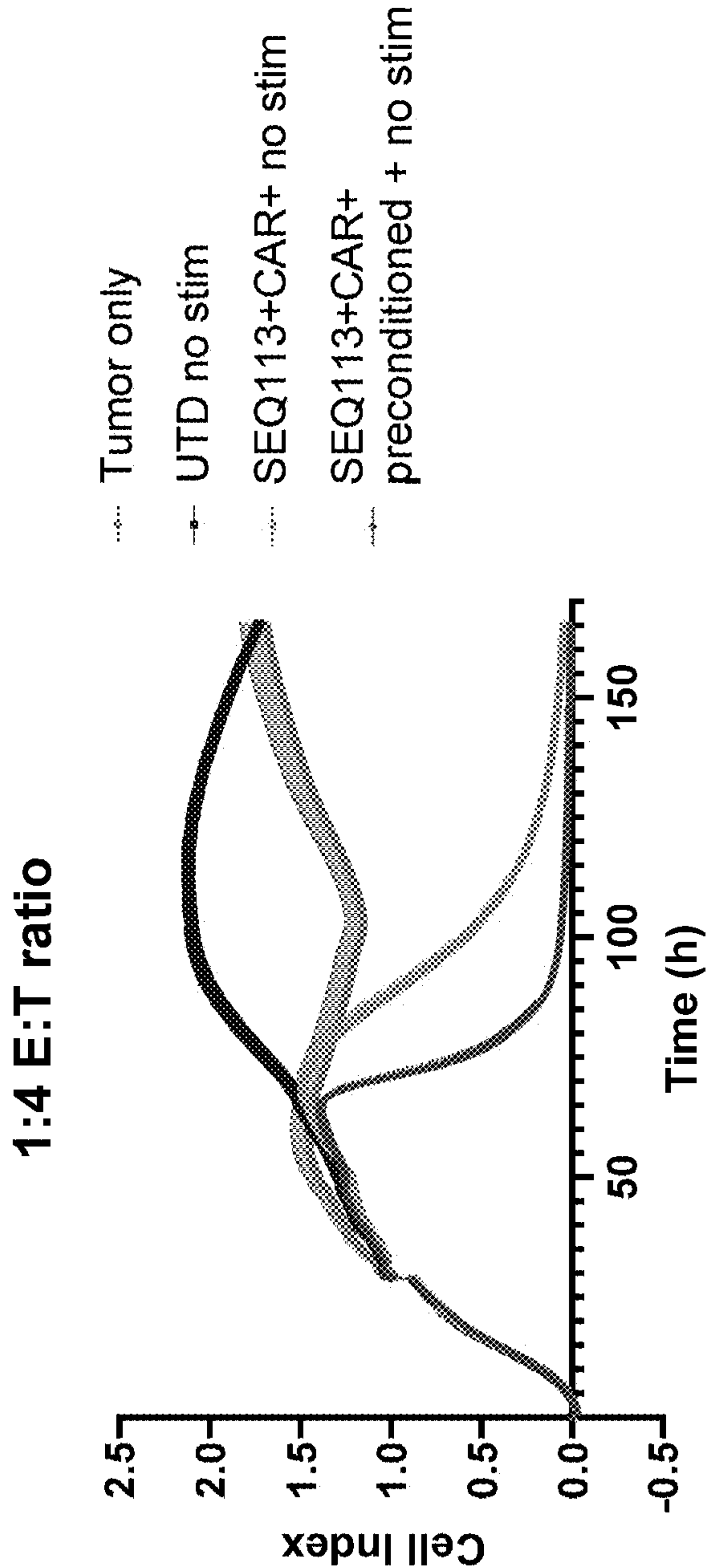
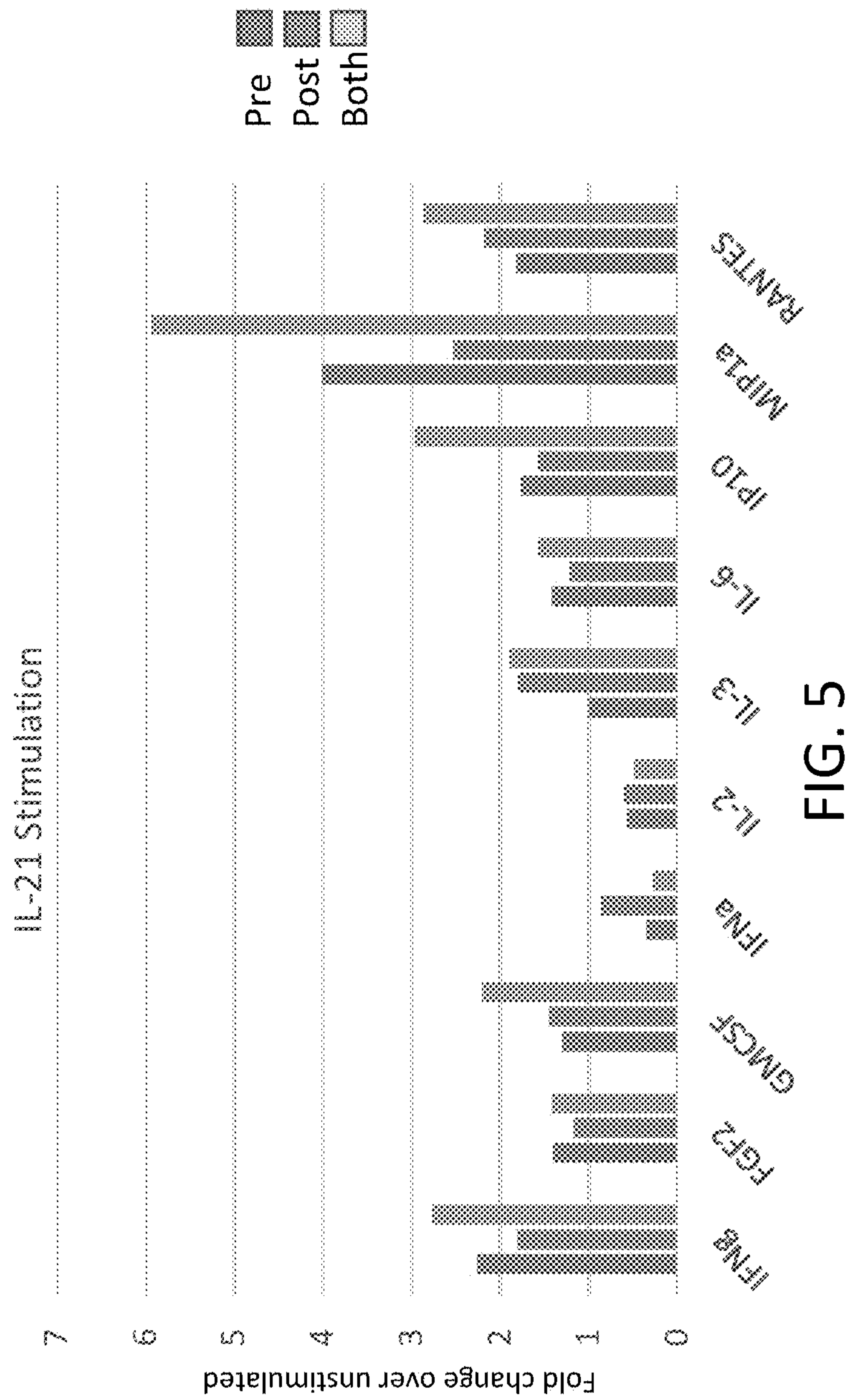


FIG. 4



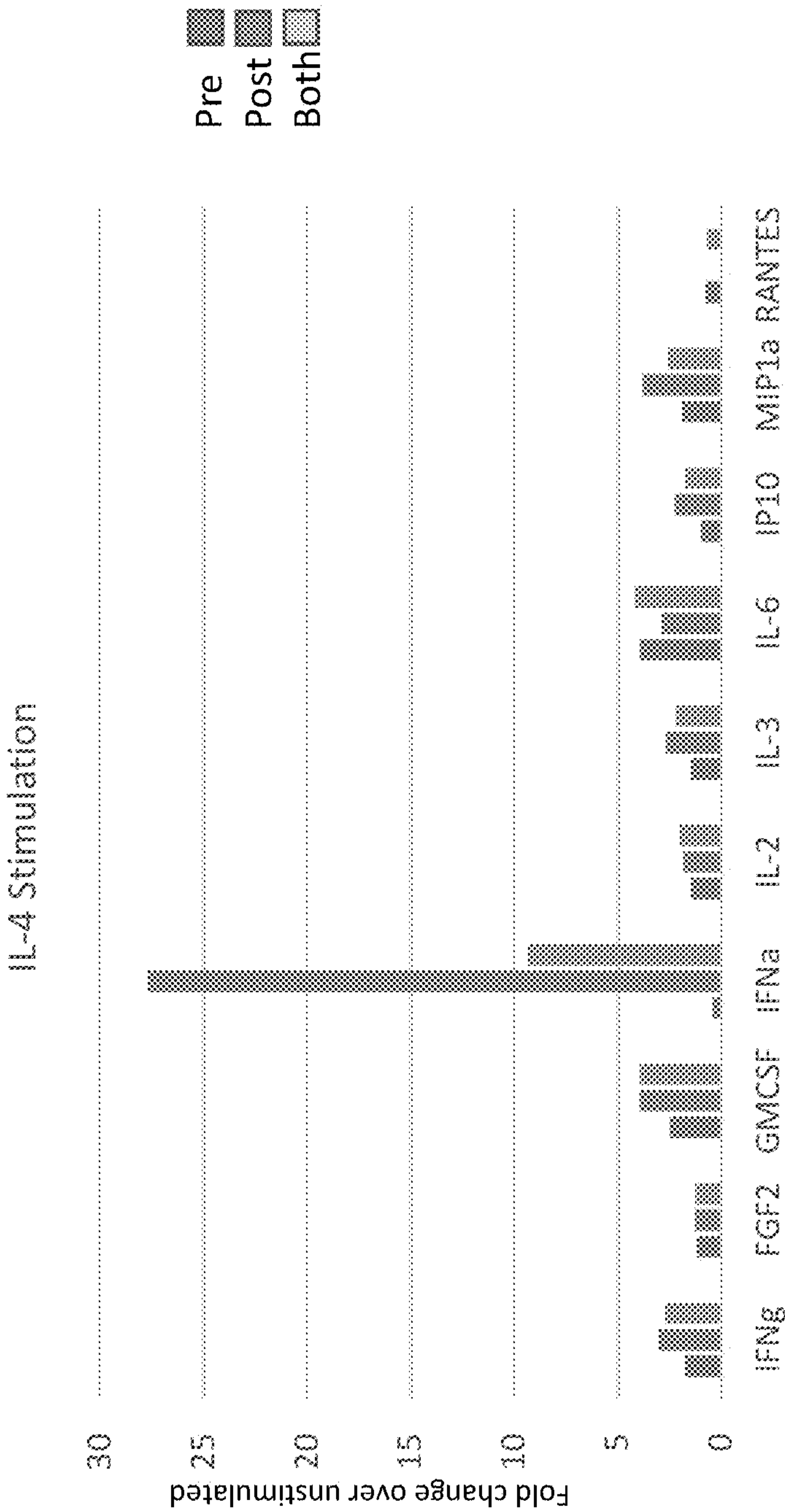


FIG. 6

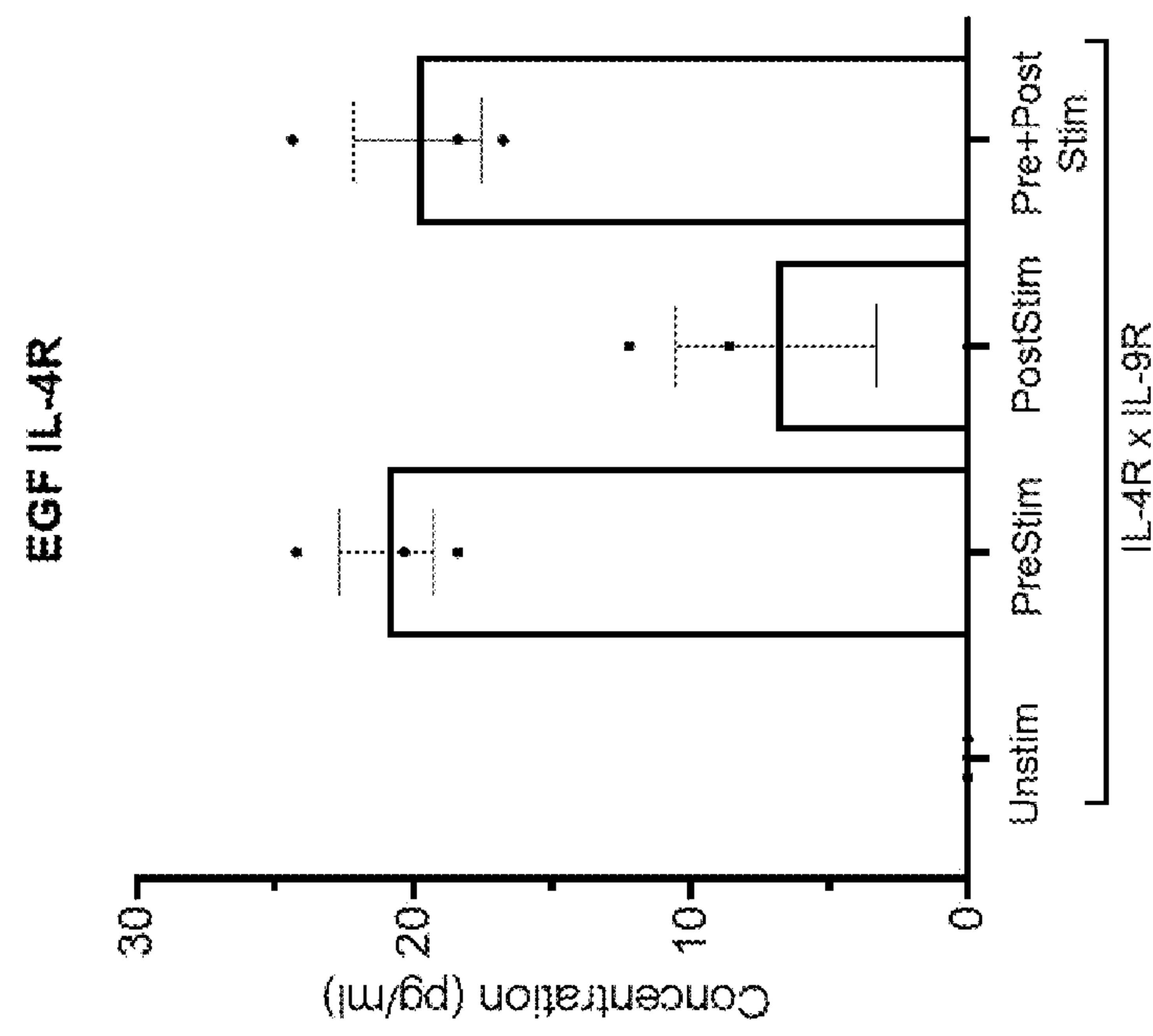


FIG. 7

FIG. 8A

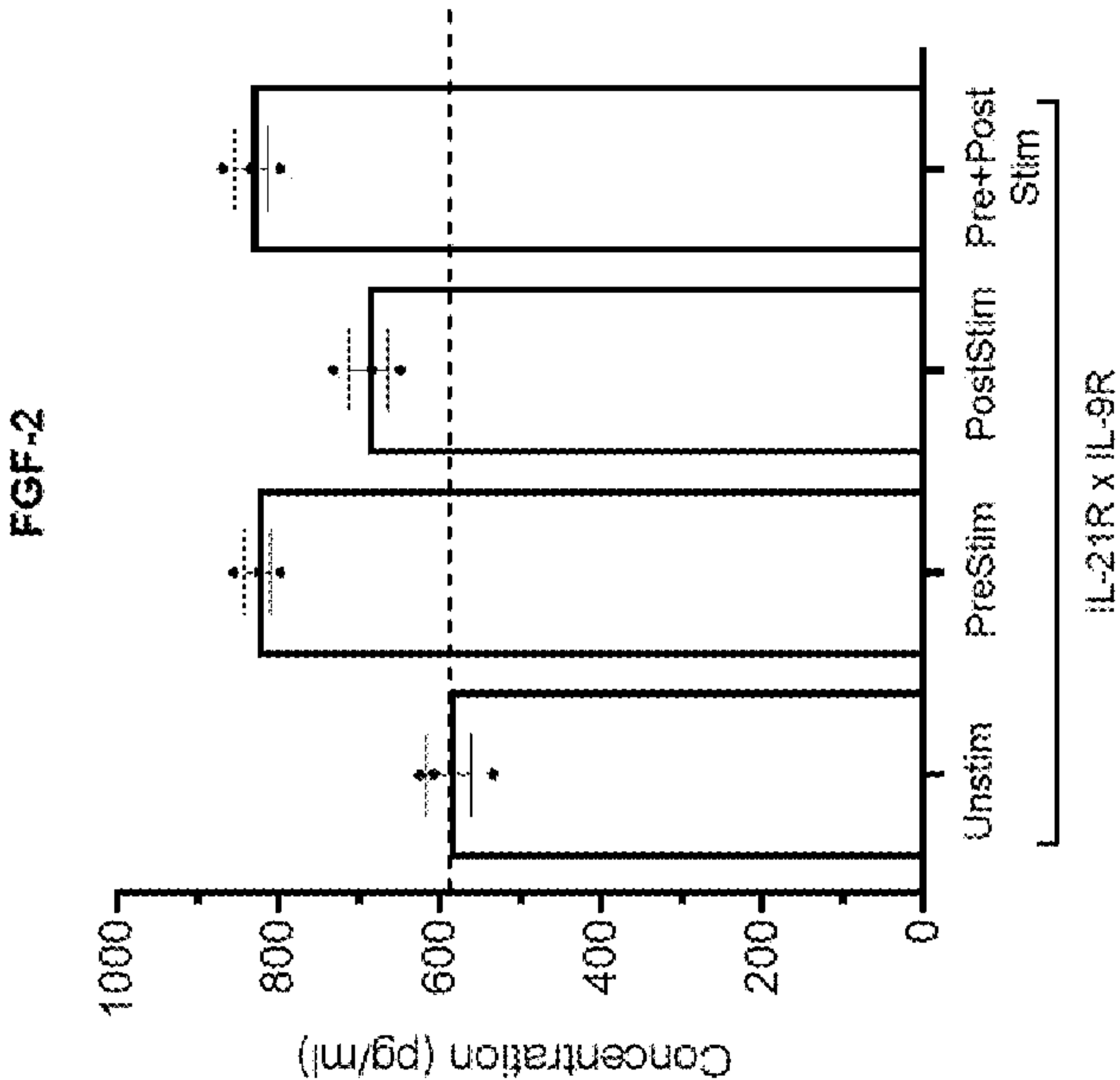


FIG. 8B

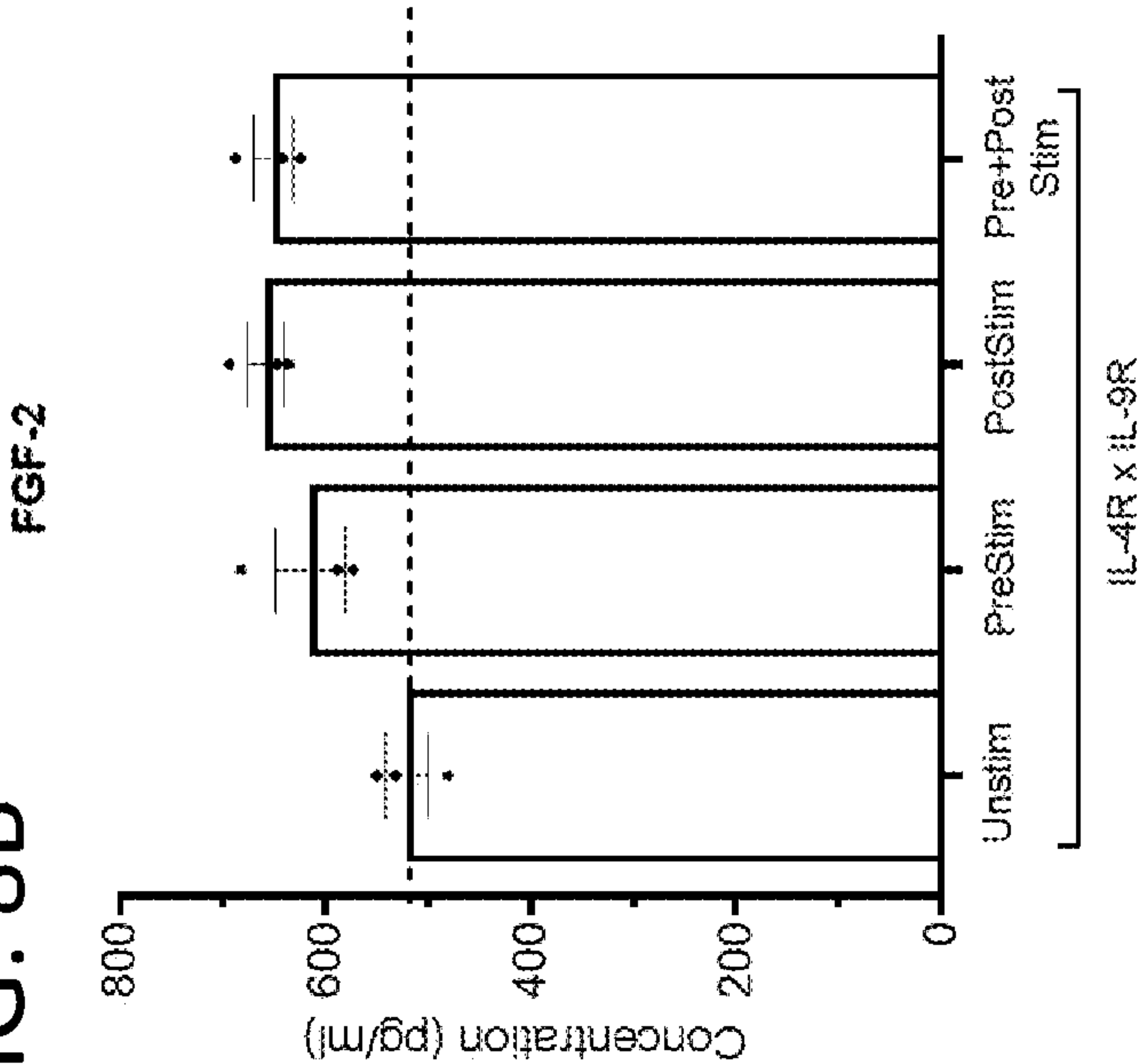


FIG. 9A

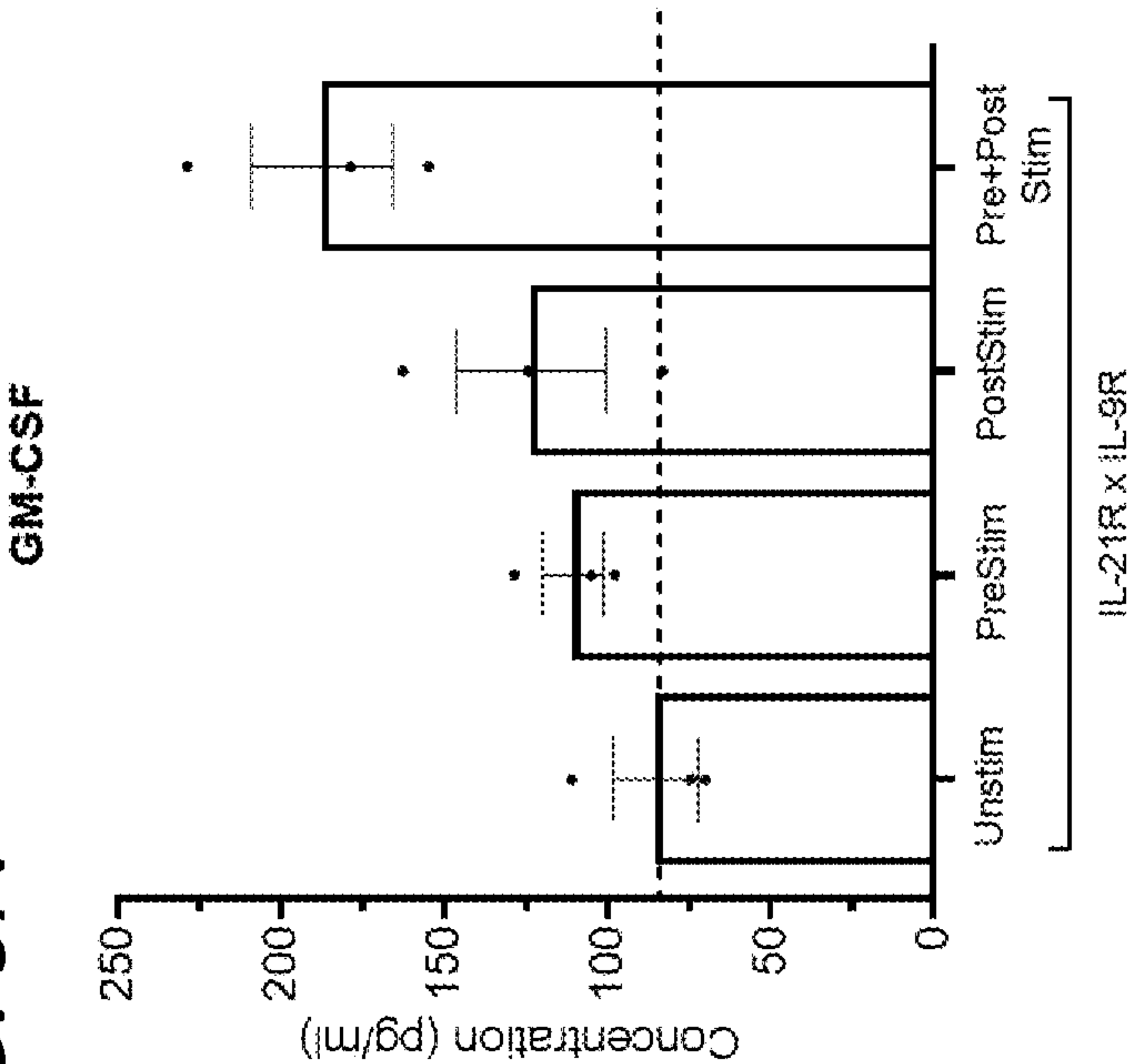
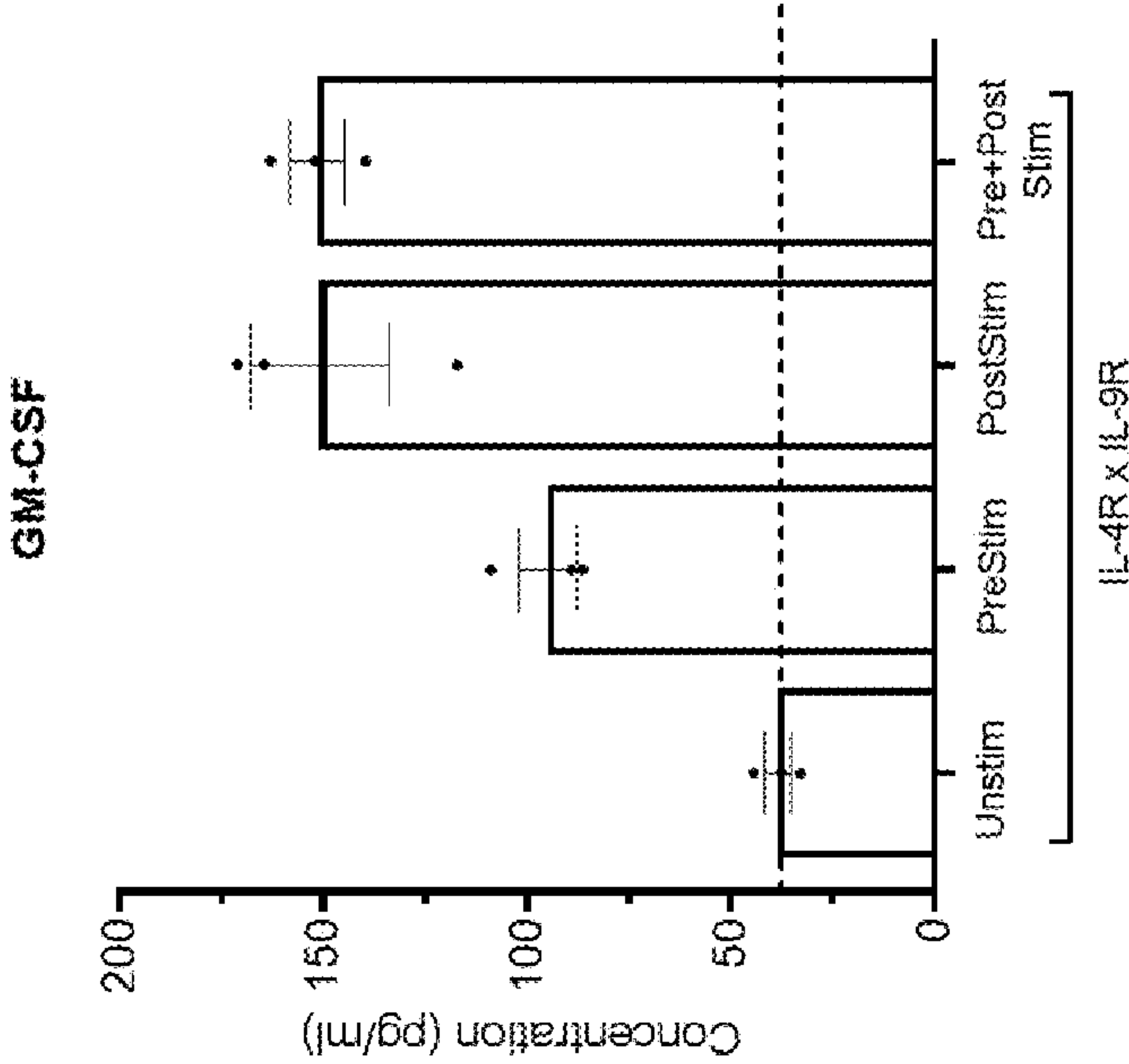


FIG. 9B



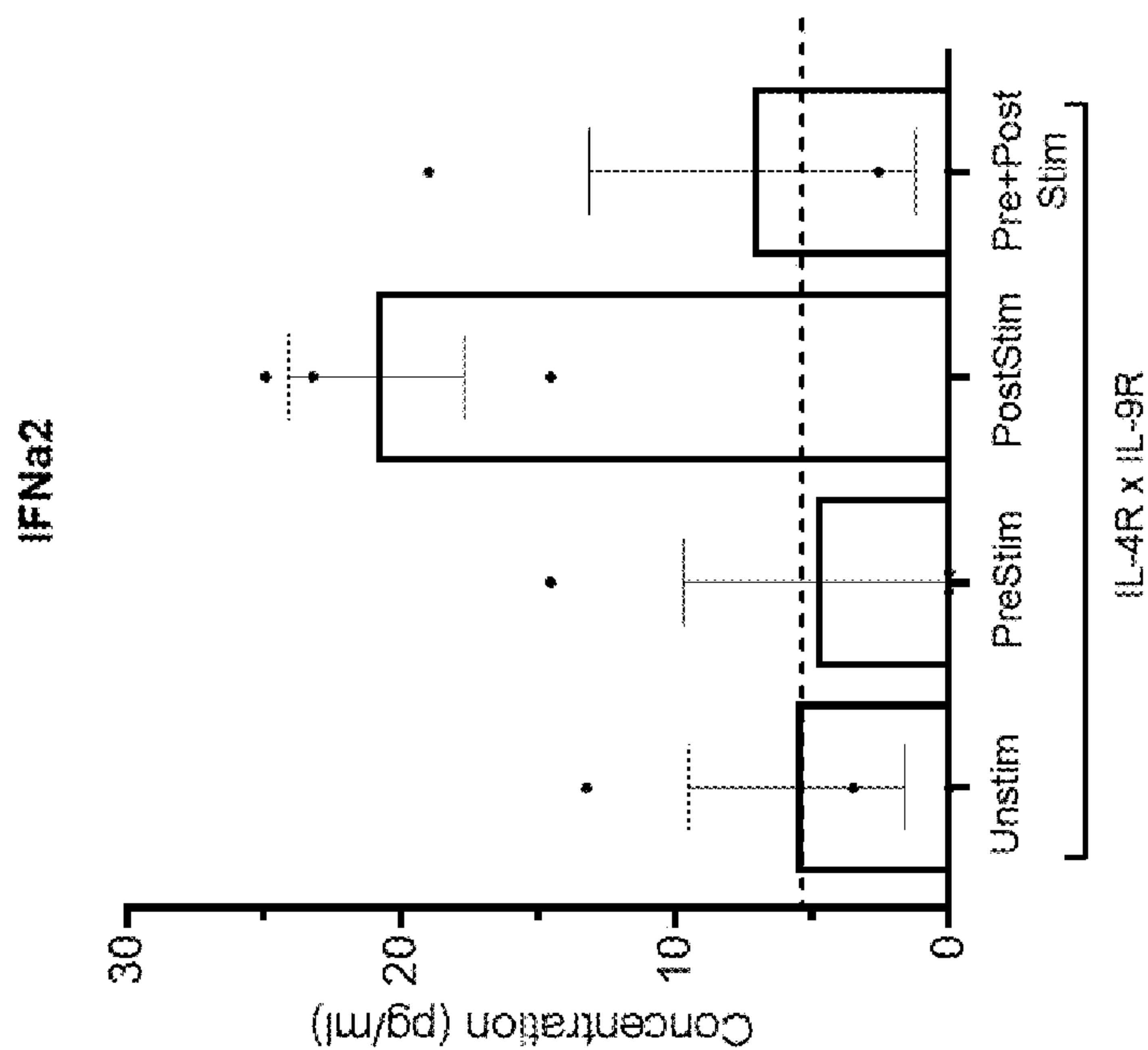


FIG. 10

FIG. 11A

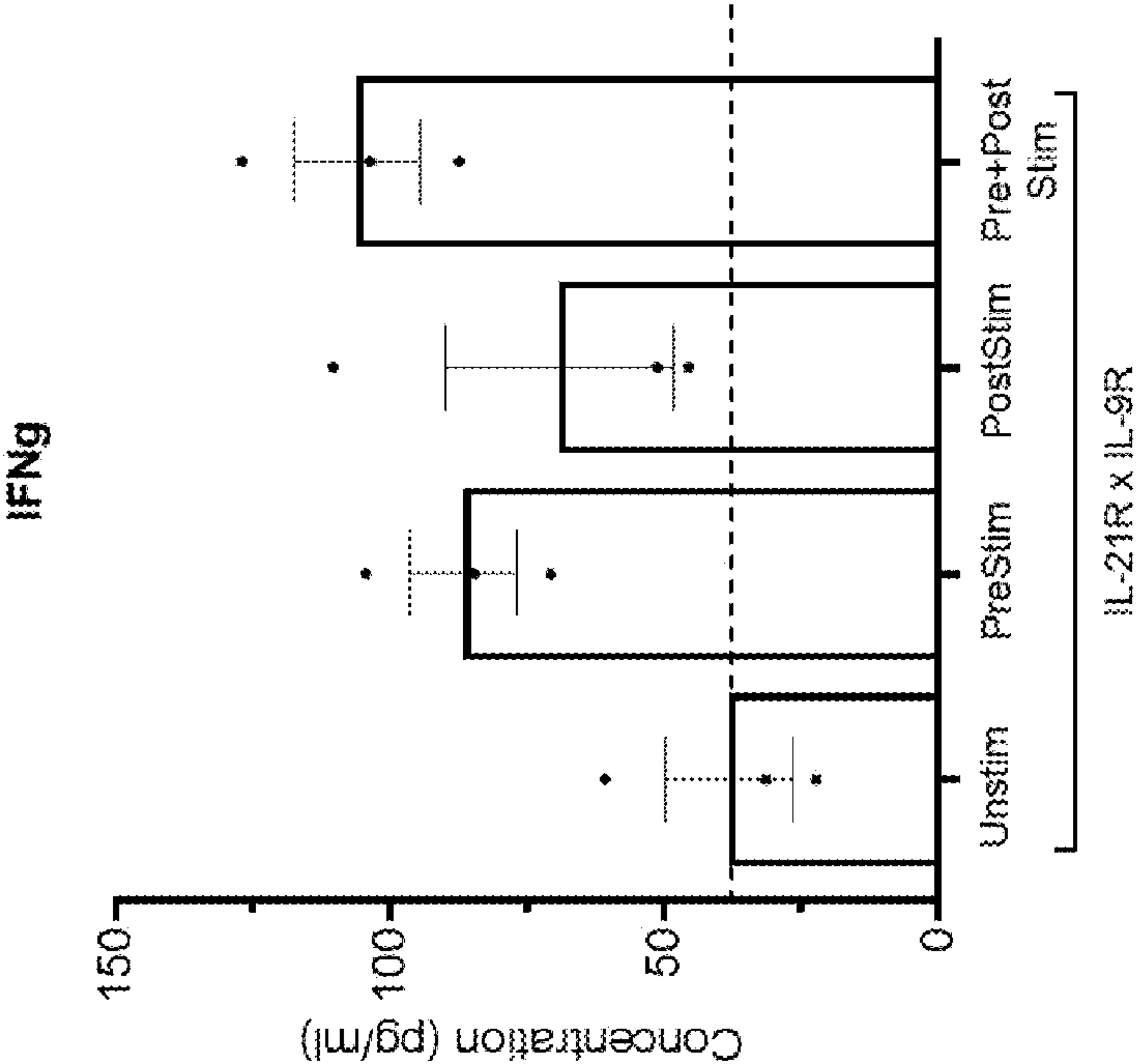
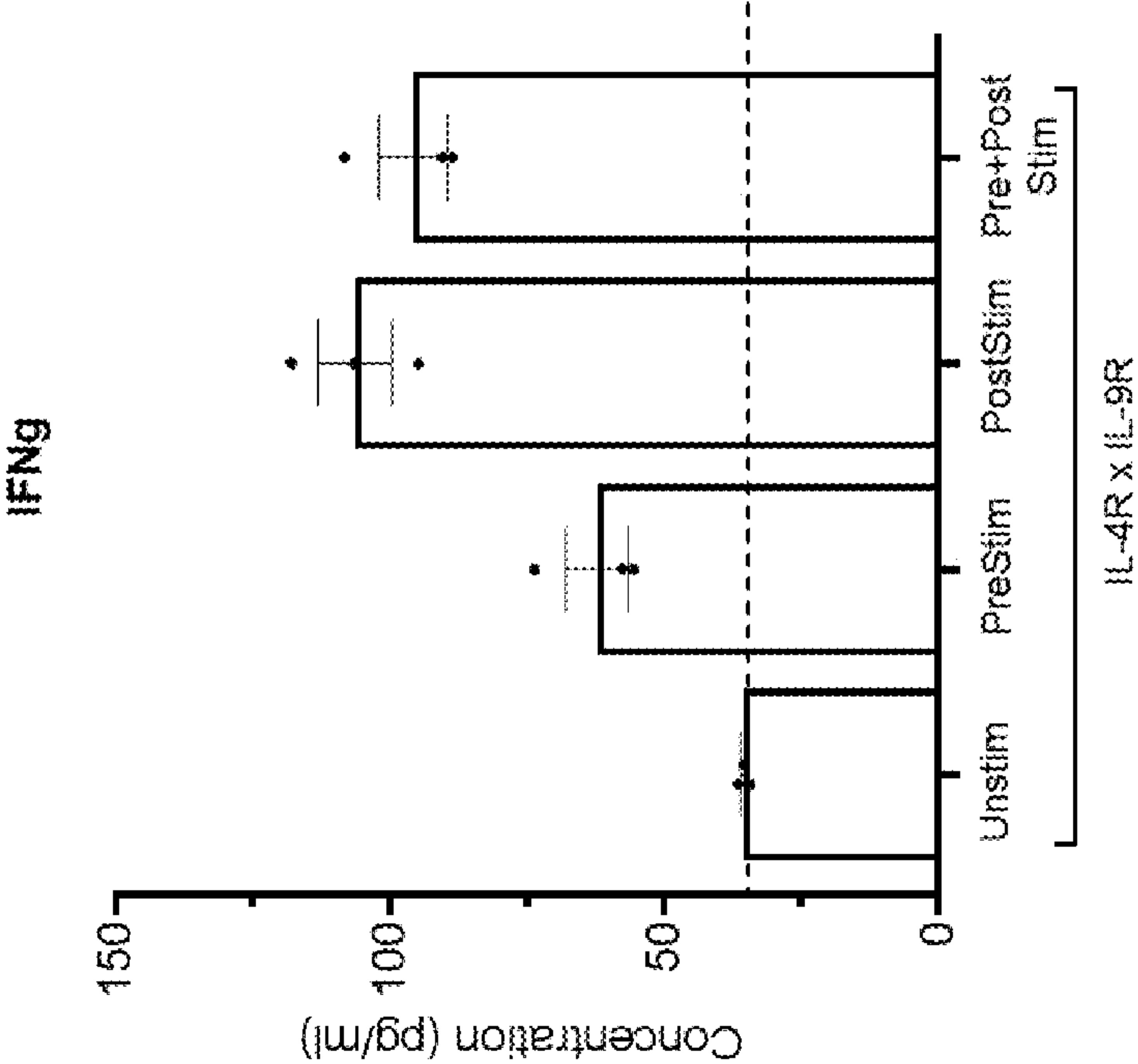


FIG. 11B



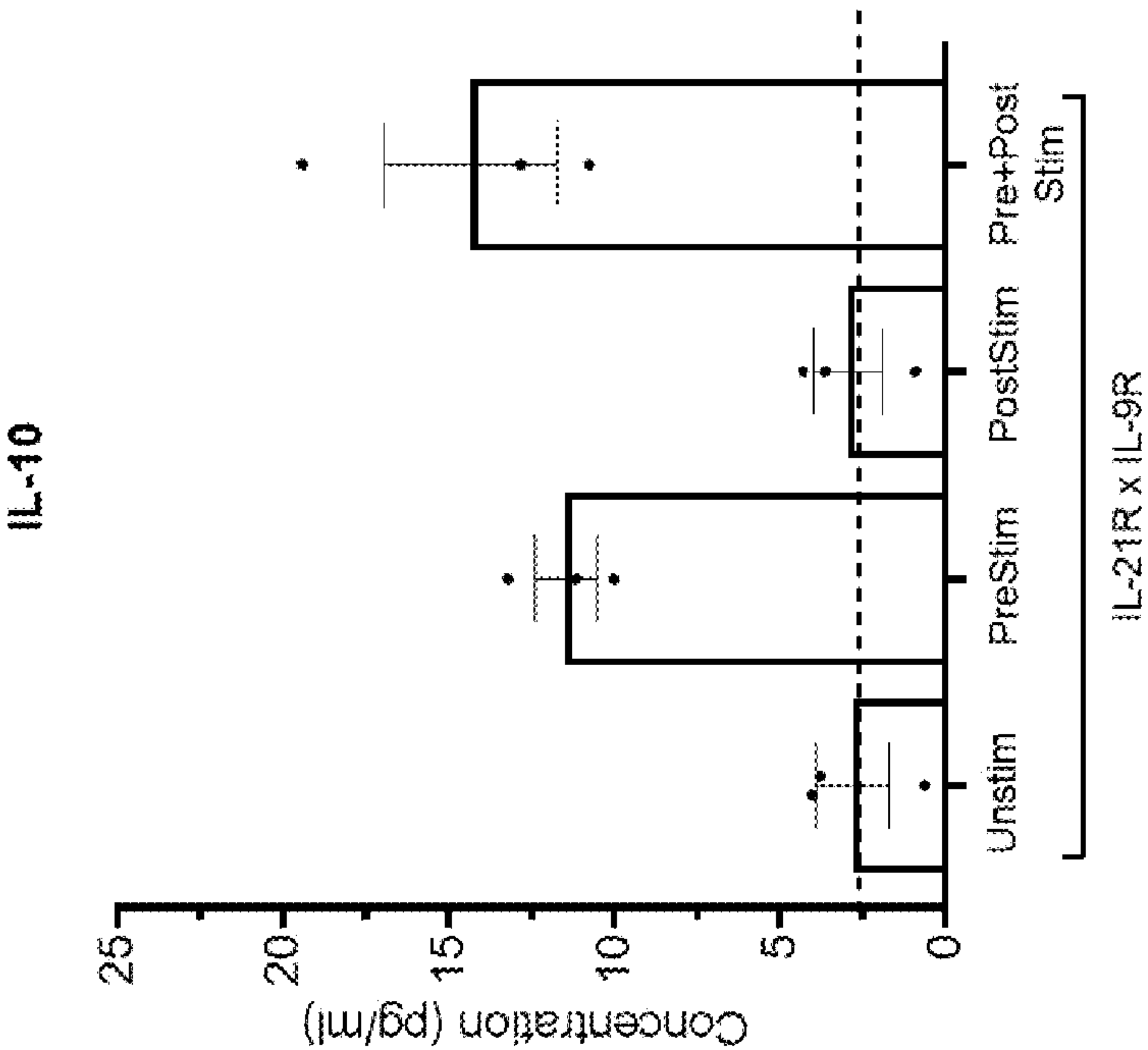


FIG. 12

FIG. 13A

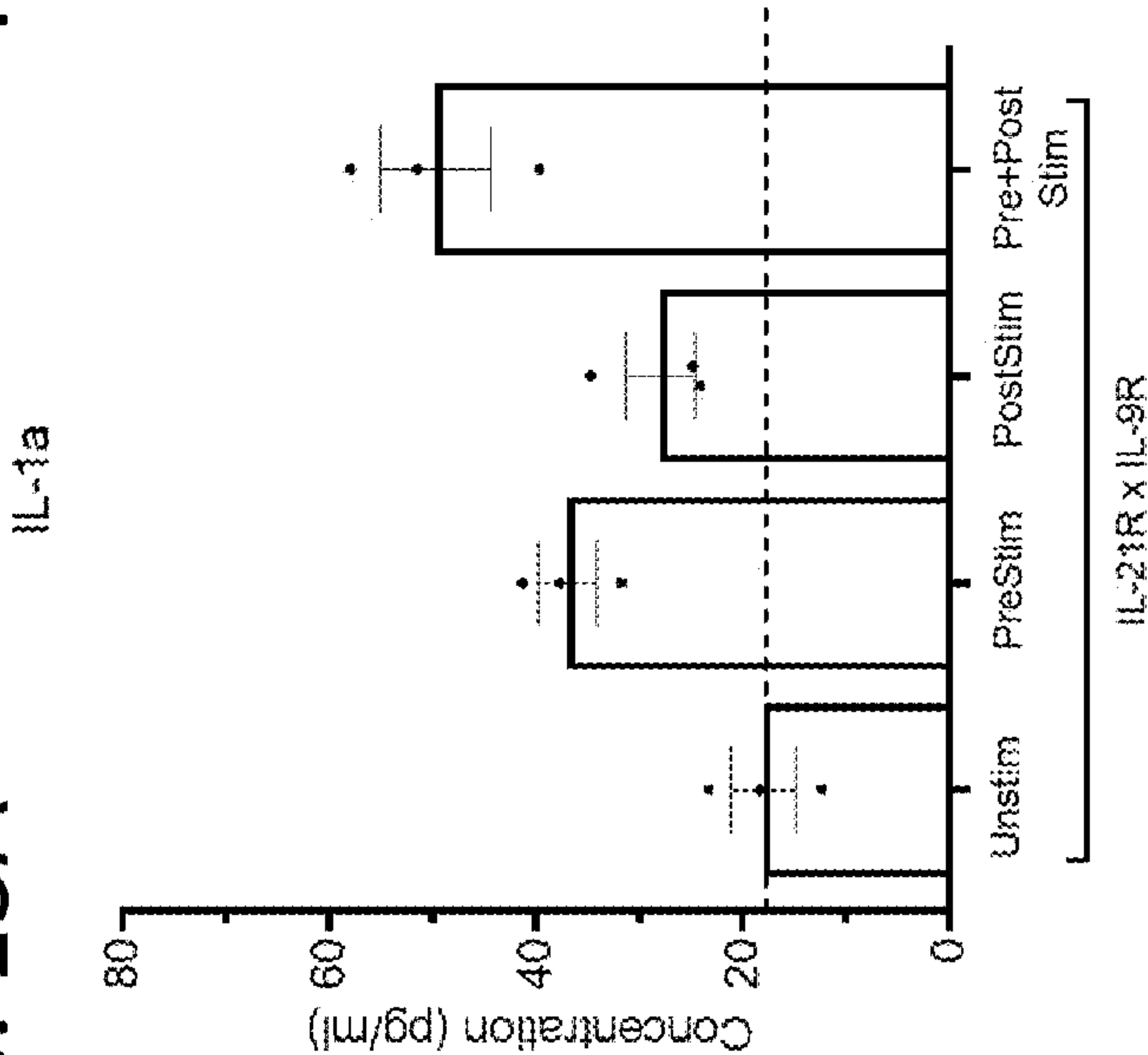
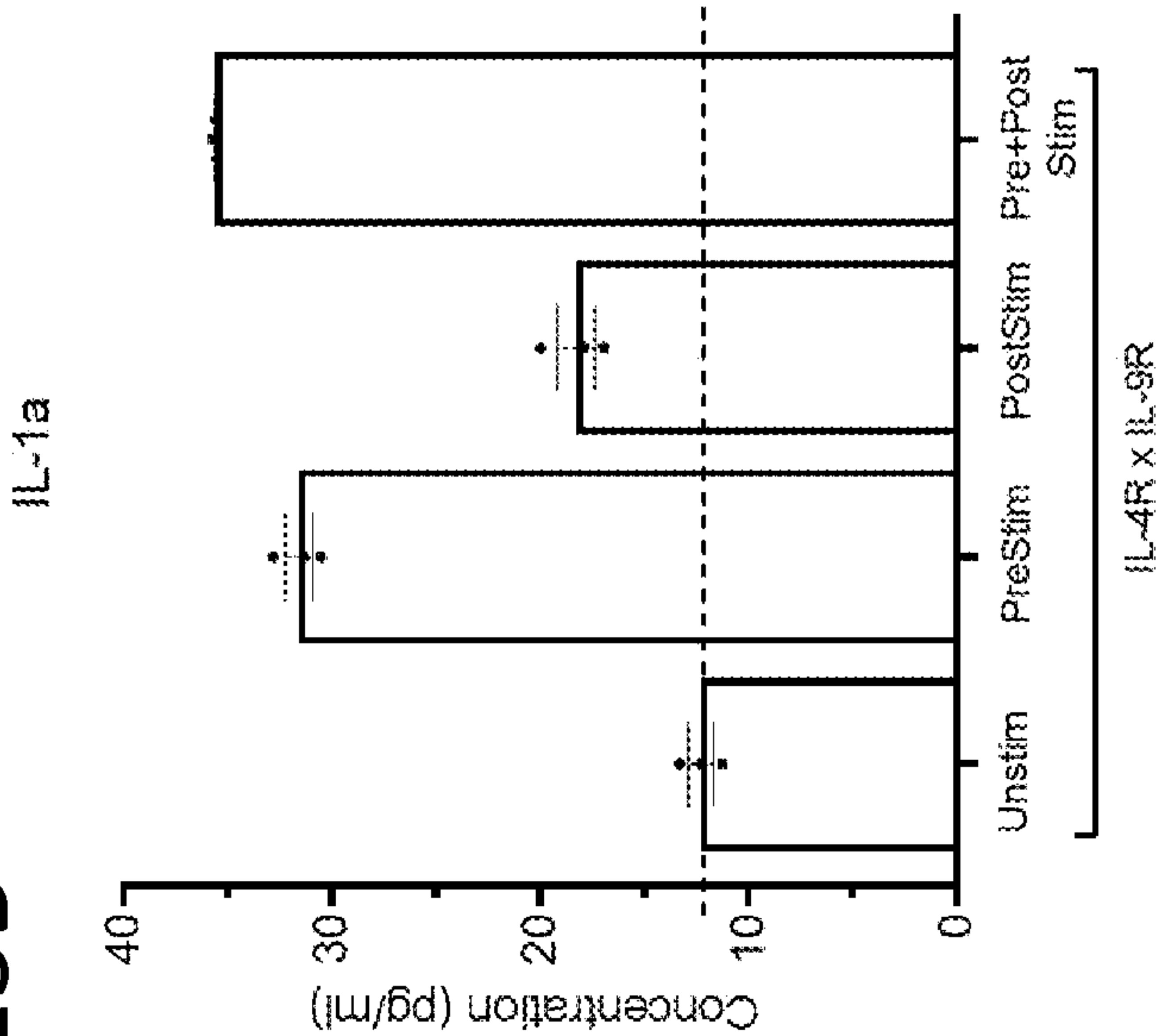


FIG. 13B



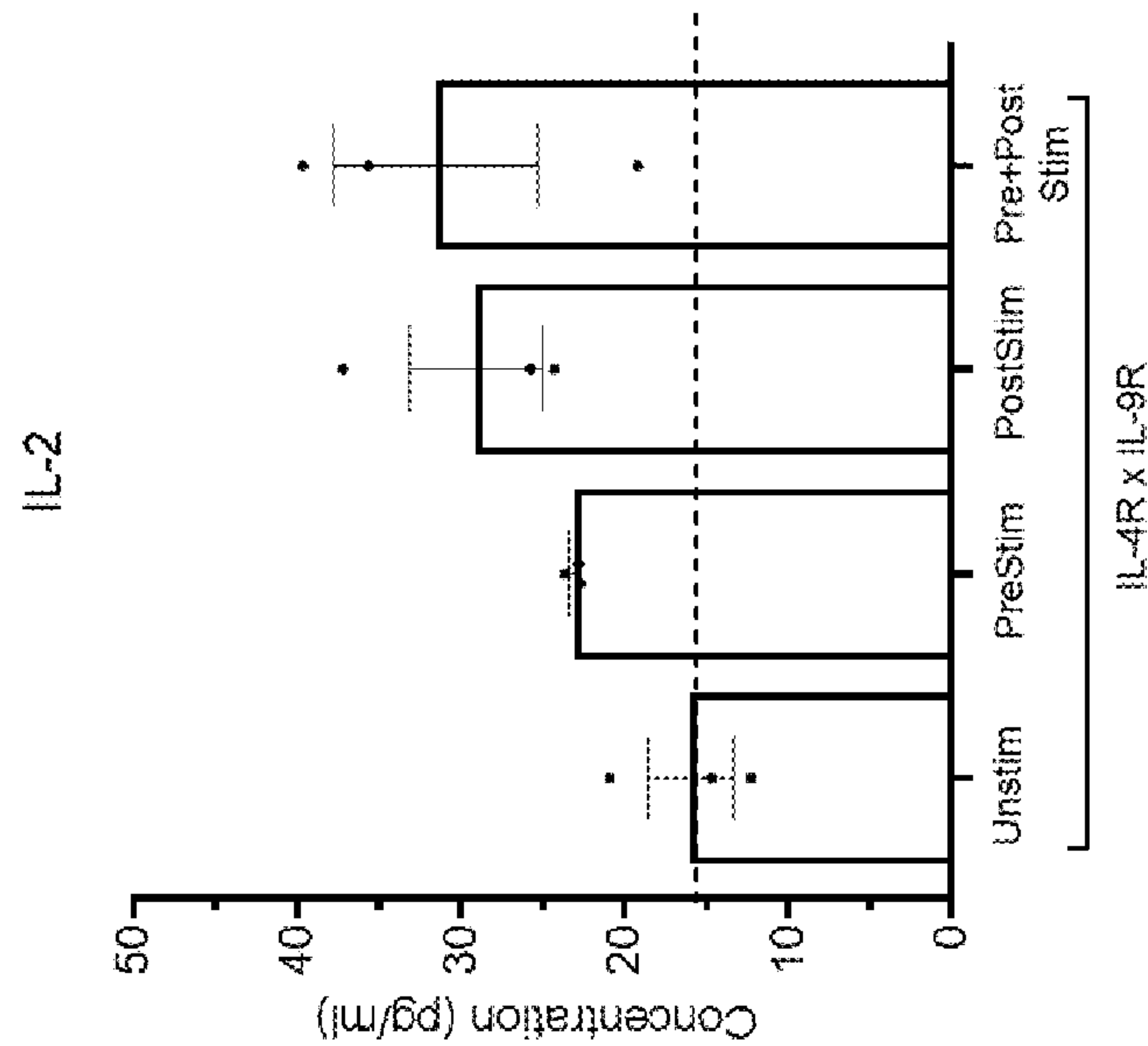


FIG. 14

FIG. 15A

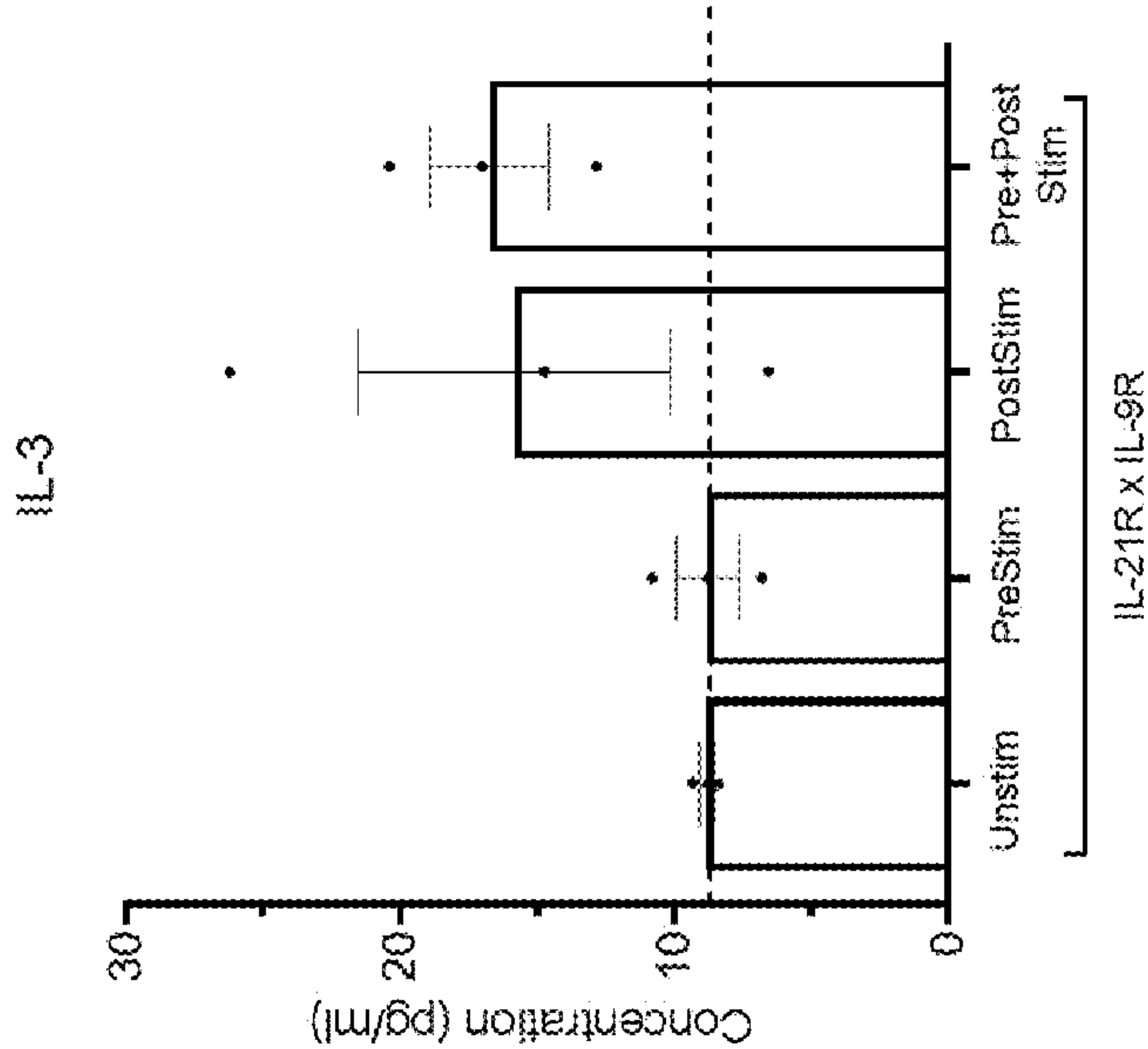


FIG. 15B

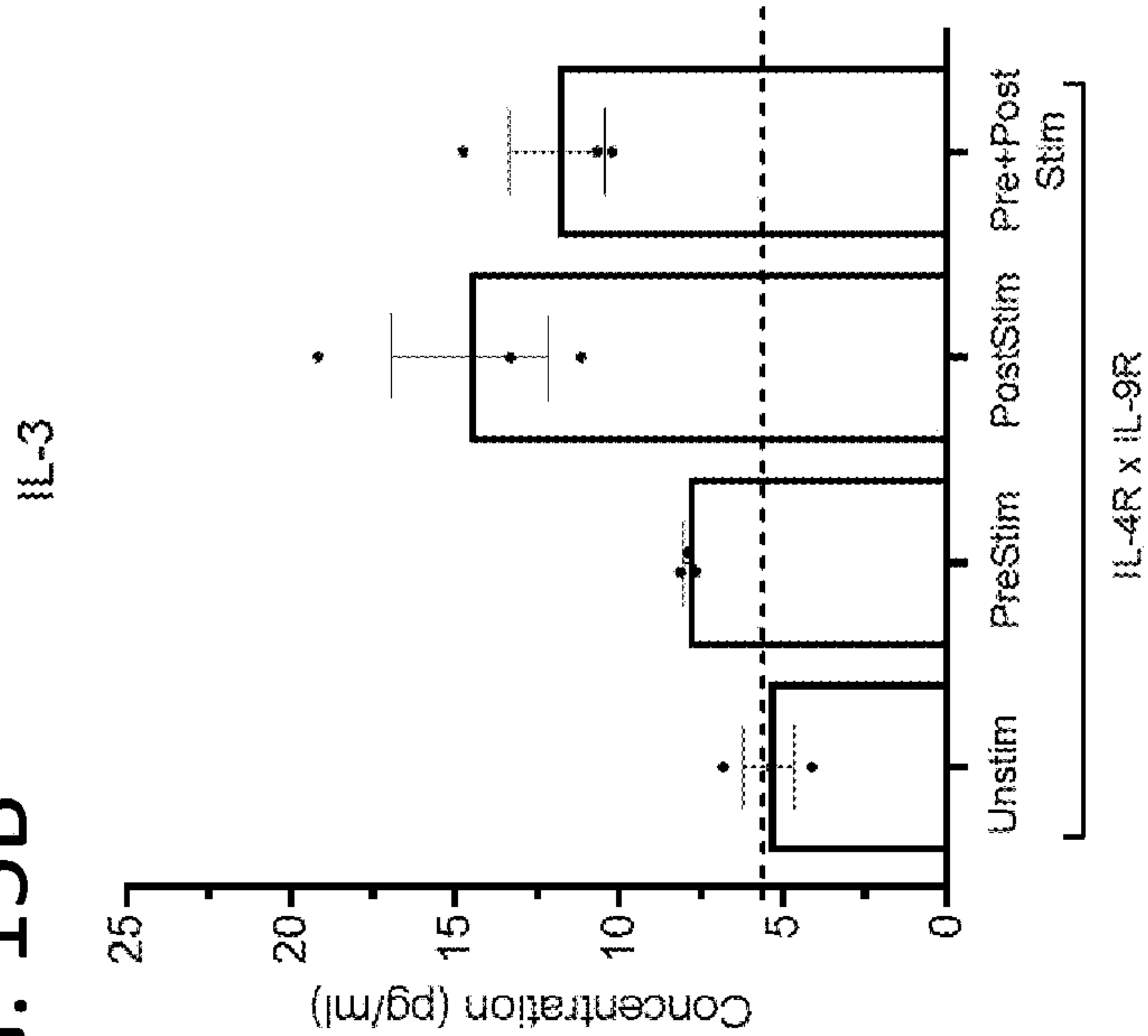


FIG. 16A

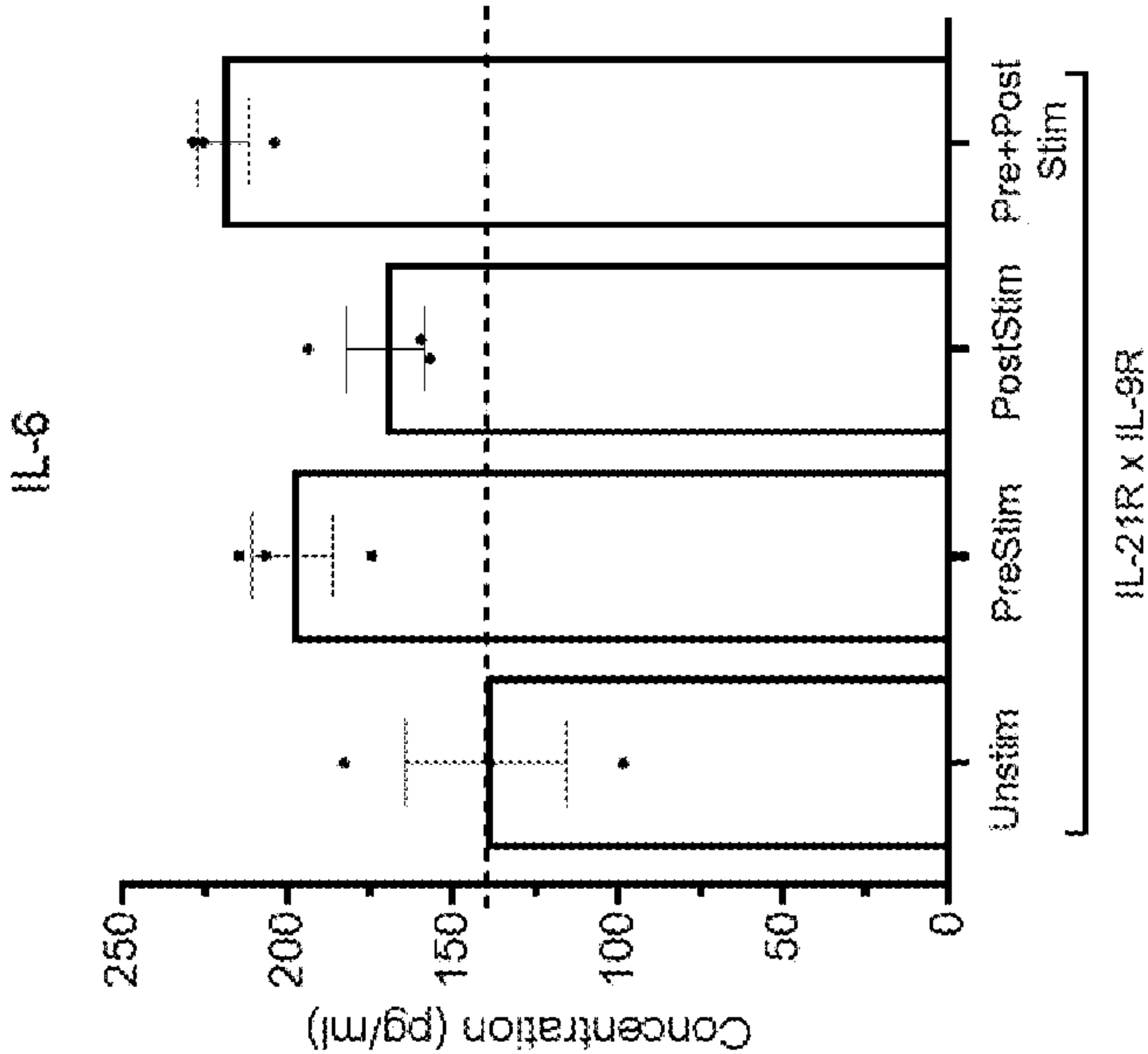


FIG. 16B

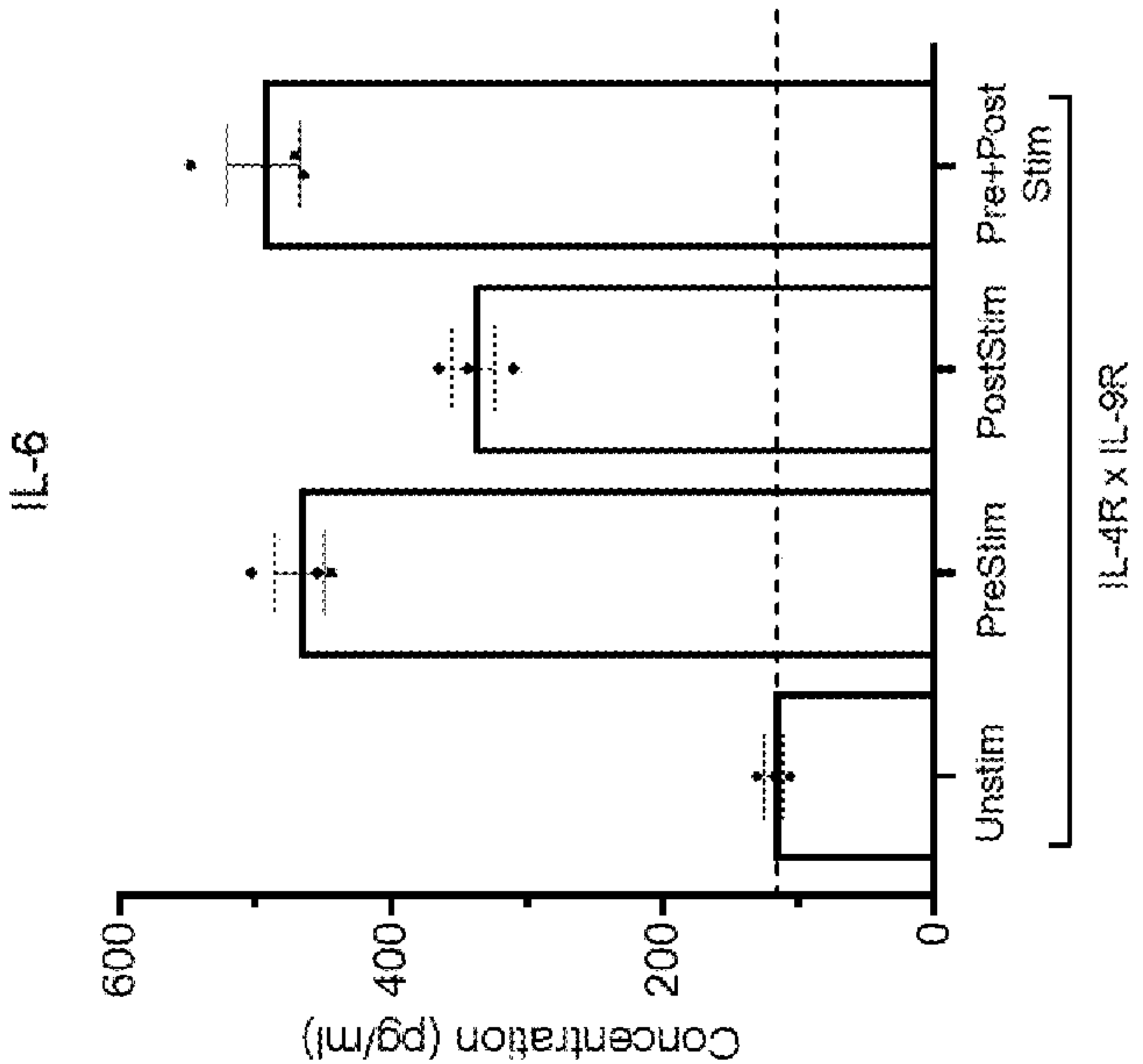


FIG. 17A

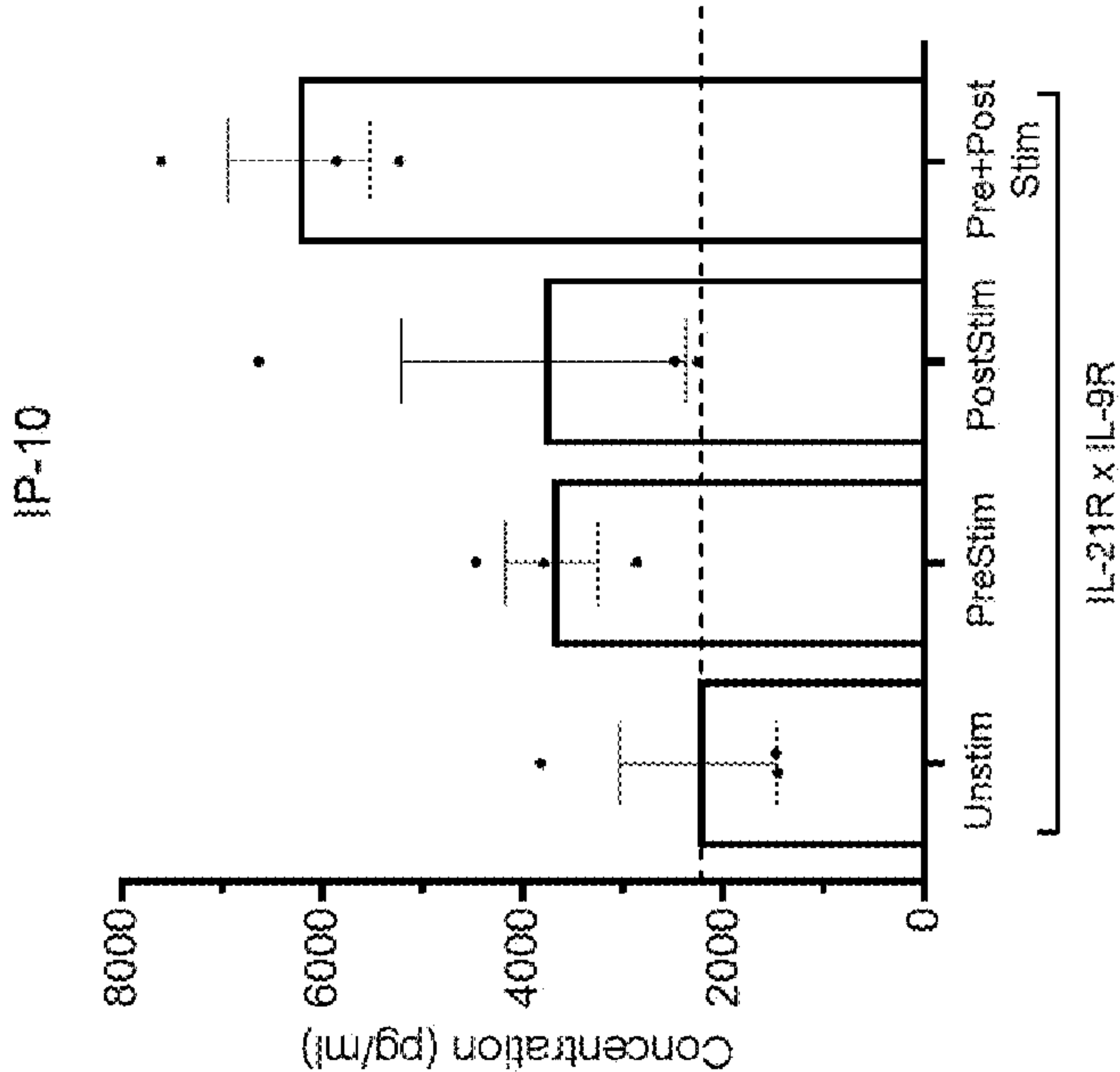


FIG. 17B

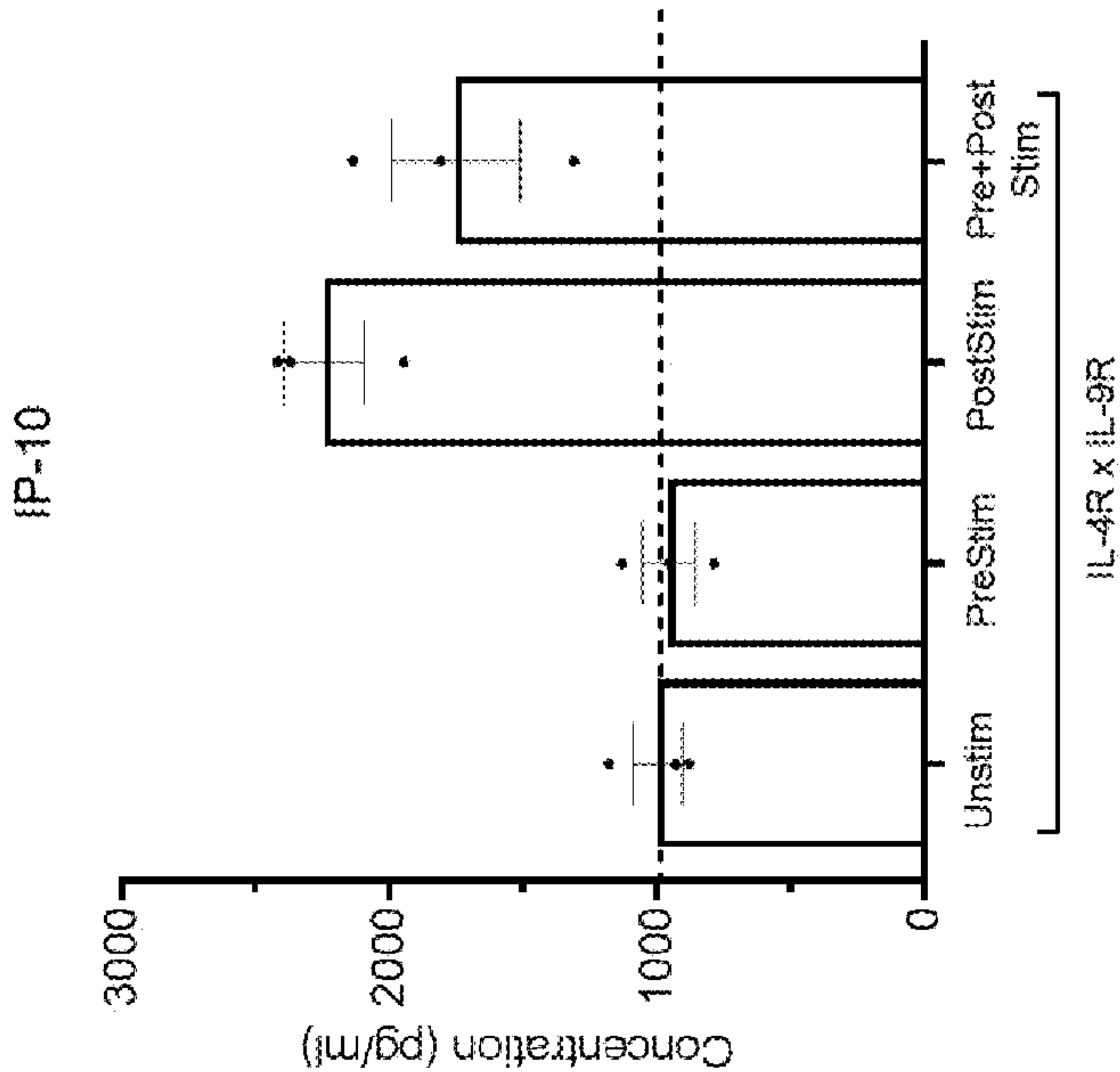


FIG. 18A

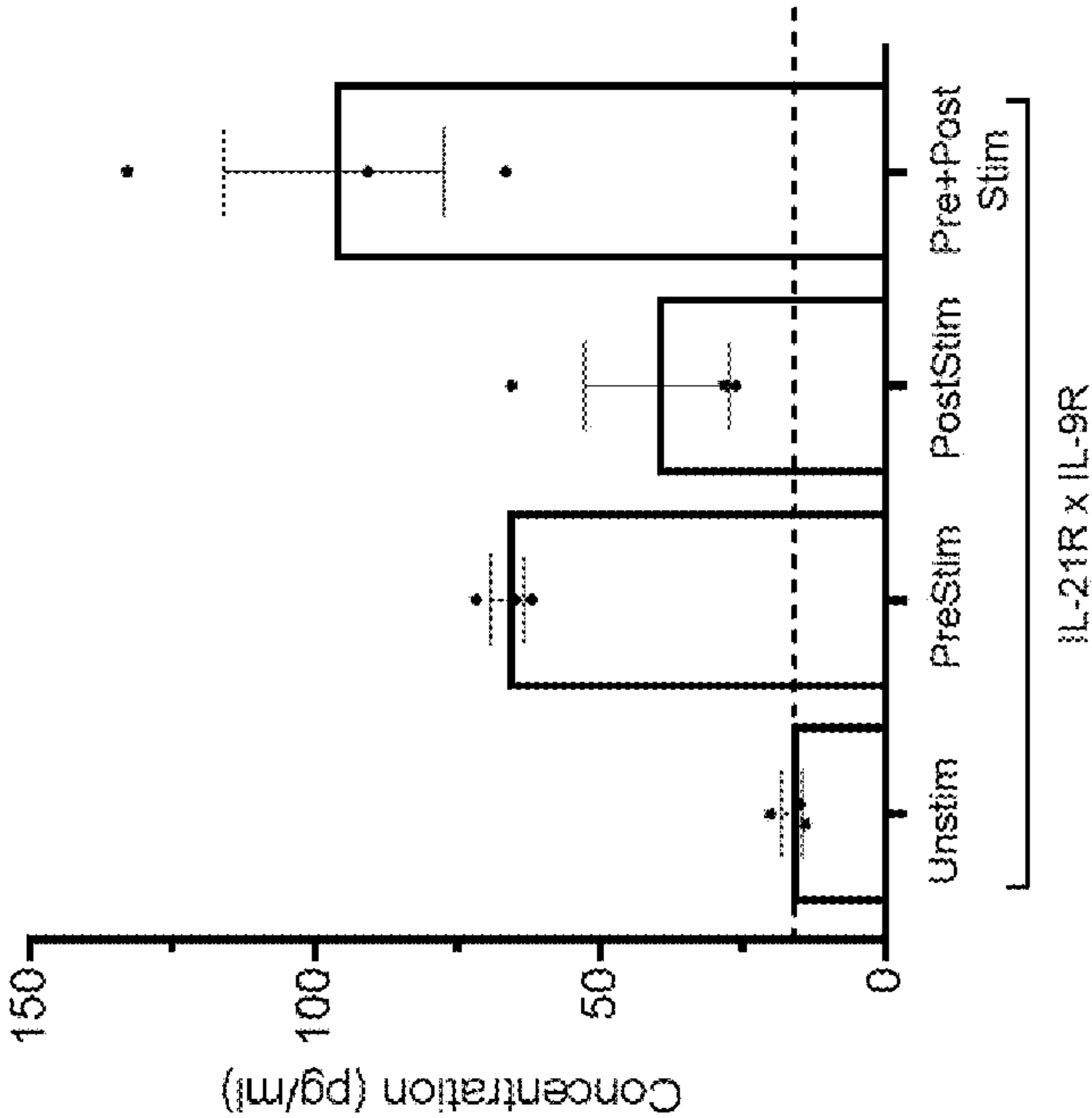
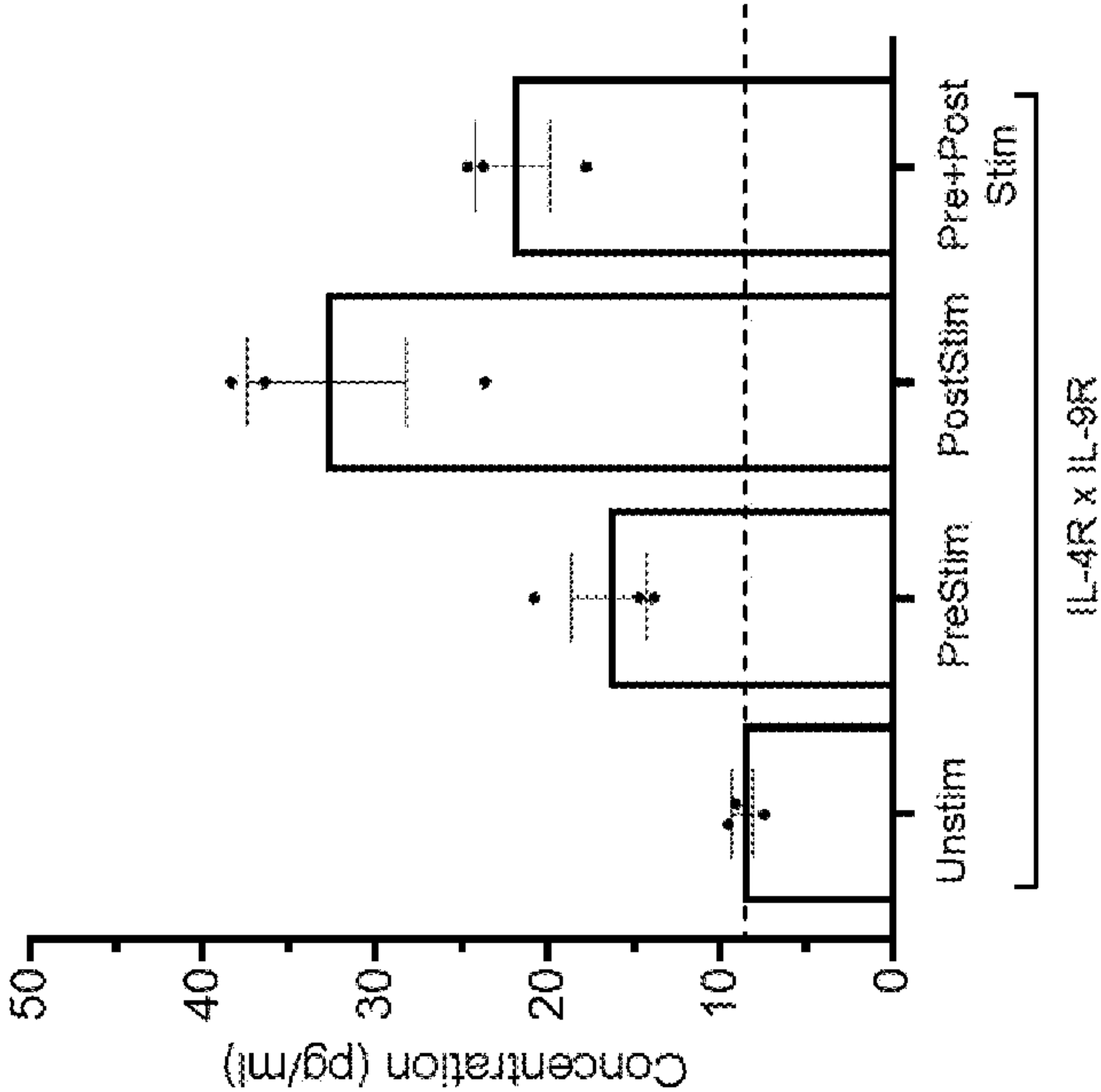


FIG. 18B



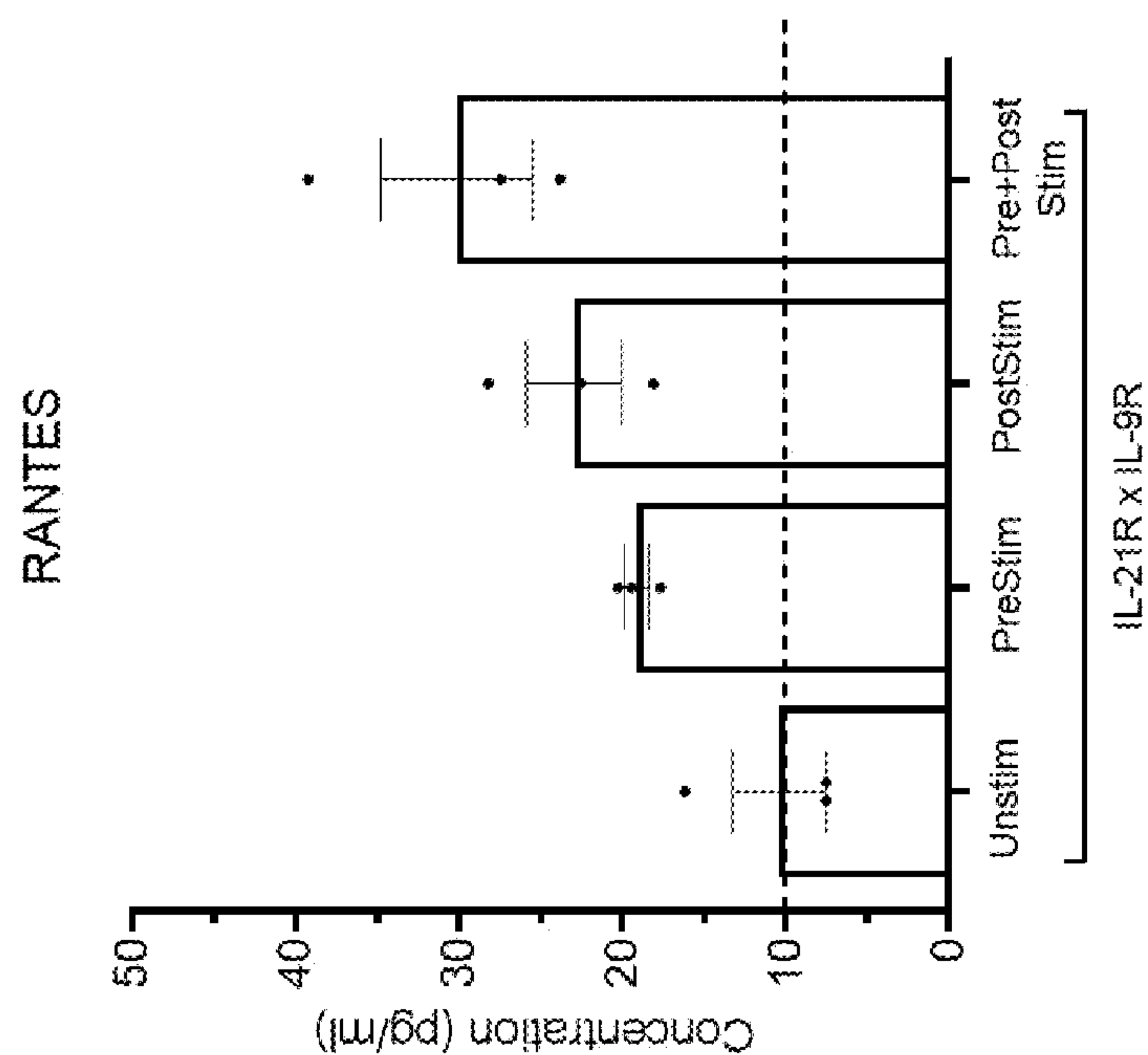


FIG. 19

SWITCH RECEPTORS USING IL-9 SIGNALING DOMAINS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/245,661, filed Sep. 17, 2021, which is incorporated herein by reference in its entirety.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

[0002] This invention was made with Government support under Contract AI051321 awarded by the National Institutes of Health. The Government has certain rights in the invention.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0003] The contents of the electronic sequence listing 051288-502001US.xml; Size: 348 Kb; and Date of Creation: Dec. 4, 2022 is hereby incorporated by reference in its entirety.

FIELD

[0004] The present disclosure relates generally to synthetic cellular receptors that bind extracellular ligands and have IL-9 endodomains. The disclosure also provides compositions and methods useful for producing such receptors, nucleic acids encoding same, host cells genetically modified with the nucleic acids, as well as methods for modulating gene expression, modulating an activity of a cell, and/or for the treatment of various health conditions or diseases.

BACKGROUND

[0005] The manipulation of cells, particularly immune cells, to differentiate, develop specialized functions and expand in numbers is of great clinical interest. Many protein factors that affect these activities are known in the art, including in particular cytokines and chemokines. However, these signaling molecules also have pleiotropic effects on cells not targeted for manipulation, and thus methods of selectively activating signaling in a targeted cell population are desirable. The ability to engineer immune cells to carry out controlled behaviors is of interest in the field. For example, in adoptive immunotherapy T cells are isolated from blood, processed ex vivo, and re-infused into patients. Such T cells have been developed for use in therapeutic applications such as the treatment of cancer, infection, and autoimmune diseases.

[0006] A critical challenge in cell based therapies is the ability to engineer receptors that respond to native molecules while also allowing the selective manipulation of immune cells. Some groups have manipulated proteins to bind and respond to modified ligands in a manner independent, or orthogonal, from the influence of the native proteins or ligands. This technology relies on the engineering of both an orthogonal cytokine and an orthogonal receptor, and, relies on the premise that native molecules will not recognize the orthogonal receptor. One of the challenges associated with generating orthogonal ligand-receptor pairs is finding muta-

tions that efficiently prevent activation by the endogenous molecule without otherwise compromising the receptor's structure or intrinsic ability to activate gene transcription. In alternative methods, to modulate signaling in immune cells, the only approach to prevent negative signals delivered by molecules such as PD-1, is to give patients systemic treatment of antagonistic antibodies that bind to PD-1. This approach has the limitation that systemic treatment prevents T cells that are present in the tumor microenvironment and the entire immune system from being inactivated, which in some patients can result in autoimmunity or systemic inflammatory syndrome (Beck et al., 2006, J Clin Oncol 24: 2283-9; Blansfield et al., 2005, J Immunother 28: 593-8; Dougan et al., 2009, Annual Review of Immunology 27: 83-117).

[0007] The disclosure provided here provides solutions to the problems existing with previous attempts to manipulate immune cells and potentially offer improved methods for treatments involving cell transfer.

SUMMARY

[0008] The present disclosure generally relates to, among other things, chimeric switch receptors containing an endodomain of an IL-9 receptor, engineered to modulate transcriptional regulation in a ligand-dependent manner. The activity of these switch receptors can be controlled by the presence of an extracellular ligand, allowing for spatial and temporal control of specific gene expression in mammalian cells, as well as for use in modulating cell activities or in treating various health conditions, such as diseases.

[0009] In one aspect, provided herein are recombinant nucleic acid molecules encoding chimeric receptors that comprise an extracellular portion comprising a binding domain of an endogenous cytokine receptor, an intracellular portion comprising an endodomain of an IL-9 receptor, and a transmembrane domain that joins the extracellular portion and intracellular portion.

[0010] In some embodiments, the recombinant nucleic acid molecule further comprises one or more linkers.

[0011] In some embodiments, the endogenous cytokine receptor is selected from IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, and IL-21ra.

[0012] In some embodiments, the endogenous cytokine receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 1-6.

[0013] In some embodiments, the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1. In some embodiments, the transmembrane domain comprises an amino acid sequence selected from SEQ ID Nos: 53-56.

[0014] In some embodiments, the chimeric receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 63-80.

[0015] Another aspect provides recombinant nucleic acid molecules encoding chimeric receptors comprising an extracellular portion comprising a binding domain of an endogenous inhibitory receptor an intracellular portion comprising an endodomain of an IL-9 receptor linked to a BOX $\frac{1}{2}$ common gamma chain domain; and a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0016] In some embodiments, the recombinant nucleic acid molecule further comprises one or more linkers.

[0017] In some embodiments, the endogenous inhibitory receptor is selected from TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, and VEGF.

[0018] In some embodiments, the endogenous inhibitory receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 7-52.

[0019] In some embodiments, the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1.

[0020] In some embodiments, the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1.

[0021] In some embodiments, the chimeric receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 81-203.

[0022] Another aspect provides recombinant nucleic acid molecules encoding chimeric receptors comprising an extracellular portion comprising a binding domain of an endogenous inhibitory receptor linked to an agent specific for the common gamma chain; an intracellular portion comprising an endodomain of an IL-9 receptor; and a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0023] In some embodiments, the recombinant nucleic acid molecule further comprises one or more linkers.

[0024] In some embodiments, the endogenous inhibitory receptor is selected from TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, and VEGF.

[0025] In some embodiments, the endogenous inhibitory receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 7-52.

[0026] In some embodiments, the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1. In some embodiments, the transmembrane domain comprises an amino acid sequence selected from SEQ ID Nos: 53-56.

[0027] In some embodiments, the agent specific for the common gamma chain comprises a nanobody, a darpin, IL-2, IL-4, IL-7, and scFV.

[0028] Another aspect relates to an expression vector comprising the recombinant nucleic acid molecules of the disclosure.

[0029] Another aspect relates to a host cell comprising the expression vector of the present disclosure. In some embodiments, the host cell is a mammalian cell. In some embodiments, the host cell is an immune cell.

[0030] Another aspect provides a composition comprising a recombinant nucleic acid of the present disclosure.

[0031] Another aspect provides a composition of cells comprising the expression vector of the present disclosure.

[0032] Another aspect provides a polypeptide encoded by the recombinant nucleic acid the present disclosure.

[0033] Another aspect provides a composition of one or more polypeptides encoded by one or more recombinant nucleic acids of the present disclosure.

[0034] Another aspect provides a composition of cells capable of expressing the chimeric receptor encoded by the recombinant nucleic acid of the present disclosure.

[0035] Another aspect provides a composition of cells comprising a chimeric receptor comprising an amino acid sequence selected from SEQ ID Nos: 63-203.

[0036] Another aspect relates to a method for modulating the activity of an immune cell comprising administering, to an immune cell, the recombinant nucleic acid of the present disclosure.

[0037] Another aspect relates to a method of treating a subject that involves administering, to the subject, a cell expressing the recombinant nucleic acid of the present disclosure.

[0038] In some embodiments, the subject is treated for cancer.

[0039] In some embodiments, the subject is treated for autoimmune disease.

[0040] In some embodiments, the subject is treated for infection.

[0041] The foregoing summary is illustrative only and is not intended to be in any way limiting. In addition to the illustrative embodiments and features described herein, further aspects, embodiments, objects and features of the disclosure will become fully apparent from the drawings and the detailed description and the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0042] FIG. 1 shows the pSTAT expression profile in either stimulated or unstimulated primary human T cells transduced with a lentiviral vector encoding switch receptors of SEQ ID NO:63+CAR+ (IL21R ECD+IL9R TM+IL9R ICD and CAR 4D5), SEQ ID NO:66 (IL15Ra+IL9R TM+IL9R ICD), SEQ ID NO:72+CAR+ (IL4R ECD+IL9R TM+IL9R ICD and CAR 4D5), or SEQ ID NO:153+CAR+ (IL10Ra ECD+IL9R TM+IL9R ICD and CAR 4D5).

[0043] FIG. 2 shows a real-time cytotoxicity assay (RTCA) with T cells co-expressing switch receptor SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) against SKOV-3 human ovarian adenocarcinoma cells expressing HER2. Double-positive T cells (SEQ63+CAR+) were left unstimulated ("no stim") before being added on SKOV-3 tumor cells at a 1:8 effector-to-target ratio, or preconditioned for 48 hours with IL21 before addition to the plate with continued ligand stimulation ("preconditioned+IL21"). Untransduced T cells (UTD) served as control and were added on tumor cells with continued IL21 stimulation ("UTD+IL21").

[0044] FIG. 3 shows a real-time cytotoxicity assay (RTCA) with T cells co-expressing switch receptor SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) against SKOV-3 human ovarian adenocarcinoma cells expressing HER2. Double-positive T cells (SEQ72+CAR+) were left unstimulated ("no stim") before being added on SKOV-3 tumor cells at a 1:8 effector-to-target ratio, or preconditioned for 48 hours with IL4 before addition to the plate with continued ligand stimulation ("preconditioned+IL4"). Untransduced T cells (UTD) served as control and were added on tumor cells with continued IL4 stimulation ("UTD+IL4").

[0045] FIG. 4 shows a real-time cytotoxicity assay (RTCA) with T cells co-expressing switch receptor SEQ113 (Fas ECD+IL9R TM+IL9R ICD) and CAR (4D5) against SKOV-3 human ovarian adenocarcinoma cells expressing

HER2. Double-positive T cells (SEQ113+CAR+) were left unstimulated (“no stim”) before being added on SKOV-3 tumor cells at a 1:4 effector-to-target ratio, or preconditioned for 48 hours with FasL before addition to the plate (“pre-conditioned+no stim”). Untransduced T cells (UTD) served as control and were added on tumor cells unstimulated (“UTD+no stim”).

[0046] FIG. 5 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with IL-21 (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graph depicts fold change over unstimulated.

[0047] FIG. 6 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with IL-4 (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graph depicts fold change over unstimulated.

[0048] FIG. 7 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with IL-4 (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of EGF in pg/mL.

[0049] FIGS. 8A-8B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 8A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 8B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of FGF-2 in pg/mL.

[0050] FIGS. 9A-9B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 9A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 9B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of GM-CSF in pg/mL.

[0051] FIG. 10 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with its respective ligand (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the

concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IFN α 2 in pg/mL.

[0052] FIGS. 11A-11B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 11A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 11B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IFN γ in pg/mL.

[0053] FIG. 12 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with its respective ligand (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IL-10 in pg/mL.

[0054] FIGS. 13A-13B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 13A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 13B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IL-1 α in pg/mL.

[0055] FIG. 14 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with its respective ligand (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IL-2 in pg/mL.

[0056] FIGS. 15A-15B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 15A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 15B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IL-3 in pg/mL.

[0057] FIGS. 16A-16B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 16A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 16B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IL-6 in pg/mL.

[0058] FIGS. 17A-17B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 17A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 17B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of IP-10 in pg/mL.

[0059] FIGS. 18A-18B show hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptors SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 18A) and SEQ72 (IL4R ECD+IL9R TM+IL9R ICD) and CAR (4D5) (FIG. 18B) and cocultured with their respective ligands (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of MIP-1a in pg/mL.

[0060] FIG. 19 shows hybrid cytokine receptors induce functional activation of T cells in response to ligand stimulation. T cells were transduced with hybrid cytokine receptor SEQ63 (IL21R ECD+IL9R TM+IL9R ICD) and CAR (4D5) and cocultured with its respective ligand (i) before, (ii) during, or (iii) before+during, co-culture with target cells for 160 hrs. Cell culture supernatants were collected and the concentrations of effector cytokines measured by Luminex assay. The graphs shows concentration of RANTES in pg/mL.

DETAILED DESCRIPTION OF THE DISCLOSURE

[0061] The present disclosure generally relates to, among other things, chimeric switch receptors containing an endodomain of an IL-9 receptor and a binding domain of an endogenous receptor, wherein the chimeric switch receptor is engineered to modulate transcriptional regulation in a ligand-dependent manner. The activity of these switch receptors can be controlled by the presence of an extracellular ligand, allowing for spatial and temporal control of specific gene expression in mammalian cells, as well as for use in modulating cell activities, immune system responses, or in treating various health conditions, such as diseases. Particularly, the chimeric switch receptor (termed “IL-9 switch receptor”), even though containing the endodomain of an IL-9 receptor, does not require IL-9 for activation and can be tailored to be activated by ligands specific for the binding domains of the endogenous receptors, such as normally inhibitory ligands. This class of chimeric switch receptors is synthetic and recombinant, and does not occur in nature. As described below, the chimeric switch receptors disclosed herein can be synthetic polypeptides, and can be engineered, designed, or modified so as to provide desired and/or improved properties, e.g., modulating transcription. The disclosure also provides compositions and methods useful for producing such receptors, nucleic acids encoding same, cells genetically modified with the nucleic acids, as well as methods for modulating an activity of a cell, modulating immune system, and/or for the treatment of various diseases.

[0062] In the following detailed description, the illustrative alternatives described in the detailed description and claims are not meant to be limiting. Other alternatives may be used and other changes may be made without departing from the spirit or scope of the subject matter presented here. It will be readily understood that the aspects, as generally described herein, can be arranged, substituted, combined, and designed in a wide variety of different configurations, all of which are explicitly contemplated and make part of this application.

Definitions

[0063] The singular form “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. For example, the term “a cell” includes one or more cells, including mixtures thereof. “A and/or B” is used herein to include all of the following alternatives: “A”, “B”, “A or B”, and “A and B.”

[0064] The terms “administration” and “administering”, as used herein, refer to the delivery of a composition or formulation as disclosed herein by an administration route including, but not limited to, intravenous, intra-arterial, intracranial, intramuscular, intraperitoneal, subcutaneous, intramuscular, or combinations thereof. The term includes, but is not limited to, administration by a medical professional and self-administration.

[0065] “Cancer” refers to the presence of cells possessing several characteristics typical of cancer-causing cells, such as uncontrolled proliferation, immortality, metastatic potential, rapid growth and proliferation rate, and certain characteristic morphological features. Cancer cells can aggregate into a mass, such as a tumor, or can exist alone within a subject. A tumor can be a solid tumor, a soft tissue tumor, or a metastatic lesion. As used herein, the term “cancer” also encompasses other types of non-tumor cancers. Non-limiting examples include blood cancers or hematological cancers, such as leukemia. Cancer can include premalignant, as well as malignant cancers.

[0066] The terms “cell”, “cell culture”, and “cell line” refer not only to the particular subject cell or cell line but also to the progeny or potential progeny of such a cell, cell culture, or cell line, without regard to the number of transfers or passages in culture. It should be understood that not all progeny are exactly identical to the parental cell. This is because certain modifications may occur in succeeding generations due to either mutations (e.g., deliberate or inadvertent mutations) or environmental influences (e.g., methylation or other epigenetic modifications), such that progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein, so long as the progeny retain the same functionality as that of the original cell, cell culture, or cell line.

[0067] As used herein “endogenous” refers to any material from or produced inside an organism, cell, tissue or system (e.g., as it would occur in nature or naturally produced).

[0068] The term “percent identity”, as used herein in the context of two or more nucleic acids or proteins, refers to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides or amino acids that are the same (e.g., about 60% sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region)

as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection. See e.g., the NCBI web site at ncbi.nlm.nih.gov/BLAST. Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a sequence. This definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. Sequence identity can be calculated over a region that is at least about 20 amino acids or nucleotides in length, or over a region that is 10-100 amino acids or nucleotides in length, or over the entire length of a given sequence. Sequence identity can be calculated using published techniques and widely available computer programs, such as the GCS program package (Devereux et al, *Nucleic Acids Res.* 12:387, 1984), BLASTP, BLASTN, FASTA (Atschul et al., *Mol Biol* 215:403, 1990). Sequence identity can be measured using sequence analysis software such as the Sequence Analysis Software Package of the Genetics Computer Group at the University of Wisconsin Biotechnology Center (1710 University Avenue, Madison, Wis. 53705), with the default parameters thereof.

[0069] As used herein, a “subject” or an “individual” includes animals, such as human (e.g., human subject) and non-human animals. In some embodiments, a “subject” or “individual” is a patient under the care of a physician. Thus, the subject can be a human patient or a subject who has, is at risk of having, or is suspected of having a disease of interest (e.g., cancer) and/or one or more symptoms of the disease. The subject can also be a subject who is diagnosed with a risk of the condition of interest at the time of diagnosis or later. The term “non-human animals” includes all vertebrates, e.g., mammals, e.g., rodents, e.g., mice, non-human primates, and other mammals, such as e.g., sheep, dogs, cows, chickens, and non-mammals, such as amphibians, reptiles, etc.

[0070] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the disclosure. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the disclosure, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure.

[0071] All ranges disclosed herein also encompass any and all possible sub-ranges and combinations of sub-ranges thereof. Any listed range can be recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, and so forth. As will also be understood by one skilled in the art all language such as “up to”, “at least”, “greater than”, “less than”, and the like include the number recited and refer to ranges which can be subsequently broken down into sub-ranges as discussed above. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 articles refers to groups having 1, 2, or 3 articles.

Similarly, a group having 1-5 articles refers to groups having 1, 2, 3, 4, or 5 articles, and so forth.

[0072] It is appreciated that certain features of the disclosure, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the disclosure, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the disclosure are specifically embraced by the present disclosure and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the present disclosure and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

IL-9 and Common Gamma Chain Receptors

[0073] Interleukin-9 (IL-9) is a member of a group of cytokines referred to as the common γ chain cytokines. Common γ chain cytokines exert numerous functions on immune cell survival, function and proliferation. The γ c family consists of six members—IL-2, IL-4, IL-7, IL-9, IL-15, and IL-21—which all have unique receptors. Upon receptor ligation, γ c cytokines through JAK1 and JAK3 activate various developmental pathways including STAT1, STAT3, STAT5, MAPK, and PI3K/AKT pathways.

[0074] An important aspect of γ c receptor signaling is positive and negative regulation of pathways to either enhance or repress signaling. Some of the γ c cytokines can mediate similar signaling pathways and transcriptional programs (Kovanen P E, Rosenwald A, Fu J, Hurt E M, Lam L T, Giltneane J M, et al. Analysis of Gamma C-Family Cytokine Target Genes. Identification of Dual-Specificity Phosphatase 5 (DUSP5) as a Regulator of Mitogen-Activated Protein Kinase Activity in Interleukin-2 Signaling. *J Biol Chem* (2003) 278(7):5205-13; Osinalde N, Sanchez-Quiles V, Akimov V, Guerra B, Blagoev B, Kratchmarova I. Simultaneous Dissection and Comparison of IL-2 and IL-15 Signaling Pathways by Global Quantitative Phosphoproteomics. *Proteomics* (2015) 15(2-3):520-31), however, physiological differences in cytokine signaling are mediated by competition for γ c between the different receptors (Gonnord P, Angermann B R, Sadtler K, Gombos E, Chappert P, Meier-Schellersheim M, et al. A Hierarchy of Affinities Between Cytokine Receptors and the Common Gamma Chain Leads to Pathway Cross-Talk. *Sci Signal* (2018) 11(524)), variability in receptor expression on T cell subsets, a bias for signaling through different STAT molecules, and differences in activation of the MAPK and PI3K pathways (Zeng R, Spolski R, Casas E, Zhu W, Levy D E, Leonard W J. The Molecular Basis of IL-21-Mediated Proliferation. *Blood* (2007) 109(10):4135-42; Gadina M, Sudarshan C, Visconti R, Zhou Y J, Gu H, Neel B G, et al. The Docking Molecule Gab2 is Induced by Lymphocyte Activation and is Involved in Signaling by Interleukin-2 and Interleukin-15 But Not Other Common Gamma Chain-Using Cytokines. *J Biol Chem* (2000) 275(35):26959-66).

[0075] The IL-9 receptor alpha (IL-9R α), a member of the type I hematopoietin receptor superfamily, has high affinity (K_d of approximately 100 pM) for IL-9. This 64-kDa glycoprotein is reported on a variety of hematopoietic cells, particularly T cells. Similar to the other members of the IL-2

receptor family, IL-9R α also forms a heterotypic receptor complex with the common gamma (γ c) chain. In the IL-9R heterocomplex, the IL-9R α chain is the ligand binding domain and γ chain serves as the signaling subunit. The IL-9R α subunit is characterized by four extracellular cysteines and the conserved WSXWS motif, while the intracellular domain contains a BOX1 consensus sequence and a serine rich region. IL-9R α is found in both membrane bound and soluble forms, whereas the γ c subunit is observed only in a membrane bound form.

[0076] IL-9 binding to IL-9R α results in the formation the IL-9R heterocomplex. A hallmark of the IL-9R heterocomplex is the absence of any intracellular enzymatic activity, and, therefore, Janus kinases (JAK) need to mediate the phosphorylation of the receptor (Knoops L., Renauld J. C. IL-9 and its receptor: From signal transduction to tumorigenesis. *Growth Factors*. 2004; 22:207-215). Upon IL-9 binding to the receptor, a conformational change occurs in the IL-9R heterocomplex, which allows JAK molecules to bind to the proline rich BOX1 motif in the membrane-proximal region of IL-9R α . JAK1 associates with IL-9R α , whereas JAK3 binds to γ c. Phosphorylated JAK1 and JAK3 then mediate the phosphorylation of receptor tyrosine residues. Phosphorylated tyrosine residues act as docking sites for the downstream Src homology 2 (SH2) domain containing signaling molecules such as Signal Transducer and Activator of Transcription (STAT) transcription factors, insulin receptor substrate (IRS), and the adaptors of the Mitogen-Activated Protein Kinase (MAPK) pathways.

COMPOSITIONS OF THE DISCLOSURE

[0077] As described in greater detail below, one aspect of the present disclosure relates to recombinant nucleic acids encoding chimeric switch receptors that include an extracellular portion comprising a binding domain of an endogenous cytokine receptor or endogenous inhibitory receptor, an intracellular portion comprising an endodomain of an IL-9 receptor, and transmembrane domain that joins the extracellular portion and the intracellular portion. Such receptors are engineered to modulate transcriptional regulation in a ligand-dependent manner with various advantages including the ability to convert an otherwise negative signal into a positive signal in the cell. Thus, the present disclosure also encompasses switch receptors that are able to switch negative signals to positive signals for enhancement of an immune response. The present disclosure also encompasses receptors that are able to bind to an endogenous or exogenously given ligand (e.g. a cytokine) and, regardless of the cytokine, result in activation of STAT5, for example, via the common gamma chain and IL-9 endodomain.

[0078] As described in the Examples, certain recombinant nucleic acids encoding chimeric receptors can be tested and validated in T cells. These chimeric receptors are expected to show similar performance in mouse models as well as models in other suitable animals or in vitro systems. The receptors disclosed herein may be engineered into various immune cell types for enhanced discrimination and elimination of tumors, or in recombinant host cells for control of autoimmunity and infection. Accordingly, recombinant host cells and compositions of cells, such as immune cells capable of expressing one of more of the chimeric receptors disclosed herein, are also within the scope of the disclosure.

In some embodiments, a composition of cells expresses the chimeric receptor encoded by the recombinant nucleic acid described herein.

Switch Receptors

[0079] The present disclosure is based, inter alia, on recombinant nucleic acid molecules encoding chimeric receptors which comprise an endodomain of an IL-9 receptor, thus creating chimeric receptors that can respond to various extracellular ligands while maintaining the ability to initiate intracellular signaling through the IL-9 receptor endodomain. Immune cells expressing these chimeric receptors may be useful in the context of modulating immune cell activity. In some embodiments, the ligand can be added exogenously and not be limited to production within the cell.

[0080] As outlined above, some embodiments of the present disclosure relate to recombinant nucleic acid molecules encoding chimeric receptors containing the endodomain of an IL-9 receptor. In particular, the chimeric receptors, even though containing an IL-9 endodomain, do not require binding of IL-9 for the functioning of the receptors. Generally, the chimeric receptors comprise an extracellular portion, an intracellular portion comprising an endodomain of an IL-9 receptor, and a transmembrane domain that joins the extracellular portion and the intracellular portion. In some embodiments, extracellular portion comprises a binding domain of an endogenous cytokine receptor. In some embodiments, the extracellular portion comprises a binding domain of an endogenous inhibitory receptor.

[0081] In some embodiments, provided herein is a recombinant nucleic acid encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous cytokine receptor; (b) an intracellular portion comprising an endodomain of an IL-9 receptor; (c) a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0082] In some embodiments, provided herein is a recombinant nucleic acid encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor; (b) an intracellular portion comprising an endodomain of an IL-9 receptor linked to a BOX1/2 common gamma chain domain; (c) a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0083] In some embodiments, provided herein is a recombinant nucleic acid encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor linked to an agent specific for the common gamma chain; (b) an intracellular portion comprising an endodomain of an IL-9 receptor; (c) a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0084] Extracellular Portions

[0085] As outlined above, the extracellular portions of the chimeric receptors (e.g., switch receptors) in some embodiments of the disclosure have a binding domain of an endogenous cytokine receptor or an endogenous inhibitory receptor. A binding domain of an endogenous cytokine receptor can be an extracellular portion of an endogenous cytokine receptor, or a fragment or truncation thereof that can bind a cytokine polypeptide sequence. In some embodiments, the endogenous cytokine receptor is a member of the common gamma chain receptor family. Members of the common gamma chain receptor family are known in the art

and are discussed supra. In some embodiments, the endogenous cytokine receptor is selected from IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, and IL-21ra. As described supra, IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, and IL-21ra are all part of the common gamma chain family. Therefore, these receptors are capable of recruiting the common gamma chain, upon ligand binding, and signaling can proceed through the IL-9 endodomain.

[0086] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-2rb (SEQ ID NO:1) below:

AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQV
HAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQ
KLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLR
LMAPISLQVVHVETHRCNISWEISQASHYFERHLE
FEARTLSPGHTWEEAPLLTLKQKQEWICLETLPD
TQYEFQVRVKPLQGEFTTWPWSQPLAFRTKPAAL
GKDT

[0087] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-2ra (SEQ ID NO:2) below:

ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFR
RIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT
KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCR
EPPPWENEATERIYHFVVGQMVYYQCVQGYRALHR
GPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGE
EKPQASPEGRPESETSCLVTTTDFQIQTEMAATME
TSIFTTEYQ

[0088] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-4 (SEQ ID NO:3) below:

MKVLQEPTCVSDYMSISTCEWKMNQPTNCSTELRL
LYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVS
ADNYTLDLWAGQQLLWKGSKPSEHVKPRAPGNLT
VHTNVSDTLLLTWSNPYPDPNYLYNHLTYAVNIWS
ENDPADFRIYNVTYPEPSLRIAASTLKSGISYRAR
VRAWAQCYNNTTSEWSPSTKWHNSYREPFEQH

[0089] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-7ra (SEQ ID NO:4) below:

ESGYAQNGDLEDAELDDYSFSCYSQLEVNQSQHSL
TCAFEDPDVNI TNLEFEICGALVEVKCLNFRKLQE
IYFIETKKFLLIGKSNICVKVGEKSLTCKKIDLTT

-continued

IVKPEAPFDLSVVYREGANDFVVTFNTSHLQKKYV
KVLMDVAYRQEKDENKWTHVNLSSTKLTLQKRL
QPAAMYEIKVRSIPDHYFKGFWSEWSPSYFFRTPE
INNSSGEMD

[0090] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-15ra (SEQ ID NO:5) below:

ITCPPMSVEHADIWVKSYSLSRERYICNSGFKR
KAGTSSLTECVLNKATNVAHWTPSLKCIRDPALV
HQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPS
SNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHES
SHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTT

[0091] In one embodiment, the endogenous cytokine receptor comprises the amino acid sequence of IL-21ra (SEQ ID NO:6) below:

CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQ
YEELKDEATSCSLHRSAHNATHATYTCHMDVFHFM
ADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPF
NVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQ
YRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDS
SYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEE
LKE

[0092] In some embodiments, the extracellular portions of the chimeric polypeptides disclosed herein (e.g., IL-9 switch receptors) having at least 80% sequence identity, such as, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or 99% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 1-6 in the Sequence Listing. In some embodiments, the extracellular portion includes an amino acid sequence having at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 1-6. In some embodiments, the extracellular portion includes an amino acid sequence having at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 1-6. In some embodiments, the extracellular portion includes an amino acid sequence having about 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 1-6. In some embodiments, the extracellular portion includes an amino acid sequence having a sequence selected from the group consisting of SEQ ID NOS: 1-6, wherein one, two, three, four, or five of the amino acid residues in any one of the SEQ ID NOS: 1-6 is substituted by a different amino acid residue.

[0093] In another aspect of the present disclosure, the extracellular portion of the chimeric receptor of the disclosure can also comprise a binding domain of an endogenous inhibitory receptor. Specifically, as described supra, in some

embodiments, provided herein is a recombinant nucleic acid encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor linked to an agent specific for the common gamma chain; (b) an intracellular portion comprising an endodomain of an IL-9 receptor; (c) a transmembrane domain that joins the extracellular portion and the intracellular portion.

[0094] As described supra, signaling through the IL-9 endodomain requires recruitment of the common gamma chain. In some embodiments, the binding domains of the extracellular portion of the inhibitory receptors described herein are not able to naturally recruit the common gamma chain in order to elicit signaling through the IL-9 endodomain of the chimeric receptor. Accordingly, in these embodiments, the binding domain of the endogenous inhibitory receptor is linked to an agent specific for the common gamma chain. The binding domain of the inhibitory receptor is linked to the agent specific for the common gamma chain such that both components are able to function in their intended way (e.g., the binding domain is able to bind a ligand and the agent specific for the common gamma chain is able to bind the common gamma chain).

[0095] In some embodiments, the agent specific for the common gamma chain comprises agent specific for the common gamma chain comprises a nanobody, a darpin, IL-2, IL-4, IL-7, or an scFv.

[0096] In some embodiments, an scFv directed to the common gamma chain is cloned in frame with the extracellular portion of the chimeric receptor, with suitable linker sequences inserted between these components. The binding of the common gamma chain to the scFv will be sufficient to induce chimeric receptor dimerization.

[0097] scFVs directed to the common gamma chain as well as their sequences are known in the art and described in WO 2017/021540. However, the use of scFVs directed to the common gamma chain with respect to switch receptors is not disclosed therein.

[0098] A binding domain of an endogenous inhibitory receptor can be an extracellular portion of an endogenous inhibitory receptor, or a fragment or truncation thereof that can bind a cytokine polypeptide sequence and subsequently decrease immune activity. For example, a natural inhibitory receptor can reduce T cell proliferation, T cell survival, cytokine release, or immune cell lytic activity upon binding of a natural agonist.

[0099] Endogenous inhibitory receptors are well known in the art and are contemplated for use in the compositions described herein (Turnis et al., "Inhibitory Receptors as Targets for Cancer Immunotherapy," Eur J Immunol 2015 45(7):1892-1905).

[0100] In some embodiments, the endogenous inhibitory receptor signals through trimerization. In some embodiments, the endogenous inhibitory receptor is a member of the TNF receptor superfamily.

[0101] In some embodiments, the endogenous inhibitory receptor signals as functional dimers of dimers. In some embodiments, the endogenous inhibitory receptor is a member of the TGF beta superfamily of receptors. Receptors in this family include, for example, Type I, Type II, and Type III receptors. Exemplary members of the Type I receptor family include, without limitation, ACVRL1, ACVR1A, BMPR1A, ACVR1B, TGFβR1, BMPR1B, and ACVR1C. Exemplary members of the Type II receptor family include,

without limitation, TGFBR2, BMPR2, ACVR2A, ACVR2B, and AMHR2. TGF βR3 is a member of the Type III family of receptors.

[0102] In some embodiments, the endogenous inhibitory receptor signal as dimers. In some embodiments, the endogenous inhibitory receptor is a member of the VEGF family of receptors. Receptors in this family include, for example, VEGFR1, VEGFR2, and VEGFR3.

[0103] In some embodiments, the endogenous inhibitory receptor is selected from TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, and VEGF. Thus, in some embodiments, the extracellular portion of the chimeric receptor of the disclosure can be a binding domain of TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, and VEGF.

[0104] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of TGFBR1 (SEQ ID NO:7) below:

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LQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHN
SMCIAEIDLIPDRPFVFCAPSSKTGSVTTTYCCNQ
DHCNKIELPTTVKSSPGLGPVEL
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[0105] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of TGFBR2 (SEQ ID NO:8) below:

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TIPPHVQKSVNNDMTVTDNNGAVKFPQLCKFCQDVR
FSTCDNQKSCMSNCSITSICEKPQEVCAVWRKND
ENITLETVCHDPKLPYHDFILEDAAAPKCMKEKK
KPGETFFMCSSSDECNDNIIFSEEYNTSNPDLLE
VIFQ
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[0106] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of IL-10ra (SEQ ID NO:9) below:

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HGTELPSPPSVWFEEFFHHILHWTPIPNQSESTC
YEVALLRYGIESWNSISNCSQTLSDLTAVTLDLY
HSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLT
VGSVNLEIHNGFILGKIQLPRPKMAPANDTYESIF
SHFREYEIAIRKVPGNFTFTHKKVKHENFSLTSG
EVGEFCVQVKPSVASRSNKGMSKEECISLTRQYF
TVTN
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[0107] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of FAS (SEQ ID NO:10) below:

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QVTDINSKGLLELRKTVTTVETQNLEGLHHDGQFCH
KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA
HFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCK
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-continued

PNFFCNSTVCEHCDPCKCEHGIIKECTLTSNTKC
KEEGSRSN

[0108] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of CTLA4 (SEQ ID NO:11) below:

KAMHVAQPAVVLASSRGIASFVCEYASPGKATEVR
VTVLRQADSQVTEVCAATYMMGNELTFLDDSICTG
TSSGNQVNLTIQGLRAMDTGLYICKVELMYPPIYY
LGIGNGTQIYVIDPEPCPDSD

[0109] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of LAG3 (SEQ ID NO:12) below:

LQPGAIEVPVWVAQEGAPQLPCSPTIPLQDLSLLR
RAGVTWQHQPDSGPPAAAPGHPLAPGPHPAAPSSW
GPRPRRYTVLSVGGGLRSGRLPLQPRVQLDERGR
QRGDFSLWLRPARRADAGEYRAAVHLRDRALSCRL
RLRLGQASMTASPPGSLRASDWVILNCSFSRPDRP
ASVHWFRNRGQGRVPVRESPHHHLAESFLFLPQVS
PMDSGPWGCILTYRDGFNVSIMYNLTVLGLEPPTP
LTVYAGAGSRVGLPCRLPAGVGTRSFLLTAKWTPPG
GGPDLLVTGDNGDFTLRLEDVSAQAQAGTYTCHIHL
QEQQLNATVTLAIITVTPKSFSGPSLGKLLCEVT
PVSGQERFVWSSLDTPSQRSFSGPWLEAQEAQLLS
QPWQCQLYQGERLLGAAYFTELSSPGAQRSGRAP
GALPAGHL

[0110] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of TIM3 (SEQ ID NO:13) below:

SEVEYRAEVGQONAYLPCFYTPAAPGNLVPVCWGKGACPVFECGNVVLRTD
ERDVNYWTSRYWLNQDFRKGDVSLTIENVTLADSGIYCCRIQIPGIMNDE
KFNLKLVIKPAKVTAPTRQRDFTAAFPRLTTRGHGPAETQTLGSLPDI
NLTQISTLANELRDSRLANDLRDSGATIRIG

[0111] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of PD1 (SEQ ID NO:14) below:

FTVTVPKDLVVEYGSNMTIECKFPVEKQLDLAALIVWEMEDKNHIQFV
HGEEDLKVQHSSYRQARLLKDQLSLGNAALQITDVKLQDAGVYRCMISY
GGADYKRI TVKVNAPYNKINQRILVVDVPTSEHELTCAEGYPKAEVIWT

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SSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDP
NHTAELVIPELPLAHPNER

[0112] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of ILT2 (SEQ ID NO:15) below:

GHLPKPTLWAEPGSVITQGSPVTLRCQGGQETQYRLYREKKTALWITRI
PQELVKKGQFPISITWEHAGRYRCYYSDDTAGRSESSDPLELVVTGAYI
KPTLSAQSPVNVNSGGNVILQCDQVAFDGFSLCKEGEDEHPQCLNSQPH
ARGSSRAIFSVGPFVSPRRWYRCYAYDSNSPYEWSLPSDLLELLVLGVS
KKPSLSVQPGPIVAPEETLTLQCGSDAGYNRFVLKDGGERDFLQLAGAQP
QAGLSQANFTLGPVSRSYGGQYRCYGAHNLSSEWSAPSDPLDILLAGQFY
DRVLSLVQPGPTVASGENVTLLCQSQGWMQTFLLTKEGAADDPWRLRSTY
QSQKYQAEFFMPGVTSAHAGTYRCYGSQSSKPYPLLTHPSDPLELVVSGPS
GGPSSPTTGPTSTSGPEDQPLTPTGSDPQSGLGRHLGV

[0113] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of ILT3 (SEQ ID NO:16) below:

QAGPLPKPTLWAEPGSVISWGNVITIWCQGTLEAREYRLDKEESPAPWDR
QNPLEPKNKARFSIPSMTEYAGRYRCYRSPVGWSQPSDPLELVMTGAY
SKPTLSALPSPLVTSGKSVTLLCQSRSPMDTFLLIKERAHPLHLRSEH
GAQQHQAEFFMSPVTSVHGGTYRCFSSHGFSHYLLSHPSDPLELIVSGSL
EDPRPSPTRSVSTAAGPEDQPLMPTGSPVPHSGLRRHWE

[0114] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of ILT4 (SEQ ID NO:17) below:

QTGTIPKPTLWAEPDVITQGSPVTLSCQGSLEAQYRLYREKKSASWIT
RIRPELVKNGQFHIPSITWEHTGRYGCQYYSRARWSELSDPLVLVMTGAY
PKPTLSAQSPVVTSGGRVTLQCESQVAFGGFILCKEGEEHPQCLNSQP
HARGSSRAIFSVGPFVSPNRRWSHRCYGYDLNSPYVWSSPSDLLELLVPGV
SKKPSLSVQPGPVVAPGESLTLQCVSDVGYDRFVLYKEGERDLRQLPGRQ
PQAGLSQANFTLGPVSRSYGGQYRCYGAHNLSSECSAPSDPLDILITGQI
RGTPFISVQPGPTVASGENVTLLCQSWRQFHTFLLTKAGAADAPLRLRSI
HEYPKYQAEFFMSPVTSAHAGTYRCYGSLSNDPYLLSHPSEPLELVVSGP
SMGSSPPPTGPISTPAGPEDQPLTPTGSDPQSGLGRHLGV

[0115] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of ILT5 (SEQ ID NO:18) below:

GPFPKPTLWAEPGSVISWGSPTIWCQGSQEAQYRLHKEGSPEPLDRNN
PLEPKNKARFSIPSMTEHHAGRYRCHYYSAGWSEPSDPLEMVTGAYSK
PTLSALPSPVVASGGNMTLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLH

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SRGFQALFPVGPVTPSHRWRFTCYYYTNTPWVWSHPSDPLEILPSGVSR
KPSLLTLQGPVLAPGQSLTLQCGSDVGYNRFVLYKEGERDFLQRPGQQPQ
AGLSQANFTLGPVSPSNGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYD
TVSLSAQPGPTVASGENVTLLCQSWWQFDTFLLTKEGAAHPPLRLRSMYG
AHKYQAEFPMSPVTSAHAGTYRCYGSYSSNPHLLSHPSEPLELVVSGHSG
GSSLPPTGPPSTPGLGRYLE

[0116] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of VEGFR1 (SEQ ID NO:19) below:

SKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESERLSI
TKSACGRNGKQFCSTLTNLTAQANHTGFYSCKYLAVPTSKKKETESAIYI
FISDTGRPFVEMYSEIPEIIHMTGRELVIPCRVTSFNITVTLKKFPLDT
LIPDGKRIIWDSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQT
NTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRA
SVRRRIDQSNSHANIFYSVLTIDKMQNKDGLYTCRVRSGPSFKSVNTSV
HIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFFSPPEVVWLKDGLPA
TEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFNLTATLIVNV
KPQIYEKAVSSFDPALYPLGSRQILTCTAYGIPQPTIKWFHPCNNHNS
EARCDFCSNNEESFILDADSNMGNRIESITQMAIEGKNKMASTLVVAD
SRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLS
CTVKNFLYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNV
SLQDSGTYACRARNVYTGEIILQKKEITIRDQEAPYLLRNLSDHTVAISS
STTLDCHANGVPEPQITWFKNNHKIQQEPGIILGPGSSTLFIERVTEEDE
GVYHCKATNQKGSVESSAYLTVQGTSDKSNLE

[0117] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of VEGFR2 (SEQ ID NO:20) below:

ASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWPNNQSG
SEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQ
DYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKR
FVPDGNRISWDSKKGFTIPSYMISYAGMVFEAKINDESYSIMYIVVVV
GYRIYDVVLSPSHGIELSVGEKLVLNCTARTELVGIDFNWEYPSSKHQH

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KKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNS
TFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPEIKWYKNGI
PLESNHTIKAGHVLTIMEVSESDTGNYSVTILTNPISKEKQSHVSVLVVYV
PPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHHIHWYQLEEECANE
PSQAVSVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVI
QAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPDMQPTEQESVSL
WCTADRSTFENLTWYKLGQPPLPIHVGEPLTPVCKNLDTLWKLNATMFSN
STNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTI
TGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGN
RNLTIRRVKKEDEGLYTCQACSVLGCAKVEAFFIIIEGAQEKTNLE

[0118] In one embodiment, the endogenous inhibitory receptor comprises the amino acid sequence of VEGFR3 (SEQ ID NO:21) below:

YSMTPTLNI TEESHVIDTGDLSLISCRGQHPLEWAWPGAQEAPATGDKD
SEDTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYKYIKARIEGTT
AASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPGLNVTLSQSS
VLWPDGQEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHI
TGNELYDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAE
RGKWVPERRSQQTHTELSSILTIHNVSQHDLGSYVCKANNGIQRFRESTE
VIVHENPFISVEWLKGPPILEATAGDELVKLPVKLAAYPPPEFQWKDGKA
LSGRHSPHALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNVPPQI
HEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTPCKMFAQRSL
RRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQ
NANVSAMYKCVSNKVGQDERLIYFYVTTIPDGFTIESKPSEELLEGQPV
LLSCQADS KYEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATPLAASL
EEVAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLVSQA
LEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEEKSGV
DLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSM
E

[0119] A number of other receptor sequences are contemplated for use in the extracellular portions of the chimeric receptors described herein. Such sequences may be used to switch the natural biology of the receptor ligand or provide for localized stimulation of a cell population. Exemplary sequences of the extracellular portions of such receptors are shown in Table 1 below.

Receptor Extracellular Portion	Amino Acid Sequence	SEQ ID NO
OPG	ETFPFKYLHYDEETSHQLLCDKPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHT SDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQ AGTPERNTV CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGI DVTLC EEAFFRFAVP TKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQT FQL LKLWKHQN	22

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Receptor Extracellular Portion	Amino Acid Sequence	SEQ ID NO
	KDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKAC KPSDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFT MYKLYQKLFLEMIGNQVQSVKISCL	
TACI	MSGLGRRRGGRRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTI CNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCAICGQHPKQCAYFCENKLR SPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYS	23
BCMA	MLQMAGQCSQNEYFDSLHACIPCQLRCSNTPPLTCQRYCNASVTNSVKGTNA	24
NGFR	KEACPTGLYTHSGECCACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPC KPCTECVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEACRVCEAGSGLVFSC QDKQNTVCEE CPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEEIPGRWITRSTPPE GSDSTAPSTQEPEAPPEQDLIASTVAGVVTVMGSSQPVVTRGTTDN	25
EDAR	EYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSGCGYGTDEDDYGCVPCPAEKFSKG GYQICRRHKDCEGFFRATVLTTPGDMENDAECGPCLPGYYIVILENRPRNIYGIVIVCY SCLLAPPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKELSGQHLATA	26
DCR2 (TNFRSF10D)	ATIPRQDEVPPQTVAPQQQRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASN NLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRG MVKVSNCTPRSDIKCKNESAASTGKTPAAEETVTTILGMLASPYH	27
DCR1 (TNFRSF10C)	ATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNAS NNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSG EVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPG TPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA	28
CD40	EPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECCLPCGESEFLDTWNRETHC HQHKYCDPNLGLRVQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVK QIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCG PQDRLR	29
DR4	ASGTEAAAATPSKVWGSSAGRIEPRGGGRGALPTSMGQHGPSARARAGRAGP RPAREASPRLRVHKTFFKVVVGVLLQVVPSSAATIKLHDQSIGTQQWEHSPLGELC PPGSHRSEHPGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTAC QCKPGTFRNDNSAEMCRKCSRGCPRGMVKVKDCTPWSDIECVHKESGNHN	30
DR6	QPEQKASNLIGHTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFT RHENGI EKCHDCSQPCPWPMIEKLPCAALTDRECTPPGMFQSNATCAPHTVCP VGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKE TDNVCGLTLPFSSTSPSPGTAFPRPEHMETHEVPSSTYVPKGMNSTESNSSASVR PKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGPHHRHILKLLPSMEA TGGEKSSTPIKGPKRGHPRQNLHKHFDINEH	31
DR5	ITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYGDYSTHWNDL LFLRCTRCDSGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRGTGCPRGMVK VGDCPTWSDIECVHKESGTHKSGEVPAVEETVTSSPGTPASPCS	32
DR3	QGGTRSPRCD CAGDFHKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQDTFLA WENHHNSECARCQACDEQASQVALENC SAVADTRCGCKPGWFVECVSQCVSS SPFYCQPCLD CGALHRHTRLLCSRRDTCGTCLPGFYEHDGCVSCPTSTLGSCPE RCAAVCGWRQ	33
TNFRSF1B	LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCD CEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTRPGWYCALSQ EGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSTTSSTDI CRPHQICNV VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFL PMGPSPPAEGSTGD	34
TNFRSF1	LVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTLYLNDCPGPGQDTCREC ESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD TVCGCRKNQYRHYWSEN LFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSELECTKLCL PQIENVKGTEDSGTT	35
BMPR1B	KKEDGESTAPTPRPKVLRCCHHCPEDSVNNICSTDGYCFMTIEEDDSGLPVVTS GCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKNRDFVDGPIHH R	36

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Receptor Extracellular Portion	Amino Acid Sequence	SEQ ID NO
BMPRI1A	QNLDSMLHGTGMKSDSDQKKSENGVTLAPEDTLPFLKCYCSGHCPDDAINNTCIT NGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYL QPTLPPVVIGPFFDGSIR	37
BMPRI2	SQNQERLCAFKDPYQQDLGIGESRISHENGITILCSKGSTCYGLWEKSKGDINLVKQ GCWSHIGDPQECHYEECVVTTTPPSIQNGTYRFCCCSTDLCNVNFTENFPPPDTP LSPPHSFNRDET	38
CSF3R	ECGHISVSAPIVHLGDPITASCIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDG TQESIITLPHLNHTQAFSLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTS SLICQWEPGPGETHLPTSFTLKSFKSRGNCQTQGDSIILDCVPKDGQSHCCIPRKHLLL YQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAG CLQLCWEPWQPGLHINQKCELRHKPQGEASWALVGPLPLEALQYELCGLLPATA YTLQIRCIRWPLPGHWSWSPSLELRRTTERAPTVRDLTWWRQRLDPRTVQLFW KVPLEEDSGRIQGYVSWRPSGQAGAILPLCNTTELSCTFHLPSAQEVALVAYNS AGTSRPTPVVFSESRGPALTRLHAMARDPHS LWVGWEPPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLENIRP FQLYEIVTPLYQDTMGPSQHVVAYSQEMAPSHAPELHLKHIGKTWAQLEWVPEP PELGKSPLTHTYTFWNTAQNQSFSAILNASSRGFVLHGLEPASLYHIHLMAASQAG ATNSTVLTLMTLTPEGSELH	39
CSF1R	IPVIEPSVPELVVKPGATVTLRCVGNNGSVWDGPPSPHWTLYSDGSSSILSTNNATF QNTGTYRCTEPGDPLGGSAAIHLVVKDPAWPWNVLAQEVVVFEDQDALLPCLLTD PVLEAGVSLVRVRGRPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSALMGGRK VMSISIRLKVQKVI PGPPALTLVPAELVRIRGEAAQIVCSASSVDVNFVFLQHNNNT KLAI PQQSDFHNNRYQKVLTLNLDQVDFQHAGNYSVASNVQGHSTSMFFRVV ESAYLNLSEQNLIQEVTVGEGNLKVMVEAYPGLQGFNWTYLGPFSDHQPEPKL ANATTKDTYRHTFTLSLPRLKPSSEAGRYSLARNPGGWRALTFELTLRYPPEVSVIW TFINGSGTLLCAASGYPPQNVTWLQCSGHTDRCDQAQVLQVWDDPYPEVLSQEP FHKVTVQSLLTVETLEHNQTYECRAHNSVSGSGSWAFIPISAGAHTHPDEFLEFTP	40
Activin R1A	MEDEKPKVNPKLYMCVCEGLSCGNEDHCEGQQCFSSLSINDGFHVYQKGCQFQVY EQGKMTCKTPPSPGQAVECCQGDWCNRNITAQLPTKGKSFPGTQNFHLE	41
Activin R1B	SGPRGVQALLCACTSCLOANYTCETDGACMVSI FNLDGMEHHVRTCIPKVELVPA GKPFYCLSSDLRNTHCYTDYCNRIDLRVPSGHLKEPEHPSMWGPVE	42
Activin R1C	LSPGLKCVCLLCDSSNFTCQTEGACWASVMLTNGKEQVIKSCVSLPELNAQVFCHS SNNVTKTECCFTDFCNNTLHLPATASPNAKLGPMEL	43
Activin R2B	SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASWRNSSGTIELVK KGCWLDDFNICYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEP PTAPTLLT	44
Activin R2A	AILGRSETQECLFFNANWEKDRTNQTVGEPCYGDKDKRRHCFATWKNISGSIEIVK QGCWLDDINCYDRDTCVEKSDSPEVYFCCCEGNMCNEKFSYFPMEVTTQPTSNP VTPKPP	45
TIGIT	MMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGW HISPSFKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRI FLEVLESSVAE HGARFQIP	46
FCGR2B	TPAAPPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPTHTQPS YRFKANMNSGEYTCQTGQTSLSDPVHLTVLSEWLVLTQPHLEFQEGETIVLRCHS WKDKPLVKVTFQNGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSKPV TITVQAP	47
FCGR1	QVDTTKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTATQTSTPSYR ITSASVNSGGEYRCQRLSGRSDPIQLEIHRGWLLQVSSRVFTEGEPLALRCHAW KDKLVYNVLYYRNGKAFKFFHWNSNLITLKTNI SHNGTYHCSGMGKHRYTSAGISV TVKELFPAPVLNASVTSPLLEGNLVTLS CETKLLQLRPLQLYFSFYMGSKTLRGRNT SSEYQILTARREDSGLYWCEATEDGNVLKRSPELELQVLGLQLPTPVWFH	48
2B4	CQGSADHVVISGVPLQLQPNISIQTKVDSIAWKLLPSQNGFHHILKWENGSLPSN TSNDRFSFIVKNLSLLIKAAQQQDSGLYCLEVTSISGKVQTATFQVFVFESLLPDKVE KPRLQGGQKILDRGRQVALSCLVSRDGNVSYAWYRGSKLIQTAGNLTYLDEEVDI NGHTYTCNVSNPVSWESHTLNLTDQDCQNAHQEFRFWP	49
LAIR1	QEEDLPRPSISAEPGTVIPLGSHVTFVCRGPVGVQTFRLERESRSTYNDTEDVSQAS PSESEARFRIDSVSEGNAGPYRCIYYKPPKWEQSDYLELLLVKETSGGPDSPDTEPG SSAGPTQRPDSNHNHAPASQGLKAEHLY	50

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Receptor Extracellular Portion	Amino Acid Sequence	SEQ ID NO
CD5	RLSWYDPDFQARLTRSNSKCQGQLEVYLKDGWHMVCSQSWGRSSKQWEDPSQ ASKVCQRLNCGVPLSLGPFLVITYTPQSSII CYGQLGSFSNCSHSRNDMCHSLGLTCL EPQKTTPPTTRPPPTTTPEPTAPPRQLVAQSGGQHCAGVVEFYSGSLGGTISYEA QDKTQDLENFLCNNLQCGSFLKHLPETEAGRAQDPGEPREHQPPLPIQWKIQNSSC TSLEHCFRKIKPKSGRVLALLCSGFQPKVQSRLVGGSSICEGTVEVRQGAQWAAL CDSSSARSSLRWEEVCREQQCGSVNSYRVLDAGDPTSRGLFCPHQKLSQCHELWE RNSYCKKVFTVCQDPNP	51
TWEAKR	EQAPGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWP	52

[0120] In some embodiments, the extracellular portions of the chimeric polypeptides disclosed herein (e.g., IL-9 switch receptors) having at least 80% sequence identity, such as, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or 99% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 7-52 in the Sequence Listing. In some embodiments, the extracellular portion includes an amino acid sequence having at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 7-52. In some embodiments, the extracellular portion includes an amino acid sequence having at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 7-52. In some embodiments, the extracellular portion includes an amino acid sequence having about 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 7-52. In some embodiments, the extracellular portion includes an amino acid sequence having a sequence selected from the group consisting of SEQ ID NOS: 7-52, wherein one, two, three, four, or five of the amino acid residues in any one of the SEQ ID NOS: 7-52 is substituted by a different amino acid residue.

bonds, hydrogen bonds, electrostatic bonds, and the like. Transmembrane domains may be a hydrophobic alpha helix that spans the cell membrane. The transmembrane domain associated with the endodomain is commonly used. However, in some embodiments, the transmembrane domain of TNFR1 is used in combination with extracellular portions from the TNF superfamily (e.g., DCR2, TNFRSF1, etc.) to stabilize the receptor structure.

[0124] The transmembrane domain can have any length. In some embodiments, the transmembrane domain includes 1 amino acid or 10 amino acids or 20 amino acids or 50 amino acids or 60 amino acids or 70 amino acids or 80 amino acids or 100 amino acids or 120 amino acids or 140 amino acids or 160 amino acids or 180 amino acids or 200 amino acids or 250 amino acids or 300 amino acids or any number therebetween.

[0125] In some embodiments, the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1. Exemplary amino sequences of transmembrane domains for use herein are shown in Table 2.

TABLE 2

Transmembrane domain sequences		
Transmembrane domain	Amino acid sequence	SEQ ID NO
IL-9	LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPR	53
IL-7ra	PILLTISILSFFSVALLVILACVLW	54
IL-2rb	IPWLGHLLVGLSGAFGFII LVYLLI	55
TNFR1	VLLPLVIFFGLCLLSLLFIGLMY	56

[0121] Transmembrane Domain (TMD)

[0122] As outlined above, the chimeric switch receptors of the disclosure also include a transmembrane domain that joins the extracellular portion and the intracellular portion of the chimeric receptor.

[0123] The transmembrane domain is a region, which can be generally hydrophobic, and crosses the cell membrane. This domain can be positioned such that it directly or indirectly connects, or joins, the extracellular portion of the chimeric switch receptor to the intracellular portion of the chimeric switch receptor. This includes, but is not limited to recombinant fusions, covalent bonds, disulfide bonds, ionic

[0126] In some embodiments, the transmembrane domain comprises the transmembrane domain of IL-9. In some embodiments, the transmembrane domain comprises the amino acid sequence of LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPR (SEQ ID NO: 53).

[0127] In some embodiments, the transmembrane domain comprises the transmembrane domain of TNFR1. In some embodiments, the transmembrane domain comprises the amino acid sequence of VLLPLVIFFGLCLLSLLFIGLMY (SEQ ID NO: 56).

[0128] In some embodiments, the transmembrane domain includes an amino acid sequence exhibiting at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least

95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to one or more of SEQ ID NOS: 53-56 in the Sequence Listing. In some embodiments, the transmembrane domain includes an amino acid sequence having at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 53-56. In some embodiments, the transmembrane domain includes an amino acid sequence having at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NOS: 53-56. In some embodiments, the transmembrane domain includes an amino acid sequence having about 100% sequence identity to one or more of SEQ ID NOS: 53-56. In some embodiments, the transmembrane domain includes an amino acid sequence having a sequence selected from the group consisting of SEQ ID NOS: 53-56, wherein one, two, three, four, or five of the amino acid residues in any one of the SEQ ID NOS: 53-56 is substituted by a different amino acid residue.

[0129] Endodomain

[0130] In some embodiments, the endodomain is responsible for receptor clustering/dimerization after antigen binding and for initiation of signal transduction to the cell.

[0131] As outlined above, the chimeric receptors of the disclosure include an endodomain of an IL-9 receptor.

[0132] In some embodiments, the amino acid sequence for the IL-9 receptor endodomain is as follows in SEQ ID NO: 57 below:

VKRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQG
ALEPCVQEATALLTGPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
CTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGRSSSSSSSSNNNNYCAL
GCYGGWHLSPALPGNTQSSGPIPALACGLSCDHQGLETTQQGVAVVLGH
CQ
RPGLHEDLQGMLLPSVLSKARSWTF

[0133] In other embodiments, amino acid numbers 292 to 521 of IL-9Rα (NCBI REFSEQ: NP_002177.2) can be used.

[0134] Alternatively, a truncated fragment of said endodomain of the IL-9 receptor chain also may be used. For example, the truncated fragment comprises up to 250 amino acids, or is 50 to 200 amino acids or 80 to 150 amino acids of the ILR cytoplasmic domain.

[0135] As described supra, one aspect of the present disclosure relates to a recombinant nucleic acid encoding a chimeric receptor including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor; (b) an intracellular portion comprising an endodomain of an IL-9 receptor linked to a BOX^{1/2} common gamma chain domain; (c) a transmembrane domain that joins the extracellular portion and the intracellular portion. Extracellular portions comprising binding domains of inhibitory receptors are described above and are useful in the chimeric receptors described infra as well. In this category of chimeric receptors, signaling through the IL-9 endodomain requires recruitment of the common gamma chain. In some embodiments, the binding domains of the extracellular portion of the chimeric receptors described herein are not able to naturally recruit the common gamma chain in order to elicit signaling through the IL-9 endodomain of the chimeric receptor. Accordingly, in these embodiments, the endodomain of the IL-9 receptor can be linked to BOX^{1/2} domain. Receptors of the common gamma chain family contain two

regions at the cytoplasmic tail, termed Box 1 and Box 2. These domains are critical for the association of JAKs with the receptor (see for example, Murakami M, Narazaki M, Hibi M, Yawata H, Yasukawa K, Hamaguchi M, Taga T, Kishimoto T (1991) Critical cytoplasmic region of the interleukin 6 signal transducer gp130 is conserved in the cytokine receptor family. *Proc Natl Acad Sci USA* 88:11349-11353). Generally, the Box1 domain contains a proline-rich segment of amino acid residues, and the Box2 domain contains a hydrophobic segment of amino acid residues.

[0136] In some embodiments, the chimeric receptor comprises a BOX^{1/2} domain of the following amino acid sequence of SEQ ID NO: 58

ERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVS
EIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

[0137] Linkers

[0138] The nucleic acid encoding the chimeric receptor can further comprise a linker between any of the portions or domains described above. As used herein, the term “linker” generally refers to an oligopeptide or polypeptide that functions to link a one region of a nucleic acid to another region of a nucleic acid. The spacer or linker may comprise up to 300 amino acids, 0-100 amino acids, 25-50 amino acids, 10-15 amino acids, for example.

[0139] Linkers useful in the chimeric receptors described herein include those in Table 3 below.

Linker	Amino acid sequence	SEQ ID NO
Gly Ser Linker	GGGGSGGGSGGGGS	59
Q-Pro Linker	QPQPQPQPQPQP	60
K-Pro Linker	KPKPKPKPKPKP	61

[0140] In some embodiments, the linker is a Gly Ser Linker. In some embodiments, the linker comprising the amino acid sequence GGGSGGGSGGGGS (SEQ ID NO:59).

[0141] In some embodiments, the linker is a Q-Pro Linker. In some embodiments, the linker comprising the amino acid sequence QPQPQPQPQPQP (SEQ ID NO:60).

[0142] In some embodiments, no linker is present.

[0143] In some embodiments, the linker can be a 2A self-cleaving peptide. 2A peptide are a class of 18-22 amino acid peptides, which can result in ribosomal skipping during translation of a protein in a cell. In some embodiments, a linker, such as a 2A peptide, can be included to link the nucleic acid region encoding the chimeric receptor of the disclosure to another nucleic acid region encoding a chimeric antigen receptor (CAR). In some embodiments, the CAR is anti-HER2 CAR (4D5).

[0144] Signal Sequence

[0145] A “signal sequence” can also included at the beginning of the coding sequence of the chimeric receptors disclosed herein. This sequence encodes a signal peptide, N-terminal to the mature polypeptide, that directs the host cell to translocate the polypeptide. Translocation signal sequences can be found associated with a variety of proteins native to eukaryotes and prokaryotes, and are often functional in both types of organisms.

[0146] An exemplary signal sequence that can be used in the chimeric receptors herein includes the amino acid sequence of: MAAPALSWRLPLLILLPLATSWASA (SEQ ID NO: 62)

Nucleic Acid Molecules

[0147] Provided herein are various nucleic acid molecules including nucleotide sequences encoding the chimeric receptors of the disclosure. In some embodiments, expression cassettes and expression vectors contain these nucleic acid molecules operably linked to heterologous nucleic acid sequences such as, for example, regulatory sequences which allow in vivo expression of the receptor in a host cell.

[0148] The terms “nucleic acid molecule” and “polynucleotide” are used interchangeably herein, and refer to both RNA and DNA molecules, including nucleic acid molecules comprising cDNA, genomic DNA, synthetic DNA, and DNA or RNA molecules containing nucleic acid analogs. A nucleic acid molecule can be double-stranded or single-stranded (e.g., a sense strand or an antisense strand). A nucleic acid molecule may contain unconventional or modified nucleotides. The terms “polynucleotide sequence” and “nucleic acid sequence” as used herein interchangeably refer to the sequence of a polynucleotide molecule. The nomenclature for nucleotide bases as set forth in 37 CFR § 1.822 is used herein.

[0149] Nucleic acid molecules of the present disclosure can be of any length, including for example, between about 1.5 Kb and about 50 Kb, between about 5 Kb and about 40 Kb, between about 5 Kb and about 30 Kb, between about 5 Kb and about 20 Kb, or between about 10 Kb and about 50 Kb, for example between about 15 Kb to 30 Kb, between about 20 Kb and about 50 Kb, between about 20 Kb and about 40 Kb, about 5 Kb and about 25 Kb, or about 30 Kb and about 50 Kb.

[0150] In some embodiments, provided herein is a nucleic acid molecule including a nucleotide sequence encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous cytokine receptor; (b) a transmembrane domain; and (c) an intracellular portion comprising an endodomain of an IL-9 receptor.

[0151] In one embodiment, the nucleic acid molecule includes a sequence encoding a chimeric polypeptide including: (a) a binding domain of IL-21; (b) a transmembrane domain of IL-9; and (c) an endodomain of an IL-9 receptor.

[0152] In one embodiment, the nucleic acid molecule includes a sequence encoding a chimeric polypeptide including: (a) a binding domain of IL-4; (b) a transmembrane domain of IL-9; and (c) an endodomain of an IL-9 receptor.

[0153] In one embodiment, the nucleic acid molecule includes a sequence encoding a chimeric polypeptide including: (a) a binding domain of IL-15Ra; (b) a transmembrane domain of IL-9; and (c) an endodomain of an IL-9 receptor.

[0154] In one embodiment, the nucleic acid molecule includes a sequence encoding a chimeric polypeptide including: (a) a binding domain of IL-10Ra; (b) a transmembrane domain of IL-9; and (c) an endodomain of an IL-9 receptor.

[0155] In some embodiments, provided herein is a nucleic acid molecule including a nucleotide sequence encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor; (b) a transmembrane domain; and (c) an intracellular portion comprising an endodomain of an IL-9 receptor linked to a BOX^{1/2} common gamma chain domain.

[0156] The orientation of the endodomain of the IL-9 receptor linked to a BOX^{1/2} common gamma chain domain may be altered depending upon desired structure and function. For example, the intracellular portion can comprise, in an N- to C-terminal direction, an endodomain of an IL-9 receptor, a linker, and a BOX^{1/2} common gamma chain domain. Alternatively, the intracellular portion can comprise, in an N- to C-terminal direction, a BOX^{1/2} common gamma chain domain, a linker, and an endodomain of an IL-9 receptor.

[0157] In one embodiment, the nucleic acid molecule includes a sequence encoding a chimeric polypeptide including: (a) a binding domain of Fas; (b) a transmembrane domain of IL-9; and (c) an endodomain of an IL-9 receptor linked to a BOX^{1/2} common gamma chain domain.

[0158] In some embodiments, provided herein is a nucleic acid molecule including a nucleotide sequence encoding a chimeric polypeptide including: (a) an extracellular portion comprising a binding domain of an endogenous inhibitory receptor linked to an agent specific for the common gamma chain; (b) a transmembrane domain; and (c) an intracellular portion comprising an endodomain of an IL-9 receptor.

[0159] The orientation of the extracellular portion comprising a binding domain of an endogenous inhibitory receptor linked to an agent specific for the common gamma chain may be altered depending upon desired structure and function. For example, the extracellular portion can comprise, in an N- to C-terminal direction, a binding domain of an endogenous inhibitory receptor, a linker, and an agent specific for the common gamma chain. Alternatively, the extracellular portion can comprise, in an N- to C-terminal direction, an agent specific for the common gamma chain, a linker, and a binding domain of an endogenous inhibitory receptor.

[0160] In some embodiments, the nucleotide sequence is incorporated into an expression cassette or an expression vector. It will be understood that an expression cassette generally includes a construct of genetic material that contains coding sequences and enough regulatory information to direct proper transcription and/or translation of the coding sequences in a recipient cell, in vivo and/or ex vivo. Generally, the expression cassette may be inserted into a vector for targeting to a desired host cell and/or into a subject. As such, in some embodiments, an expression cassette of the disclosure include a coding sequence for the chimeric polypeptide as disclosed herein, which is operably linked to expression control elements, such as a promoter, and optionally, any or a combination of other nucleic acid sequences that affect the transcription or translation of the coding sequence.

[0161] In some embodiments, the nucleotide sequence is incorporated into a cloning vector or an expression vector. It will be understood by one skilled in the art that the term “vector” generally refers to a recombinant polynucleotide construct designed for transfer between host cells, and that may be used for the purpose of transformation, e.g., the introduction of heterologous DNA into a host cell. As such, in some embodiments, the vector can be a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. In some embodiments, the expression vector can be an integrating vector. In some embodiments, the nucleotide sequence is incorporated into a cloning vector.

[0162] As described above in relation to linkers, the nucleic acid sequence encoding a chimeric receptor as described herein can also encode a CAR. Each may each be provided on separate expression vectors, each nucleic acid sequence being operably linked to one or more expression control elements to achieve expression of the CAR and chimeric receptor in the target cell, the vectors being co-transfected into the target cell. Alternatively, the nucleic acid sequences encoding the CAR and the chimeric receptor may each be provided on a single vector each nucleic acid sequence under the control of one or more expression control elements to achieve expression of the associated nucleic acid sequence. Alternatively, both nucleic acid sequences may be under the control of a single promoter with intervening or downstream control elements that facilitate co-expression of the two sequences from the vector.

[0163] In some embodiments, the expression vector can be a viral vector. As will be appreciated by one of skill in the art, the term “viral vector” is widely used to refer either to a nucleic acid molecule (e.g., a transfer plasmid) that includes virus-derived nucleic acid elements that generally facilitate transfer of the nucleic acid molecule or integration into the genome of a cell or to a viral particle that mediates nucleic acid transfer. Viral particles will generally include various viral components and sometimes also host cell components in addition to nucleic acid(s). The term viral vector may refer either to a virus or viral particle capable of transferring a nucleic acid into a cell or to the transferred nucleic acid itself. Viral vectors and transfer plasmids contain structural and/or functional genetic elements that are primarily derived from a virus. The term “retroviral vector” refers to a viral vector or plasmid containing structural and functional genetic elements, or portions thereof, that are primarily derived from a retrovirus. The term “lentiviral vector” refers to a viral vector or plasmid containing structural and functional genetic elements, or portions thereof, including LTRs that are primarily derived from a lentivirus, which is a genus of retrovirus.

[0164] In some embodiments, provided herein are nucleic acid molecules encoding a polypeptide with an amino acid sequence having at least about 80%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a chimeric receptor disclosed herein. In some embodiments, provided herein are nucleic acid molecules encoding a polypeptide with an amino acid sequence having at least about 80%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOS: 63-203 as identified in the Sequence Listing.

[0165] The nucleic acid sequences encoding the chimeric receptors can be optimized for expression in the host cell of interest. For example, the G-C content of the sequence can be adjusted to average levels for a given cell, as calculated by reference to known genes expressed in the host cell. Methods for codon usage optimization are known in the art. Codon usages within the coding sequence of the chimeric receptor disclosed herein can be optimized to enhance expression in the host cell, such that about 1%, about 5%, about 10%, about 25%, about 50%, about 75%, or up to 100% of the codons within the coding sequence have been optimized for expression in a particular host cell.

[0166] Some embodiments disclosed herein relate to vectors or expression cassettes including a recombinant nucleic acid molecule encoding the chimeric receptors disclosed herein. The expression cassette generally contains coding

sequences and sufficient regulatory information to direct proper transcription and/or translation of the coding sequences in a recipient cell, in vivo and/or ex vivo. The expression cassette may be inserted into a vector for targeting to a desired host cell and/or into a subject. An expression cassette can be inserted into a plasmid, cosmid, virus, autonomously replicating polynucleotide molecule, phage, as a linear or circular, single-stranded or double-stranded, DNA or RNA polynucleotide molecule, derived from any source, capable of genomic integration or autonomous replication, including a nucleic acid molecule where one or more nucleic acid sequences has been linked in a functionally operative manner, i.e., operably linked.

[0167] Also provided herein are vectors, plasmids, or viruses containing one or more of the nucleic acid molecules encoding a chimeric receptor disclosed herein. The nucleic acid molecules can be contained within a vector that is capable of directing their expression in, for example, a cell that has been transformed/transduced with the vector. Suitable vectors for use in eukaryotic and prokaryotic cells are known in the art and are commercially available, or readily prepared by a skilled artisan. See for example, Sambrook, J., & Russell, D. W. (2012). *Molecular Cloning: A Laboratory Manual* (4th ed.). Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory and Sambrook, J., & Russell, D. W. (2001). *Molecular Cloning: A Laboratory Manual* (3rd ed.). Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory (jointly referred to herein as “Sambrook”); Ausubel, F. M. (1987). *Current Protocols in Molecular Biology*. New York, N.Y.: Wiley (including supplements through 2014); Bollag, D. M. et al. (1996). *Protein Methods*. New York, N.Y.: Wiley-Liss; Huang, L. et al. (2005). *Nonviral Vectors for Gene Therapy*. San Diego: Academic Press; Kaplitt, M. G. et al. (1995). *Viral Vectors: Gene Therapy and Neuroscience Applications*. San Diego, Calif.: Academic Press; Lefkowitz, I. (1997). *The Immunology Methods Manual: The Comprehensive Sourcebook of Techniques*. San Diego, Calif.: Academic Press; Doyle, A. et al. (1998). *Cell and Tissue Culture: Laboratory Procedures in Biotechnology*. New York, N.Y.: Wiley; Mullis, K. B., Ferré, F. & Gibbs, R. (1994). *PCR: The Polymerase Chain Reaction*. Boston: Birkhauser Publisher; Greenfield, E. A. (2014). *Antibodies: A Laboratory Manual* (2nd ed.). New York, N.Y.: Cold Spring Harbor Laboratory Press; Beaucage, S. L. et al. (2000). *Current Protocols in Nucleic Acid Chemistry*. New York, N.Y.: Wiley, (including supplements through 2014); and Makrides, S. C. (2003). *Gene Transfer and Expression in Mammalian Cells*. Amsterdam, NL: Elsevier Sciences B.V., the disclosures of which are incorporated herein by reference).

[0168] DNA vectors can be introduced into eukaryotic cells via conventional transformation or transfection techniques. Suitable methods for transforming or transfecting host cells can be found in Sambrook et al. (2012, supra) and other standard molecular biology laboratory manuals, such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction, nucleoporation, hydrodynamic shock, and infection.

[0169] Viral vectors that can be used in the disclosure include, for example, retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, lentivirus vectors, herpes virus, simian virus 40 (SV40), and bovine papilloma

virus vectors (see, for example, Gluzman (Ed.), *Eukaryotic Viral Vectors*, CSH Laboratory Press, Cold Spring Harbor, N.Y.). For example, a chimeric receptor as disclosed herein can be produced in a eukaryotic host, such as a mammalian cells (e.g., COS cells, NIH 3T3 cells, or HeLa cells). These cells are available from many sources, including the American Type Culture Collection (Manassas, Va.). In selecting an expression system, care should be taken to ensure that the components are compatible with one another. Artisans of ordinary skill are able to select and design expression systems suitable and functional in a selected engineered cell. If further guidance is required in selecting an expression system, skilled artisans may consult P. Jones, "Vectors: Cloning Applications", John Wiley and Sons, New York, N.Y., 2009).

[0170] The nucleic acid molecules provided can contain naturally occurring sequences, or sequences that differ from those that occur naturally, but, due to the degeneracy of the genetic code, encode the same polypeptide, e.g., antibody. These nucleic acid molecules can consist of RNA or DNA (for example, genomic DNA, cDNA, or synthetic DNA, such as that produced by phosphoramidite-based synthesis), or combinations or modifications of the nucleotides within these types of nucleic acids. In addition, the nucleic acid molecules can be double-stranded or single-stranded (e.g., either a sense or an antisense strand).

Recombinant Cells and Cell Cultures

[0171] The nucleic acid of the present disclosure can be introduced into a host cell, such as, for example, a human T lymphocyte, to produce a host cell containing the recombinant nucleic acid molecule. Accordingly, some embodiments of the disclosure relate to methods for making a host cell, including (a) providing a cell capable of protein expression and (b) contacting the provided cell with a recombinant nucleic acid of the disclosure.

[0172] Introduction of the nucleic acid molecules of the disclosure into cells can be achieved by methods known to those skilled in the art such as, for example, viral infection, transfection, conjugation, protoplast fusion, lipofection, electroporation, nucleofection, calcium phosphate precipitation, polyethyleneimine (PEI)-mediated transfection, DEAE-dextran mediated transfection, liposome-mediated transfection, particle gun technology, calcium phosphate precipitation, direct micro-injection, nanoparticle-mediated nucleic acid delivery, and the like.

[0173] Accordingly, in some embodiments, the nucleic acid molecules can be delivered by viral or non-viral delivery vehicles known in the art. For example, the nucleic acid molecule can be stably integrated in the host genome, or can be episomally replicating, or present in the recombinant cell as a mini-circle expression vector for transient expression. Accordingly, in some embodiments, the nucleic acid molecule is maintained and replicated in the recombinant cell as an episomal unit. In some embodiments, the nucleic acid molecule is stably integrated into the genome of the recombinant cell. Stable integration can be achieved using classical random genomic recombination techniques or with more precise techniques such as guide RNA-directed CRISPR/Cas9 genome editing, or DNA-guided endonuclease genome editing with NgAgo (*Natronobacterium gregoryi* Argonaute), or TALENs genome editing (transcription activator-like effector nucleases). In some embodiments, the nucleic

acid molecule is present in the recombinant cell as a mini-circle expression vector for transient expression.

[0174] The nucleic acid molecules can be encapsulated in a viral capsid or a lipid nanoparticle, or can be delivered by viral or non-viral delivery means and methods known in the art, such as electroporation. For example, introduction of nucleic acids into cells may be achieved by viral transduction. In a non-limiting example, adeno-associated virus (AAV) is engineered to deliver nucleic acids to target cells via viral transduction. Several AAV serotypes have been described, and all of the known serotypes can infect cells from multiple diverse tissue types. AAV is capable of transducing a wide range of species and tissues in vivo with no evidence of toxicity, and it generates relatively mild innate and adaptive immune responses.

[0175] Lentiviral-derived vector systems are also useful for nucleic acid delivery and gene therapy via viral transduction. Lentiviral vectors offer several attractive properties as gene-delivery vehicles, including: (i) sustained gene delivery through stable vector integration into host genome; (ii) the capability of infecting both dividing and non-dividing cells; (iii) broad tissue tropisms, including important gene- and cell-therapy-target cell types; (iv) no expression of viral proteins after vector transduction; (v) the ability to deliver complex genetic elements, such as polycistronic or intron-containing sequences; (vi) a potentially safer integration site profile; and (vii) a relatively easy system for vector manipulation and production.

[0176] In some embodiments, host cells can be genetically engineered (e.g., transduced or transformed or transfected) with, for example, a vector construct of the present application that can be, for example, a viral vector or a vector for homologous recombination that includes nucleic acid sequences homologous to a portion of the genome of the host cell, or can be an expression vector for the expression of the polypeptides of interest. These cells can be either untransformed cells or cells that have already been transfected with at least one nucleic acid molecule.

[0177] In some embodiments, the recombinant cell is a prokaryotic cell or a eukaryotic cell. In some embodiments, the cell is in vivo. In some embodiments, the cell is ex vivo. In some embodiments, the cell is in vitro. In some embodiments, the recombinant cell is a prokaryotic cell including a recombinant nucleic acid as disclosed herein. In some embodiments, the recombinant prokaryotic cell includes a recombinant nucleic acid which is a cloning vector. In some embodiments, the recombinant cell is a eukaryotic cell. In some embodiments, the recombinant cell is an animal cell. In some embodiments, the animal cell is a mammalian cell. In some embodiments, the animal cell is a human cell. In some embodiments, the cell is a non-human primate cell. In some embodiments, the mammalian cell is an immune cell, a neuron, an epithelial cell, and endothelial cell, or a stem cell. In some embodiments, the recombinant cell is an immune system cell, e.g., a lymphocyte (e.g., a T cell or NK cell), or a dendritic cell. In some embodiments, the immune cell is a B cell, a monocyte, a natural killer (NK) cell, a basophil, an eosinophil, a neutrophil, a dendritic cell, a macrophage, a regulatory T cell, a helper T cell (T_H), a cytotoxic T cell (T_{CTL}), or other T cell. In some embodiments, the immune system cell is a T lymphocyte.

[0178] In some embodiments, the cell is a stem cell. In some embodiments, the cell is a hematopoietic stem cell. In some embodiments of the cell, the cell is a lymphocyte. In

some embodiments, the cell is a precursor T cell or a T regulatory (Treg) cell. In some embodiments, the cell is a CD34+, CD8+, or a CD4+ cell. In some embodiments, the cell is a CD8+T cytotoxic lymphocyte cell selected from the group consisting of naïve CD8+ T cells, central memory CD8+ T cells, effector memory CD8+ T cells, and bulk CD8+ T cells. In some embodiments of the cell, the cell is a CD4+T helper lymphocyte cell selected from the group consisting of naïve CD4+ T cells, central memory CD4+ T cells, effector memory CD4+ T cells, and bulk CD4+ T cells. In some embodiments, the cell can be obtained by leukapheresis performed on a sample obtained from a subject. In some embodiments, the subject is a human patient.

[0179] In one embodiment, the cell expressing the recombinant nucleic acid molecule described herein is a T-cell which has been modified to surface express a chimeric antigen receptor (a 'CAR-T' cell). As used herein, a CAR-T cell may be engineered to express a chimeric receptor of the present disclosure. CARs useful in the practice of the present disclosure can be prepared in accordance with principles well known in the art. See e.g., Eshhaar et al. U.S. Pat. No. 7,741,465 B1 issued Jun. 22, 2010; Sadelain, et al (2013) *Cancer Discovery* 3(4):388-398; Jensen and Riddell (2015) *Current Opinions in Immunology* 33:9-15; Gross, et al. (1989) *PNAS(USA)* 86(24): 10024-10028; Curran, et al. (2012) *J Gene Med* 14(6): 405-15. Examples of commercially available CAR-T cell products that may be modified to incorporate a chimeric receptor of the present disclosure include axicabtagene ciloleucel (marketed as Yescarta® commercially available from Gilead Pharmaceuticals) and tisagenlecleucel (marketed as Kymriah® commercially available from Novartis).

[0180] In some embodiments, the recombinant cell further includes a first and a second nucleic acid molecule as disclosed herein, wherein the first nucleic acid molecule and the second nucleic acid molecule do not have the same sequence. In some embodiments, the recombinant cell further includes a first and a second chimeric polypeptide as disclosed herein, wherein the first chimeric polypeptide and the second chimeric polypeptide do not have the same sequence. In some embodiments, the first second chimeric polypeptide is a CAR. In some embodiments, the first chimeric polypeptide modulates the expression and/or activity of the second chimeric polypeptide.

[0181] In some embodiments, the recombinant cell further includes an expression cassette or vector encoding a protein of interest operably linked to a promoter, wherein expression of the protein is modulated by the chimeric receptor's transcriptional effector. In some embodiments, the protein of interest is heterologous to the recombinant cell. In some embodiments, the heterologous protein is one that is not normally found in the cell, e.g., not normally produced by the cell. In some embodiments, the expression vector encodes a copy of a protein that is already present in the cell. Exemplary types of proteins suitable for use with the compositions and methods disclosed herein include cytokines, cytotoxins, chemokines, immunomodulators, pro-apoptotic factors, anti-apoptotic factors, hormones, differentiation factors, dedifferentiation factors, immune cell receptors, or reporters.

[0182] In another aspect, provided herein are compositions of cells comprising an expression vector described herein. Cell cultures including at least one host cell as disclosed herein, and a culture medium are also con-

templated. Generally, the culture medium can be any suitable culture medium for culturing the cells described herein. Techniques for transforming a wide variety of the above-mentioned cells and species are known in the art and described in the technical and scientific literature. Accordingly, cell cultures including at least one recombinant cell as disclosed herein are also within the scope of this application. Methods and systems suitable for generating and maintaining cell cultures are known in the art.

Pharmaceutical Compositions

[0183] In some embodiments, the nucleic acids, host cells, and/or polypeptides (i.e., chimeric receptors) of the disclosure can be incorporated into compositions, including pharmaceutical compositions. Such compositions include one or more of the recombinant nucleic acids, host cells, and/or polypeptides (i.e., chimeric receptors) as disclosed herein. The composition can also contain a pharmaceutically acceptable excipient, e.g., a carrier.

[0184] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.), or phosphate buffered saline (PBS). In all cases, the composition should be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants, e.g., sodium dodecyl sulfate. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be generally to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[0185] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle, which contains a basic dispersion medium and the required other ingredients from those enumerated above.

[0186] In some embodiments, the chimeric receptors of the disclosure can also be administered by transfection or infection using methods known in the art, including but not limited to the methods described in McCaffrey et al. (*Nature* 418:6893, 2002), Xia et al. (*Nature Biotechnol.* 20:1006-10, 2002), or Putnam (*Am. J. Health Syst. Pharm.* 53:151-60, 1996, erratum at *Am. J. Health Syst. Pharm.* 53:325, 1996).

[0187] As described in greater detail below, in some embodiments, the host cells of the disclosure can be formulated for administration to a subject using techniques known to the skilled artisan. For example, formulations comprising populations of recombinant cells can include pharmaceutically acceptable excipient(s). Excipients included in the formulations will have different purposes depending, for example, on the recombinant cells used and the mode of administration. Examples of generally used excipients included, without limitation: saline, buffered saline, dextrose, water-for-injection, glycerol, ethanol, and combinations thereof, stabilizing agents, solubilizing agents and surfactants, buffers and preservatives, tonicity agents, bulking agents, and lubricating agents. The formulations comprising recombinant cells can have been prepared and cultured in the absence of non-human components, e.g., in the absence of animal serum. A formulation can include one population of recombinant cells, or more than one, such as two, three, four, five, six or more populations of recombinant cells.

[0188] Formulations comprising population(s) of recombinant cells can be administered to a subject using modes and techniques known to the skilled artisan. Exemplary modes include, but are not limited to, intravenous injection. Other modes include, without limitation, intratumoral, intradermal, subcutaneous (S.C., s.q., sub-Q, Hypo), intramuscular (i.m.), intraperitoneal (i.p.), intra-arterial, intramedullary, intracardiac, intra-articular (joint), intrasynovial (joint fluid area), intracranial, intraspinal, and intrathecal (spinal fluids). Devices useful for parenteral injection of infusion of the formulations can be used to effect such administration.

Methods of the Disclosure

Methods for Modulating an Activity of a Cell

[0189] In one aspect, provided herein are methods for modulating an activity of an immune cell. The methods involve administering, to an immune cell, the recombinant nucleic acid as described herein. One skilled in the art upon reading the present disclosure will appreciate that the disclosed methods can be carried out in vivo, ex vivo, or in vitro.

[0190] Non-limiting exemplary cellular activities that can be modulated using the methods provide herein include, but are not limited to, gene expression, proliferation, apoptosis, non-apoptotic death, differentiation, dedifferentiation, migration, secretion of a gene product, cellular adhesion, and cytolytic activity.

[0191] In some embodiments, the expression of a gene product of the cell is modulated.

[0192] In some embodiments, the gene product in the cell is selected from the group consisting of a chemokine, a chemokine receptor, a chimeric antigen receptor, a cytokine, a cytokine receptor, a differentiation factor, a growth factor, a growth factor receptor, a hormone, a metabolic enzyme, a pathogen-derived protein, a proliferation inducer, a receptor, an RNA guided nuclease, a site-specific nuclease, a T cell receptor (TCR) or a component thereof, a chimeric antigen receptor (CAR), a toxin, a toxin-derived protein, a transcriptional effector, a transcriptional activator, a transcriptional repressor, a translation regulator, a translational activator, a translational repressor, an activating immuno-receptor, an antibody, an apoptosis inhibitor, an apoptosis inducer, an

engineered T cell receptor, an immuno-activator, an immuno-inhibitor, and an inhibiting immuno-receptor.

[0193] In cases where expression of a chemokine or a cytokine is modulated, in some embodiments, the expression of cytokines and chemokines is modulated such that there is an increase in type-1 polarization following ligand stimulation relative to controls. Exemplary cytokine and chemokines that can be modulated include, without limitation, FGF2, GMCSF, IFN α , IFN γ , IL-10, IL-17, IL-12, IL-2, IL-3, IL-6, IP-10, MIP1 α , and RANTES.

[0194] Methods of measuring levels of cytokines and chemokines are known in the art. Levels of cytokines and chemokines can be measured, for example, by enzyme-linked immunosorbent assay (ELISA), bead based systems (e.g. Luminex), the Cytokine Bead Array (Pharmingen) and array-based systems (e.g., EMD Biosciences' ProteoPlex).

[0195] In some embodiments, the modulation of an activity of an immune cell can involve alteration of cell signaling events within the cell. As described herein, the IL-9 receptor endodomain signals through JAK1 and JAK3 to activate various developmental pathways including STAT1, STAT3, STAT5, MAPK, and PI3K/AKT pathways. Activation of STAT family members through ligand mediated phosphorylation is believed to confer advantages in effector function, polarization and proliferation to T cells. This, in some embodiments, administration of the recombinant nucleic acid encoding the chimeric switch receptor described herein induces phosphorylation of STAT1, STAT3, and/or STAT5 when stimulated with ligand. Methods for measuring the phosphorylation status of one or more proteins is known in the art and includes, for example, western blot and phospho flow cytometry as described in the Examples herein.

[0196] Cell death (e.g., apoptosis and non-apoptotic cell death) can also be modulated by the methods described herein. In some embodiments, administration of the recombinant nucleic acid encoding the chimeric switch receptor described herein can result in increased cell death of a target cell. By way of example, real-time cytotoxicity assays can be used to analyze whether or not cells expressing a chimeric switch receptor of the present disclosure show increased cytotoxicity when exposed to ligand. In some embodiments, cells expressing a chimeric switch receptor of the present disclosure demonstrate improved killing of target cells when stimulated with ligand over unstimulated controls.

Methods of Treatment

[0197] Administration of any one of the therapeutic compositions described herein, e.g., chimeric receptors, nucleic acids, host cells, and pharmaceutical compositions, can be used to treat patients for relevant diseases, such as cancers, autoimmune diseases, and infections. In some embodiments, the recombinant nucleic acids, host cells, and pharmaceutical compositions described herein can be incorporated into therapeutic agents for use in methods of treating or aiding in the treatment of a subject who has, who is suspected of having, or who may be at high risk for developing one or more diseases.

[0198] One aspect of the present disclosure is directed to a method of treating a subject that involves administering, to the subject, a chimeric switch receptor of the present disclosure or a cell expressing the recombinant nucleic acid of the present disclosure.

[0199] In one embodiment, the subject is treated for cancer. A cancer may be any unwanted cell proliferation (or any

disease manifesting itself by unwanted cell proliferation), neoplasm or tumor or increased risk of or predisposition to the unwanted cell proliferation, neoplasm or tumor. The cancer may be benign or malignant and may be primary or secondary (metastatic). A neoplasm or tumor may be any abnormal growth or proliferation of cells and may be located in any tissue. Examples of tissues include the adrenal gland, adrenal medulla, anus, appendix, bladder, blood, bone, bone marrow, brain, breast, cecum, central nervous system (including or excluding the brain) cerebellum, cervix, colon, duodenum, endometrium, epithelial cells (e.g. renal epithelia), gallbladder, oesophagus, glial cells, heart, ileum, jejunum, kidney, lacrimal gland, larynx, liver, lung, lymph, lymph node, lymphoblast, maxilla, mediastinum, mesentery, myometrium, nasopharynx, omentum, oral cavity, ovary, pancreas, parotid gland, peripheral nervous system, peritoneum, pleura, prostate, salivary gland, sigmoid colon, skin, small intestine, soft tissues, spleen, stomach, testis, thymus, thyroid gland, tongue, tonsil, trachea, uterus, vulva, white blood cells.

[0200] Tumors to be treated may be nervous or non-nervous system tumors. Nervous system tumors may originate either in the central or peripheral nervous system, e.g. glioma, medulloblastoma, meningioma, neurofibroma, ependymoma, Schwannoma, neurofibrosarcoma, astrocytoma and oligodendroglioma. Non-nervous system cancers/tumors may originate in any other non-nervous tissue, examples include melanoma, mesothelioma, lymphoma, myeloma, leukemia, Non-Hodgkin's lymphoma (NHL), Hodgkin's lymphoma, chronic myelogenous leukemia (CML), acute myeloid leukemia (AML), myelodysplastic syndrome (MDS), cutaneous T-cell lymphoma (CTCL), chronic lymphocytic leukemia (CLL), hepatoma, epidermoid carcinoma, prostate carcinoma, breast cancer, lung cancer, colon cancer, ovarian cancer, pancreatic cancer, thymic carcinoma, NSCLC, haematologic cancer and sarcoma. In particular, treatment of melanoma, kidney cancer (e.g. renal carcinoma) or bladder cancer is contemplated.

[0201] In some embodiments the cancer is an EBV or HPV positive cancer.

[0202] In one embodiment, the subject is treated for autoimmune disease. Exemplary autoimmune diseases include Crohn's disease and Multiple Sclerosis.

[0203] In one embodiment, the subject is treated for infection. An infection may be any infection or infectious disease, e.g. bacterial, viral, fungal, or parasitic infection. In some embodiments it may be particularly desirable to treat chronic/persistent infections, e.g. where such infections are associated with T cell dysfunction or T cell exhaustion. It is well established that T cell exhaustion is a state of T cell dysfunction that arises during many chronic infections (including viral, bacterial and parasitic), as well as in cancer (Wherry Nature Immunology Vol. 12, No. 6, p 492-499, June 2011).

[0204] Examples of bacterial infections that may be treated include infection by *Bacillus* spp., *Bordetella pertussis*, *Clostridium* spp., *Corynebacterium* spp., *Vibrio* cholerae, *Staphylococcus* spp., *Streptococcus* spp., *Escherichia*, *Klebsiella*, *Proteus*, *Yersinia*, *Erwinia*, *Salmonella*, *Listeria* sp, *Helicobacter pylori*, mycobacteria (e.g. *Mycobacterium tuberculosis*) and *Pseudomonas aeruginosa*. For example, the bacterial infection may be sepsis or tuberculosis. Examples of viral infections that may be treated include infection by Epstein-Barr virus, influenza virus, measles

virus, hepatitis B virus (HBV), hepatitis C virus (HCV), human immunodeficiency virus (HIV), lymphocytic choriomeningitis virus (LCMV), Herpes simplex virus and human papilloma virus.

[0205] Examples of fungal infections that may be treated include infection by *Alternaria* sp, *Aspergillus* sp, *Candida* sp and *Histoplasma* sp. The fungal infection may be fungal sepsis or histoplasmosis. Examples of parasitic infections that may be treated include infection by *Plasmodium* species (e.g. *Plasmodium falciparum*, *Plasmodium yoeli*, *Plasmodium ovale*, *Plasmodium vivax*, or *Plasmodium chabaudi*). The parasitic infection may be a disease such as malaria, leishmaniasis and toxoplasmosis

Administration of Recombinant Cells to a Subject

[0206] In some embodiments, the methods of the disclosure involve administering an effective amount or number of the recombinant cells to a subject in need of such treatment. This administering step can be accomplished using any method of implantation delivery in the art. For example, the recombinant cells can be infused directly in the subject's bloodstream or otherwise administered to the subject.

[0207] In some embodiments, the methods disclosed herein include administering, which term is used interchangeably with the terms "introducing", "implanting", and "transplanting", recombinant cells into a subject, by a method or route that results in at least partial localization of the introduced cells at a desired site such that a desired effect(s) is/are produced. The recombinant cells or their differentiated progeny can be administered by any appropriate route that results in delivery to a desired location in the subject where at least a portion of the administered cells or components of the cells remain viable. The period of viability of the cells after administration to a subject can be as short as a few hours, e.g., twenty-four hours, to a few days, to as long as several years, or even the lifetime of the subject, i.e., long-term engraftment.

[0208] When provided prophylactically, the recombinant cells described herein can be administered to a subject in advance of a symptom of a disease or condition to be treated. Accordingly, in some embodiments the prophylactic administration of a recombinant cell population prevents the occurrence of symptoms of the disease or condition.

[0209] When provided therapeutically in some embodiments, recombinant cells are provided at (or after) the onset of a symptom or indication of a disease or condition, e.g., upon the onset of disease or condition.

[0210] For use in the various embodiments described herein, an effective amount of recombinant cells as disclosed herein, can be at least 10^2 cells, at least 5×10^2 cells, at least 10^3 cells, at least 5×10^3 cells, at least 10^4 cells, at least 5×10^4 cells, at least 10^5 cells, at least 2×10^5 cells, at least 3×10^5 cells, at least 4×10^5 cells, at least 5×10^5 cells, at least 6×10^5 cells, at least 7×10^5 cells, at least 8×10^5 cells, at least 9×10^5 cells, at least 1×10^6 cells, at least 2×10^6 cells, at least 3×10^6 cells, at least 4×10^6 cells, at least 5×10^6 cells, at least 6×10^6 cells, at least 7×10^6 cells, at least 8×10^6 cells, at least 9×10^6 cells, or multiples thereof. The recombinant cells can be derived from one or more donors or can be obtained from an autologous source. In some embodiments, the recombinant cells are expanded in culture prior to administration to a subject in need thereof.

[0211] In some embodiments, the delivery of a recombinant cell composition (e.g., a composition including a plu-

rality of recombinant cells according to any of the cells described herein) into a subject by a method or route results in at least partial localization of the cell composition at a desired site. A composition including recombinant cells can be administered by any appropriate route that results in effective treatment in the subject, e.g., administration results in delivery to a desired location in the subject where at least a portion of the composition delivered, e.g., at least 1×10^4 cells, is delivered to the desired site for a period of time. Modes of administration include injection, infusion, instillation. “Injection” includes, without limitation, intravenous, intramuscular, intra-arterial, intrathecal, intraventricular, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intra-articular, subcapsular, subarachnoid, intraspinal, intracerebrospinal, and intrasternal injection and infusion. In some embodiments, the route is intravenous. For the delivery of cells, delivery by injection or infusion is a standard mode of administration.

[0212] In some embodiments, the recombinant cells are administered systemically, e.g., via infusion or injection. For example, a population of recombinant cells are administered other than directly into a target site, tissue, or organ, such that it enters the subject’s circulatory system and, thus, is subject to metabolism and other similar biological processes.

[0213] The efficacy of a treatment including any of the compositions provided herein for the treatment of a disease or condition can be determined by a skilled clinician. However, one skilled in the art will appreciate that a treatment is considered effective if any one or all of the signs or symptoms or markers of disease are improved or ameliorated. Efficacy can also be measured by failure of a subject to worsen as assessed by decreased hospitalization or need for medical interventions (e.g., progression of the disease is halted or at least slowed). Methods of measuring these indicators are known to those of skill in the art and/or described herein. Treatment includes any treatment of a disease in a subject or an animal (some non-limiting examples include a human, or a mammal) and includes: (1) inhibiting the disease, e.g., arresting, or slowing the progression of symptoms; or (2) relieving the disease, e.g., causing regression of symptoms; and (3) preventing or reducing the likelihood of the development of symptoms.

[0214] In some embodiments of the disclosed methods, the subject is a mammal. In some embodiments, the mammal is a human.

Additional Therapies

[0215] As discussed above, the recombinant cells, and pharmaceutical compositions described herein can be administered in combination with one or more additional therapeutic agents such as, for example, chemotherapeutics or anti-cancer agents or anti-cancer therapies. Administration “in combination with” one or more additional therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order. In some embodiments, the one or more additional therapeutic agents, chemotherapeutics, anti-cancer agents, or anti-cancer therapies is selected from the group consisting of chemotherapy, radiotherapy, immunotherapy, hormonal therapy, toxin therapy, and surgery. “Chemotherapy” and “anti-cancer agent” are used interchangeably herein. Various classes of anti-cancer agents can be used. Non-limiting examples include: alkyl-

ating agents, antimetabolites, anthracyclines, plant alkaloids, topoisomerase inhibitors, podophyllotoxin, antibodies (e.g., monoclonal or polyclonal), tyrosine kinase inhibitors (e.g., imatinib mesylate (Gleevec® or Glivec®)), hormone treatments, soluble receptors and other antineoplastics.

[0216] Accordingly, in some embodiments, the disclosed treatment methods further include administering to the subject a second therapy. Generally, the second therapy can be any therapy known in the art. Non-limiting examples of therapies suitable for use in combination with the therapeutic compositions disclosed herein include chemotherapy, radiotherapy, immunotherapy, hormonal therapy, toxin therapy, and surgery. In some embodiments, the second therapy includes one or more additional therapeutic agents such as, for example, chemotherapeutics or anti-cancer agents or anti-cancer therapies. In some embodiments, the first therapy and the second therapy are administered together in the same composition. In some embodiments, the first therapy and the second therapy are administered in separate compositions. In some embodiments, the first therapy and the second therapy are administered at the same time. In some embodiments, the first therapy and the second therapy are administered sequentially. In some embodiments, the first therapy is administered before the second therapy. In some embodiments, the first therapy is administered after the second therapy. In some embodiments, the first therapy and the second therapy are administered in rotation.

Systems and Kits

[0217] Also provided herein are kits including the recombinant nucleic acids, recombinant cells, or pharmaceutical compositions provided and described herein as well as written instructions for making and using the same. For example, provided herein, in some embodiments, are kits that include one or more of the following: (i) a recombinant nucleic acids as described herein, (ii) a recombinant cell as described herein, and (iii) a pharmaceutical composition as described herein. In some embodiments, the systems and/or kits of the disclosure further include one or more syringes (including pre-filled syringes) and/or catheters (including pre-filled syringes) used to administer one any of the provided recombinant nucleic acids, recombinant cells, or pharmaceutical compositions to a subject. In some embodiments, a kit can have one or more additional therapeutic agents that can be administered simultaneously or sequentially with the other kit components for a desired purpose, e.g., for modulating an activity of a cell, inhibiting a target cancer cell, or treating a disease in a subject in need thereof.

[0218] Any of the above-described systems and kits can further include one or more additional reagents, where such additional reagents can be selected from: dilution buffers; reconstitution solutions, wash buffers, control reagents, control expression vectors, negative control polypeptides, positive control polypeptides, reagents for in vitro production of the chimeric receptor polypeptides.

[0219] In some embodiments, a system or kit can further include instructions for using the components of the kit to practice the methods. The instructions for practicing the methods are generally recorded on a suitable recording medium. For example, the instructions can be printed on a substrate, such as paper or plastic, etc. The instructions can be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (i.e., associ-

ated with the packaging or sub-packaging), etc. The instructions can be present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, flash drive, etc. In some instances, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source (e.g., via the internet), are provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded. As with the instructions, this means for obtaining the instructions can be recorded on a suitable substrate.

[0220] No admission is made that any reference cited herein constitutes prior art. The discussion of the references states what their authors assert, and the inventors reserve the right to challenge the accuracy and pertinence of the cited documents. It will be clearly understood that, although a number of information sources, including scientific journal articles, patent documents, and textbooks, are referred to herein; this reference does not constitute an admission that any of these documents forms part of the common general knowledge in the art.

[0221] The discussion of the general methods given herein is intended for illustrative purposes only. Other alternative methods and alternatives will be apparent to those of skill in the art upon review of this disclosure, and are to be included within the spirit and purview of this application.

[0222] Throughout this specification, various patents, patent applications and other types of publications (e.g., journal articles, electronic database entries, etc.) are referenced. The disclosure of all patents, patent applications, and other publications cited herein are hereby incorporated by reference in their entirety to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

EXAMPLES

[0223] The practice of the present disclosure will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, cell biology, biochemistry, nucleic acid chemistry, and immunology, which are well known to those skilled in the art. Such techniques are explained fully in the literature cited above.

[0224] Additional embodiments are disclosed in further detail in the following examples, which are provided by way of illustration and are not in any way intended to limit the scope of this disclosure or the claims.

Example 1

[0225] Cloning of chimeric receptors. DNA encoding the binding domains of IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, IL-21ra, TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, VEGF; the transmembrane domains of IL-9, IL-7ra and IL-2rb; the endodomain of the IL-9 receptor; the BOX 1/2 common gamma chain domain; and an agent specific for the common gamma chain are cloned, in various configurations, into mammalian expression vectors driven by a CMV or elongation factor (EF)-1 promoter. The vector contains a mammalian selection cassette.

[0226] Similarly, DNA encoding the binding domains of IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, IL-21ra, TGF-beta R1, TGF-beta R2, IL-10ra, FAS, CTLA4, LAG3, TIM3, PD1, ILT2, ILT3, ILT4, ILT5, VEGF; the transmembrane

domains of IL-9, IL-7ra and IL-2rb; the endodomain of the IL-9 receptor; the BOX 1/2 common gamma chain domain; and an agent specific for the common gamma chain are cloned, in various configurations, into lentiviral vectors.

Example 2

[0227] Lentivirus expression. Lentivirus is produced as previously described in [Tiscornia G. et al. Nature Protocols 27 Jun. 2006; doi: 10.1038/nprot.2006.37].

Example 3

[0228] Assessment of surface expression of chimeric receptors. Mammalian expression constructs encoding for chimeric receptors are transfected into 293 cells using methods well known in the art such as lipofection 2000 (Invitrogen) or electroporation. 24 to 48 hours later, cell surface expression is assessed by flow cytometry using fluorescently labeled antibodies specific for the ectodomains chimeric receptors. An example would be FITC labeled anti-IL4R antibody for 293 cells transduced with construct 73.

[0229] Alternatively, Jurkat T cell are transduced with purified lentivirus expressing the chimeric receptors of interest at an MOI of 20. 24 to 48 hours later, cell surface expression is assessed by flow cytometry using fluorescently labeled antibodies specific for the ectodomains chimeric receptors.

Example 4

[0230] Ligand stimulation and STAT5 activation. Transfected 293 cells and virally transduced Jurkat T cells are stimulated with individual ligands to analyze the ability of the ligands to bind the chimeric receptors and induce STAT5 activation. Briefly, after stimulation with ligand for various time points, cells are lysed and protein is collected. The phosphorylation status of STAT5 is analyzed by Western Blot using phosphor STAT5 specific antibodies and assessed relative to a negative control comprising an empty vector. STAT5 phosphorylation status of ligand activated cells relative to empty vector controls is also assessed by flow cytometry as previously described. (<http://rhlcflow.facilities.northwestern.edu/files/2011/09/intracellular-phospho-protein-staining.pdf>)

Example 5

[0231] STAT5 reporter assay. STAT5 reporter assays are done in 293 cells for activated JAK1-3 induced activity. Cells are seeded in a 48 well plate. The next day, cells are transfected by Lipofectamine 2000 (Invitrogen) with the STAT5-Luciferase vector and an internal control plasmid together with other plasmids expressing genes of interest. 24 hours later, the cells are stimulated with appropriate ligand for various time points, then lysed and subjected to internal control fluorescence and luciferase luminescence measurement using a plate reader. The reporter gene activity is shown after being normalized against internal control readings.

Example 6

[0232] Ligand stimulation and cytokine expression. Jurkat T cell are transduced with purified lentivirus expressing the chimeric receptors of interest. 24 to 48 hours later, cells are

stimulated with appropriate ligands for various time points from 0, 15, 30 45 and 60 minutes. Cells are then collected for analysis of expression of IFN γ , IL-4, IL-5, IP-10, IL-2, MIP1 α , MIP1 β , and TNF α using intracellular flow cytometry. Supernatants from the culture are collected analyzed for the expression of 30 cytokines and chemokines (Thermo Fisher) (<https://www.thermofisher.com/order/catalog/product/LHC6003M#/LHC6003M>) by Luminex analysis.

Example 7

[0233] Cytotoxicity Assays. The ability of the recombinant nucleic acids described herein to stimulate CTL cytotoxicity can be measured by methods known to the skilled person. Cytotoxicity of a T cell to a given target cell can be investigated, for example, using any of the methods reviewed in Zaritskaya et al. Expert Rev Vaccines (2011), 9(6):601-616, hereby incorporated by reference in its entirety. Additionally, the ability of the chimeric cytokine receptor to enhanced cell killing of a GPC3 CAR is assessed by measuring cellular killing of cell line targets in real time by electrical impedance as described in (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5834184/>). GPC3 CAR (scFv-41BB-CD3) expressing Lentivirus will be purchased from Creative Biolabs (CAR-M0158-YC) and used to transduce T cells. Briefly, T cells will be isolated from the PBMC fraction of peripheral blood by negative selection. Cells will be stimulated with TransAct (Miltenyi) for 72 hours in the presence of IL-2 prior to Lentiviral transduction. Cells will be incubated for 48 hours and CAR expressing cells sorted by FACS. The CAR positive fraction will then be transduced with the chimeric cytokine receptor constructs. Cell surface expression of the chimeric cytokine receptor will be assessed 48 hours post transduction, by flow cytometry. Cells will be stimulated with the appropriate ligand for an additional 48 hours, washed and cultured with HEPG2 target cells on XCelligence plates (<https://www.agilent.com/en/product/cell-analysis/real-time-cell-analysis/rtca-analyzers/xcelligence-rtca-mp-multiple-plates-741230>). Transduced T cells and target cells will be cocultured for 96 hours. Target killing will be measured in real time according to the manufacturer's protocol.

Example 8

Materials and Methods for Examples 9-12

[0234] Cloning of chimeric receptors. DNA encoding the binding domains of various endogenous cytokine and inhibitory receptors; the transmembrane domains of IL-9 or TNFR1; the endodomain of the IL-9 receptor; and/or the BOX 1/2 common gamma chain domain; were cloned, in various configurations, into pTRPE backbone lentiviral transfer plasmid. Some receptors were co-expressed with anti-HER2 CAR (4D5) via a 2A linker sequence. The 4D5 amino acid sequence is as follows:

(SEQ ID NO: 204)
MDFQVQIFSLLISASVIMSRGDIQMTQSPSSLSASVGRVITITCRASQD
VNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSRSGTDFTLTISSL
QPEDFATYYCQOHYTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQL
VESGGGLVQPGGSLRLSCAASGFGNIKDTYIHWVRQAPGKGLEWVARIYPT

-continued

NGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGF
GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK
QPFMRPVQTYAMDVWGQGTLLVTVSSTTTPAPRPPTPAPTIASQPLSLRPE
ACRPAATQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNE
LNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSE
IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR*

[0235] Similarly, DNA encoding the binding domains of IL-21R, IL-15ra, IL-4ra, IL-10ra, IL-7ra, TWEAKR, CTLA4, TIM3, LAG3, PD1, DCR1, CD40, Fas, Dr4, TNFRSF1B, TGFBR2, TIGIT, 2B4; the transmembrane domains of IL-9 and TNFR1; the endodomain of the IL-9 receptor; the BOX 1/2 common gamma chain domain; were cloned, in various configurations, into lentiviral vectors.

[0236] Assessment of surface expression of chimeric receptors. Lentiviral transfer plasmids encoding for chimeric receptors were transfected into 293 cells using Lipofectamine 3000 and 500 ng of lentiviral expression plasmids. 24 hours later, cell surface expression was assessed by flow cytometry using fluorescently labeled antibodies specific for the ectodomains of the chimeric receptors. Expression of chimeric receptors on primary human T cells was measured by transducing primary human T cells with a dilution series of lentiviral supernatants and analyzed by flow cytometry 72 hours later.

[0237] Lentivirus. Lentiviruses for transduction of primary human CD3+ T cells were produced in 293T cells by lipofection (Lipofectamine 3000, Thermo Fisher Scientific) of transfer and packaging plasmids, and purified by ultracentrifugation. T cells activated with human CD3/CD28 Dynabeads (3:1 beads to cell ratio) in the presence of recombinant IL-7 and IL-15 were infected with lentiviruses one day after activation, de-beaded on Day 3, and expanded until Day 5.

[0238] Flow Cytometry. Flow cytometric detection of chimeric cytokine receptors and chimeric antigen receptors was performed by incubating lentivirally transduced primary human T cells with receptor-specific antibodies for 20 minutes in room temperature in the dark followed by acquisition of at least 10,000 events on FACSsymphony A3 flow cytometer (BD Biosciences). Data was analyzed with FlowJo software (BD Biosciences). Transiently transfected 293T cells were treated similarly to detect chimeric cytokine receptors and chimeric antigen receptors 24 hours after lipofection (Lipofectamine 3000, Thermo Fisher Scientific) of 500 ng of lentiviral expression plasmids.

[0239] pSTAT Detection. In phosphoflow experiments, transduced human T cells were stimulated by addition of ligands for 30 minutes at 37° C., and the reaction was terminated by fixation with 1.5% paraformaldehyde (PFA) for 15 min at room temperature with agitation. Cells were washed and permeabilized with ice-cold 100% methanol for 60 minutes on ice or stored at -80° C. overnight. Cells were washed with FACS buffer before staining with pSTAT antibodies (Thermo Fisher Scientific) for 1 h at 4° C. in the dark. Cells were washed and analyzed on FACSsymphony A3 flow cytometer. Data represent the mean fluorescence intensity (MFI).

[0240] xCELLigence Real-Time Cell Analysis. Tumor cell killing was assessed using the xCELLigence Real-Time Cell

Analysis (RTCA) Analyzer (Agilent). SKOV-3 human ovarian adenocarcinoma tumor cells were seeded on a 96-well xCELLigence E-Plate at 10,000 cells per well. Twenty-four hours later, transduced T cells with or without 48 hours of pre-incubation with ligands for switch receptors were added in triplicate at various effector-to-target ratios with or without continued ligand stimulation. At the end of the assay, supernatant from each experimental well of the E-Plate was harvested, centrifuged to remove debris, then immediately frozen at -80°C .

[0241] Cytokine Multiplex Analysis. Samples were analyzed for cytokines and chemokines using the Milliplex cytokine assay kit (Millipore) as per manufacturer's protocol. Briefly, samples were diluted 1:2.5 assay diluent buffer and loaded onto a Millipore Multiscreen BV 96-well filter plate. Serial dilutions of cytokine standards were prepared in parallel and added to the plate. Milliplex 42-Plex Cytokine beads were vortexed for 30 sec. and 25 μl was added to each well with culture supernatants. Samples were then incubated on a plate shaker at 600 rpm in the dark at room temperature for 2 hours. The plate was applied to a Millipore Multiscreen Vacuum Manifold, washed twice with 50 μl of assay buffer (PBS, pH7.4, 1% BSA, 0.05% Tween20, 0.05% sodium azide), and each well resuspended with 75 μl assay buffer. 25 μl of biotinylated Anti-Human Multi-Cytokine Reporter was added to each well. The plate was incubated on a plate

shaker at 600 rpm in the dark at room temperature for 1.5 hours. Streptavidin-Phycoerythrin was diluted 1:12.5 in assay buffer, and then 25 μl was added directly to each well. The plate was incubated on a plate shaker at 600 rpm in the dark at room temperature for 30 minutes. 25 μl of stop solution (0.2% (v/v) formaldehyde in PBS, pH 7.4) was added to each well and incubated at room temperature for 5 minutes. The plate was then applied to the vacuum manifold and each well resuspended in 125 μl assay buffer and shaken for 1 minute. Assay plate was then transferred to the Bio-Plex Luminex 200 XYP instrument for analysis. Cytokine concentrations were calculated using Bio-Plex Manager 6.2 software with a 5 parameter curve fitting algorithm applied for standard curve calculations.

Example 9

Chimeric Switch Receptors are Expressed on the Surface of Cells

[0242] In order to analyze whether the chimeric switch receptors were able to be correctly folded and expressed on the surface of cells, 293T cells were transiently transfected with lentiviral transfer plasmids encoding for the chimeric switch receptors. 24 hours later, cell surface expression was assessed by flow cytometry. The expression levels of various constructs are shown in Table 4 below.

TABLE 4

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	% expression transduced sample	% expression control sample	% positive cells	% double-positive cells
SEQ63 + CAR+	IL21R	IL9R	IL9R	N/A	45.4	0.031		45.369
SEQ72 + CAR+	IL4Ra	IL9R	IL9R	N/A	16.7	0.5		16.2
SEQ89 + CAR+	CTLA4	IL9R	IL9R	G ₄ S	28.8	0.72		28.08
SEQ90 + CAR+	CTLA4	IL9R	IL9R	QP	26.6	0.22		26.38
SEQ91	TIM3	IL9R	IL9R	G ₄ S	21.5	3.42	18.08	
SEQ93	LAG3	IL9R	IL9R	QP	1.33	0.13	1.2	
SEQ94	LAG3	IL9R	IL9R	G ₄ S	3.35	2.25	1.1	
SEQ95 + CAR+	PD1	IL9R	IL9R	G ₄ S	18.3	0.49		17.81
SEQ96 + CAR+	PD1	IL9R	IL9R	QP	12.2	0.21		11.99
SEQ109	DCR1	IL9R	IL9R	G ₄ S	26	11.2	14.8	
SEQ110	DCR1	IL9R	IL9R	QP	17.6	7.66	9.94	
SEQ111	CD40	IL9R	IL9R	G ₄ S	24	1.42	22.58	
SEQ112	CD40	IL9R	IL9R	QP	19.2	0.31	18.89	
SEQ113 + CAR+	Fas	IL9R	IL9R	G ₄ S	22.9	1.1		21.8
SEQ114 + CAR+	Fas	IL9R	IL9R	QP	24.9	1.03		23.87
SEQ115	DR4	IL9R	IL9R	G ₄ S	54.5	34.7	19.8	
SEQ116	DR4	IL9R	IL9R	QP	38.3	21.4	16.9	
SEQ123	TNFRSF1B	IL9R	IL9R	G ₄ S	44.9	1.59	43.31	
SEQ124	TNFRSF1B	IL9R	IL9R	QP	52.2	1.11	51.09	
SEQ153 + CAR+	IL10Ra	IL9R	IL9R	G ₄ S	19.2	0.68		18.52
SEQ155	TGFBR2	IL9R	IL9R	G ₄ S	6.22	0.45	5.77	
SEQ156	TGFBR2	IL9R	IL9R	QP	10.7	0.17	10.53	
SEQ159 + CAR+	TIGIT	IL9R	IL9R	G ₄ S	13.8	0.16		13.64
SEQ160 + CAR+	TIGIT	IL9R	IL9R	QP	19.9	0.023		19.877
SEQ165	2B4	IL9R	IL9R	G ₄ S	30.4	28.5	1.9	
SEQ166	2B4	IL9R	IL9R	QP	18.1	15.3	2.8	
SEQ187	DCR1	TNFR1	IL9R	G ₄ S	35.3	15.5	19.8	
SEQ188	DCR1	TNFR1	IL9R	QP	47	11.4	35.6	

TABLE 4-continued

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	% expression transduced sample	% expression control sample	% positive cells	% double-positive cells
SEQ189	CD40	TNFR1	IL9R	G ₄ S	31.1	1.03	30.07	
SEQ190	CD40	TNFR1	IL9R	QP	29	1.45	27.55	
SEQ193	DR4	TNFR1	IL9R	G ₄ S	65.8	45.3	20.5	
SEQ194	DR4	TNFR1	IL9R	QP	63.7	49.6	14.1	
SEQ200	TNFRSF1B	TNFR1	IL9R	G ₄ S	29.1	1.31	27.79	
SEQ201	TNFRSF1B	TNFR1	IL9R	QP	47.3	0.95	46.35	

[0243] As demonstrated by the data in Table 4, all constructs exhibited some level of cell surface expression in 293T cells. These results indicate that the constructs produced properly folded proteins capable of endocytic transport and resistant to general proteolysis.

[0244] Constructs that exhibited cell surface expression in 293T cells were then packaged in lentivirus and titered on human primary T cells. The expression analysis over transduced primary human T cells is show in Table 5 below

TABLE 5

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	Fold-dilution of lentivirus	% positive T cells	% double-positive T cells (average of duplicates)	% positive T cells in unstained T cells (average of duplicates)	% positive T cells in stained un-transduced T cells (endogenous expression)
SEQ63 + CAR+	IL21R	IL9R	IL9R	N/A	2		61	0.46	20.6
					6		39.85		
					18		28.4		
					54		14.8		
					162		4.725		
					486		0.845		
					1458		0.495		
SEQ66	IL15Ra	IL9R	IL9R	N/A	2	63.1		0.2	32.3
					6	60.6			
					18	33.85			
					54	40.6			
					162	39.6			
					486	38			
					1458	36			
SEQ69	IL7Ra	IL9R	IL9R	N/A	2	90.6		1.02	55.5
					6	83.4			
					18	77.25			
					54	66.6			
					162	60.45			
					486	54.4			
					1458	52.8			
SEQ72 + CAR+	IL4Ra	IL9R	IL9R	N/A	2		38.95	0.15	44.6
					6		29.85		
					18		18.1		
					54		10.8		
					162		7.01		
					486		2.915		
					1458		1.41		
SEQ89 + CAR+	CTLA4	IL9R	IL9R	G ₄ S	2		30	N/A	N/A
					6		18.45		
					18		9.895		
					54		3.97		
					162		1.355		
					486		0.635		
					1458		0.485		
SEQ90 + CAR+	CTLA4	IL9R	IL9R	QP	2		41.3	0.058	0.63
					6		31.5		
					18		20.05		
					54		12.6		
					162		3.06		
					486		1.255		
					1458		0.68		
SEQ91	TIM3	IL9R	IL9R	G ₄ S	2	83.4		1.71	88.4
					6	84.15			
					18	85.5			
					54	81.8			
					162	88.3			

TABLE 5-continued

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	Fold-dilution of lentivirus	% positive T cells	% double-positive T cells (average of duplicates)	% positive T cells in unstained T cells (average of duplicates)	% positive T cells in stained un-transduced T cells (endogenous expression)
SEQ95 + CAR+	PD1	IL9R	IL9R	G ₄ S	486	86.6			
					1458	77			
					4374	84.9			
					2		32.45	0.027	0.64
					6		18.75		
					18		14.45		
					54		6.965		
SEQ96 + CAR+	PD1	IL9R	IL9R	QP	162		2.43		
					486		1.19		
					1458		0.88		
					2		30.5	0.01	85.8
					6		25.1		
					18		12.85		
					54		9.4		
SEQ109	DCR1	IL9R	IL9R	G ₄ S	162		3.31		
					486		1.33		
					1458		0.645		
					2	77.8		0.033	0.7
					6	60.95			
					18	44.6			
					54	29.45			
SEQ110	DCR1	IL9R	IL9R	QP	162	13.4			
					486	4.285			
					1458	2.985			
					2	89.1		0.059	1.14
					6	74.9			
					18	49.65			
					54	28.9			
SEQ111	CD40	IL9R	IL9R	G ₄ S	162	15.6			
					486	10.755			
					1458	8.61			
					2	50.25		0.44	12.1
					6	48.2			
					18	38.1			
					54	40.25			
SEQ112	CD40	IL9R	IL9R	QP	162	21.8			
					486	9.285			
					1458	9.3			
					2	85.05		0.049	3.41
					6	78.2			
					18	62.4			
					54	39.1			
SEQ113 + CAR+	Fas	IL9R	IL9R	G ₄ S	162	31.75			
					486	13.65			
					1458	12.13			
					2		42.45	N/A	N/A
					6		17.3		
					18		8.735		
					54		4.84		
SEQ114 + CAR+	Fas	IL9R	IL9R	QP	162	2.05			
					486	0.98			
					1458	0.625			
					2	87.15		0.34	98.1
					6	81.25			
					18	71.4			
					54	54.15			
SEQ116	DR4	IL9R	IL9R	QP	162	30			
					486	13			
					1458	4.52			
					2	93.1		0.2	33.9
					6	87.85			
					18	77.75			
					54	63.8			
SEQ123	TNFRSF1B	IL9R	IL9R	G ₄ S	162	50.1			
					486	39			
					1458	34.6			
					2	90.9		0.019	68.5
					6	86.45			
					18	77.85			

TABLE 5-continued

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	Fold-dilution of lentivirus	% positive T cells	% double-positive T cells (average of duplicates)	% positive T cells in unstained T cells (average of duplicates)	% positive T cells in stained un-transduced T cells (endogenous expression)
SEQ124	TNFRSF1B	IL9R	IL9R	QP	54	57.75			
					162	78			
					486	72.45			
					1458	72.5			
					2	81.05		0.086	72.7
					6	78.25			
					18	70			
					54	70.75			
					162	71.9			
					486	73.6			
SEQ154 + CAR+	IL10Ra	IL9R	IL9R	QP	1458	71.65			
					2		28.2	0.33	1.34
					6		22.4		
					18		10.9		
					54		4.49		
					162		1.635		
SEQ155	TGFBFR2	IL9R	IL9R	G ₄ S	486		1.055		
					1458		1.075		
					2	27.55		0.67	0.68
					6	17.6			
					18	14.14			
					54	4.305			
SEQ156	TGFBFR2	IL9R	IL9R	QP	162	1.425			
					486	2.1			
					1458	1.6			
					2	77.45		0.056	68.9
					6	76.8			
					18	70.55			
SEQ171	TWEAKR	IL9R	IL9R	G ₄ S	54	70.9			
					162	63.45			
					486	67.5			
					1458	71.05			
					2	77.35		0.54	62.8
					6	68.45			
SEQ172	TWEAKR	IL9R	IL9R	QP	18	53.65			
					54	46.8			
					162	59.7			
					486	63.4			
					1458	63.75			
					2	74		0.39	32.9
SEQ173	TWEAKR	TNFR1	IL9R	G ₄ S	6	53.85			
					18	44.9			
					54	47.4			
					162	36.45			
					486	34.75			
					1458	34.1			
SEQ174	TWEAKR	TNFR1	IL9R	QP	2	92.7		0.37	30.5
					6	80.85			
					18	64.65			
					54	46.55			
					162	36.1			
					486	32.95			
SEQ187	DCR1	TNFR1	IL9R	G ₄ S	1458	31			
					2	87.2		0.29	23.6
					6	68.95			
					18	47.75			
					54	37.15			
					162	30			
SEQ188	DCR1	TNFR1	IL9R	QP	486	25.7			
					1458	26.75			
					2	86.65		0.16	4.81
					6	70.25			
					18	50.15			
					54	29			

TABLE 5-continued

Sequence ID	Ligand-binding domain	Trans-membrane domain	Intra-cellular domain	Linker	Fold-dilution of lentivirus	% positive T cells	% double-positive T cells (average of duplicates)	% positive T cells in unstained T cells (average of duplicates)	% positive T cells in stained un-transduced T cells (endogenous expression)
SEQ189	CD40	TNFR1	IL9R	G ₄ S	18	48.65			
					54	35.7			
					162	15.08			
					486	14.7			
					1458	8.65			
					2	91.05		0.079	11.9
					6	79			
					18	55.8			
					54	24.3			
					162	20.55			
SEQ190	CD40	TNFR1	IL9R	QP	486	10.65			
					1458	10.365			
					2	58.15		0.32	34
					6	56.3			
					18	53.5			
					54	48.5			
					162	38.65			
					486	33.15			
					1458	31.3			
					2	86		0.22	40
SEQ193	DR4	TNFR1	IL9R	G ₄ S	6	69.3			
					18	61			
					54	50.3			
					162	48.85			
					486	47			
					1458	43.2			
					2	87		0.089	60.6
					6	84.3			
					18	83.4			
					54	84.15			
SEQ194	DR4	TNFR1	IL9R	QP	162	75.6			
					486	74			
					1458	64.85			
					2	96.95		1.84	93.6
					6	95.35			
					18	93.65			
					54	94.25			
					162	92.7			
					486	91.65			
					1458	92			
SEQ200	TNFRSF1B	TNFR1	IL9R	G ₄ S	2	95.85		0.39	92.8
					6	96.2			
					18	94.15			
					54	93.5			
					162	94.15			
					486	92.1			
					1458	93.8			
SEQ201	TNFRSF1B	TNFR1	IL9R	QP					

[0245] As demonstrated in Table 5 above, lentiviruses for all constructs were successfully produced and transduced primary human T cells exhibited at least some level of cell surface expression. Despite their general resistance to viral transduction and sensitivity unfolded protein responses (UPR) [Lopez-Soto et al., “Cancer-induced Endoplasmic Reticulum Stress in T Cells Subverts Immunosurveillance,” Cell Metabolism 28(6):803-805 (2018); Li et al., “The Emerging Roles of Endoplasmic Reticulum Stress in Balancing Immunity and Tolerance in Health and Diseases: Mechanisms and Opportunities,” Front. Immunol. Volum 10, Article 3154], the constructs produced properly folded proteins capable of endocytic transport and resistant to general proteolysis in primary T cells.

Example 10
Expression of Chimeric Switch Receptors Results in Phosphorylation of Stat RECEPTORS
[0246] Some constructs were then tested for their ability to induce phosphorylation of STAT1, STAT3, and/or STAT5. Briefly, primary human T cells were transduced with a lentiviral vector encoding switch receptors of SEQ ID NO:63+CAR+ (IL21R ECD+IL9R TM+IL9R ICD and CAR 4D5), SEQ ID NO:66 (IL15Ra+IL9R TM+IL9R ICD), SEQ ID NO:72+CAR+ (IL4R ECD+IL9R TM+IL9R ICD and CAR 4D5), or SEQ ID NO:153+CAR+ (IL10Ra ECD+IL9R TM+IL9R ICD and CAR 4D5). Cells transduced with SEQ ID NO:63+CAR+ were left either unstimulated or stimulated with 200 ng/mL IL-21 for 30 minutes. Cells transduced with SEQ ID NO:66 were left either unstimu-

lated or stimulated with 200 ng/mL IL-15 for 30 minutes. Cells transduced with SEQ ID NO:72+CAR+ were left either unstimulated or stimulated with 200 ng/mL IL-4 for 30 minutes. Cells transduced with SEQ ID NO:153+CAR+ were left either unstimulated or stimulated with 200 ng/mL IL-4 for 30 minutes. The fold increase in gMFI of ligand stimulated versus no stimulation was calculated and is shown in FIG. 1.

[0247] As shown in FIG. 1, all constructs induced phosphorylation of STAT1, STAT3, and STAT5 when stimulated with ligand. Activation of STAT family members through ligand mediated phosphorylation is believed to confer advantages in effector function, polarization and proliferation to T cells.

Example 11

Primary T Cells Expressing Chimeric Switch Receptors Exhibit Enhanced Tumor Cell Killing

[0248] Real-time cytotoxicity assays were then used to analyze whether or not cells expressing a chimeric switch receptor of the present disclosure would show increased cytotoxicity when exposed to ligand. As shown in FIGS. 2-4, upon stimulation with ligand, cells expressing either SEQ ID NO:63+CAR+ (IL21R ECD+IL9R TM+IL9R ICD and CAR 4D5) (FIG. 2), SEQ ID NO:72+CAR+ (IL4R ECD+IL9R TM+IL9R ICD and CAR 4D5) (FIG. 3), or SEQ ID NO:113+CAR+ (Fas ECD+IL9R TM+IL9R ICD and CAR 4D5) (FIG. 4), demonstrated an increase in killing of SKOV-3 human ovarian adenocarcinoma cells expressing HER2 when preconditioned with ligand as compared to untransduced, stimulated cells. Consistent with the observed activation of STAT transcription factors following ligand stimulation, T cells transduced with hybrid IL9R receptors demonstrated improved killing over unstimulated controls. It should be noted that in the case of Seq ID NO 113, the presence of natural ligand (TNFSF6) increases background killing in the assay. That said, the addition of exogenous ligand enhances T cell killing above controls.

Example 12

Primary T Cells Expressing Chimeric Switch Receptors Exhibit Increased Cytokine and Chemokine Activity

[0249] Culture supernatants from primary human T cells transduced with either SEQ ID NO:63+CAR+ (IL21R ECD+IL9R TM+IL9R ICD and CAR 4D5) (FIG. 5) or SEQ ID NO:72+CAR+ (IL4R ECD+IL9R TM+IL9R ICD and CAR 4D5) (FIG. 6) were then analyzed for the presence of cytokines and chemokines. Supernatants were taken from cells stimulated with ligand before the real-time cytotoxicity assay of Example 11 (first bar, “pre”), cells stimulated with ligand during the real-time cytotoxicity assay of Example 11 (second bar, “post”), or cells stimulated at both points in the real-time cytotoxicity assay of Example 11 (third bar, “both”). The fold increase over unstimulated was calculated and is shown in FIGS. 5 and 6. As shown in FIGS. 5 and 6, several cytokines and chemokines, such as IFNg, FGF2, GMCSF, IL-3, IL-6, IP10, MIP1a, and RANTES, demonstrated increased production. The magnitude and quality of cytokines produced following ligand stimulation (either “pre”, “post” or “both”) indicates a robust improvement in T cell response with hybrid-IL9R engagement. Furthermore,

the pattern of cytokine response indicates an increase in type-1 polarization following ligand stimulation relative to controls.

[0250] FIGS. 7-19 depict results from the same experiment, however, the data is shown in concentration of cytokine or chemokine (in pg·mL) for each of the above described experimental conditions. Similarly, the magnitude and quality of cytokines produced following ligand stimulation (either “pre”, “post” or “both”) indicates a robust improvement in T cell response with hybrid-IL9R engagement, and the pattern of cytokine response indicates an increase in type-1 polarization following ligand stimulation relative to controls.

Informal Sequence Listing
IL21r/IL9R
SEQ ID NO: 63
CPDLVCYTDYLTQVICILEMWNLHPSTLTTLTWQDQ
YEELKDEATSCSLHRSAHNATHATYTCHMDVFHFM
ADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPF
NVTVTFSGQYNISWRSDYEDPAFYMLKGKLOQYELQ
YRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDS
SYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEE
LKELIPPWGPGNTLVAVSIFLLLTGPTYLLFKLS
PRVKRIFYQNVSPAMFFQPLYSVHNGNFQTMGMA
HGAGVLLSQDCAGTPQGALEPCVQEATALLTCGPA
RPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCTE
WRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSS
SSSSNNNNYCALGCYGGWHLSPALPGNTQSSGPIPA
LACGLSCDHQGLETOQGVAVVLAGHCQRPGLHEDL
QGMLLPVLSKARSWTF
IL21r/IL9R/IL7RaTM
SEQ ID NO: 64
CPDLVCYTDYLTQVICILEMWNLHPSTLTTLTWQDQ
YEELKDEATSCSLHRSAHNATHATYTCHMDVFHFM
ADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPF
NVTVTFSGQYNISWRSDYEDPAFYMLKGKLOQYELQ
YRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDS
SYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEE
LKEPILLTISILSFFSVALLVILACVLWVKRIFYQ
NVPSPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQ
DCAGTPQGALEPCVQEATALLTCGPAPWKSVALE
EEQEGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYL
PQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNY
CALGCYGGWHLSPALPGNTQSSGPIPALACGLSCDH
QGLETOQGVAVVLAGHCQRPGLHEDLQGMLLPVLS
KARSWTF

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IL21r/IL9R/IL2RbTM
CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQ
YEELKDEATSCSLHRSAHNATHATYTCMDVFHFM
ADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPF
NVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQ
YRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDS
SYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEE
LKEIPWLGHLLVGLSGAFGFIIILVYLLIVKRIFYQ
NVPSPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQ
DCAGTPQGALEPCVQEATALLTCGPARPWKSVALE
EEQEGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYL
PQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNY
CALGCYGGWHL SALPGNTQSSGPIPALACGLSCDH
QGLETQQGVAVVLAGHCQRPGLHEDLQGM LPSVL
SKARSWTF

IL15r-alpha/IL9R
ITCPPPMSVEHADIWVKSYSLSRERYICNSGFKR
KAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALV
HQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPS
SNNTAATTAAI VPGSQLMPSKSPSTGTTEISSHES
SHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTT
LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSS
SNMNNYCALGCYGGWHL SALPGNTQSSGPIPALAC
GLSCDHQGLETQQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL15r-alpha/IL9R/IL7RaTM
ITCPPPMSVEHADIWVKSYSLSRERYICNSGFKR
KAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALV
HQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPS
SNNTAATTAAI VPGSQLMPSKSPSTGTTEISSHES
SHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTT
PILLTISILSFFSVALLVILACVLWVKRIFYQNV
SPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCA
GTPQGALEPCVQEATALLTCGPARPWKSVALEEEQ
EGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLPQE

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DWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCAL
GCYGGWHL SALPGNTQSSGPIPALACGLSCDHQGL
ETQQGVAVVLAGHCQRPGLHEDLQGM LPSVLSKA
RSWTF

IL15r-alpha/IL9R/IL2RbTM
ITCPPPMSVEHADIWVKSYSLSRERYICNSGFKR
KAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALV
HQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPS
SNNTAATTAAI VPGSQLMPSKSPSTGTTEISSHES
SHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTT
IPWLGHLLVGLSGAFGFIIILVYLLIVKRIFYQNV
SPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCA
GTPQGALEPCVQEATALLTCGPARPWKSVALEEEQ
EGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLPQE
DWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCAL
GCYGGWHL SALPGNTQSSGPIPALACGLSCDHQGL
ETQQGVAVVLAGHCQRPGLHEDLQGM LPSVLSKA
RSWTF

IL7r-alpha/IL9R
ESGYAQNGDLEDAELDDYSFSCYSQLEVNGSQHSL
TCAFEDPDVNI TNLEFEICGALVEVKCLNFRKLQE
IYFIETKKFLLIGKSNICVKVGEKSLTCKKIDLTT
IVKPEAPFDLSVVYREGANDFVVTFNTSHLQKKYV
KVLMDVAYRQEKDENKWTHVNLSSTKLTL LQRKL
QPAAMY EIKVRSIPDHYFKGFWSEWSPSYFFRTPE
INNSSGEMDLIPPWGWP GNTLVAVSIFLLLTGPTY
LLFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNF
QTMGAHGAGVLLSQDCAGTPQGALEPCVQEATAL
LTCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
PAAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEG
SRSSSSSSSSNNNNYCALGCYGGWHL SALPGNTQS
SGPIPALACGLSCDHQGLETQQGVAVVLAGHCQRP
GLHEDLQGM LPSVLSKARSWTF

IL7r-alpha/IL9R/IL7RaTM
ESGYAQNGDLEDAELDDYSFSCYSQLEVNGSQHSL
TCAFEDPDVNI TNLEFEICGALVEVKCLNFRKLQE
IYFIETKKFLLIGKSNICVKVGEKSLTCKKIDLTT
IVKPEAPFDLSVVYREGANDFVVTFNTSHLQKKYV
KVLMDVAYRQEKDENKWTHVNLSSTKLTL LQRKL

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QPAAMYEIKVRSIPDHYFKGFWSEWSPSYFRTPE
INNSSGEMDPILLTISILSFFSVALLVILACVLWV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTGPARPW
KSVALEEEQEGPGTRLPGNLSSDVLPACTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGRSSSSSSSS
SNMNNYCALGCYGGWHLALPGNTQSSGPIPALAC
GLSCDHQGLETTQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL7r-alpha/IL9R/IL2RbTM
SEQ ID NO: 71
ESGYAQNGDLEDAELDDYSFSCYSQLEVNQSQSL
TCAFEDPDVNI TNLEFEICGALVEVKCLNFRKLQE
IYFIETKKFLLIGKSNICVKVGEKSLTCKKIDLT
IVKPEAPFDLSVVYREGANDFVVTFTNTSHLQKKYV
KVLMDVAVRQEKDENKTHVNLSTKLTLQKRL
QPAAMYEIKVRSIPDHYFKGFWSEWSPSYFRTPE
INNSSGEMDIPWLGHLVGLSGAFGFIIIVYLLIV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTGPARPW
KSVALEEEQEGPGTRLPGNLSSDVLPACTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGRSSSSSSSS
SNMNNYCALGCYGGWHLALPGNTQSSGPIPALAC
GLSCDHQGLETTQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL4r-alpha/IL9R
SEQ ID NO: 72
MKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRL
LYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVS
ADNYTLDLWAGQQLLWKGSKPSEHVKPRAPGNLT
VHTNVSDTLLL TWSNPYPDPNYLYNHLTYAVNIWS
ENDPADFRIYNTYLEPSLRIAASTLKSGISYRAR
VRAWAQCYNTTWSEWSPSTKWHNSYREPFEQHLIP
PWGWPGNTLVAVSIFLLLTGPTYLLFKLSRVKRI
FYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTGPARPWKS
VALEEEQEGPGTRLPGNLSSDVLPACTEWRVQTL
AYLPQEDWAPTSLTRPAPPDSEGRSSSSSSSSNN
NNYCALGCYGGWHLALPGNTQSSGPIPALACGLS
CDHQGLETTQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

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IL4r-alpha/IL9R/IL7RaTM
SEQ ID NO: 73
MKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRL
LYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVS
ADNYTLDLWAGQQLLWKGSKPSEHVKPRAPGNLT
VHTNVSDTLLL TWSNPYPDPNYLYNHLTYAVNIWS
ENDPADFRIYNTYLEPSLRIAASTLKSGISYRAR
VRAWAQCYNTTWSEWSPSTKWHNSYREPFEQHPIL
LTISILSFFSVALLVILACVLWVKRIFYQNVPSA
MFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTGPARPWKS
VALEEEQEGPGTRLPGNLSSDVLPACTEWRVQTLAYLP
QEDWAPTSLTRPAPPDSEGRSSSSSSSSNNMNNYCALGCY
GGWHLALPGNTQSSGPIPALACGLSCDHQGLETTQ
GVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL4r-alpha/IL9R/IL2RbTM
SEQ ID NO: 74
MKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRL
LYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVS
ADNYTLDLWAGQQLLWKGSKPSEHVKPRAPGNLT
VHTNVSDTLLL TWSNPYPDPNYLYNHLTYAVNIWS
ENDPADFRIYNTYLEPSLRIAASTLKSGISYRAR
VRAWAQCYNTTWSEWSPSTKWHNSYREPFEQH
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MFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTGPARPWKS
VALEEEQEGPGTRLPGNLSSDVLPACTEWRVQTLAYLP
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GVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL2r-beta Ectodomain /IL9R
SEQ ID NO: 75
AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQV
HAWPDRRRWNQTCCELLPVSQASWACNLILGAPDSQ
KLTTVDIVTLRVLCREGVRVRVMAIQDFKPFENLR
LMAPIQLQVHVETHRCNISWEISQASHYFERHLE
FEARTLSPGHTWEEAPLLTLKQKQEWICLETLPD
TQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAAL
GKDTLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKL
SPRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMG

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AHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLSPGNTQSSGPIP
ALACGLSCDHQGLETOQGVAWVLAGHCQRPGLHED
LQGMLLPSVLSKARSWTF

IL2r-beta Ectodomain /IL9R/IL7RaTM
SEQ ID NO: 76
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HAWPDRRRWNQTCCELLPVSQASWACNLILGAPDSQ
KLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLR
LMAPIQLQVVHVETHRCNISWEISQASHYFERHLE
FEARTLSPGHTWEEAPLLTLKQKQEWICLETLPD
TQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAAL
GKDTPIILLTISILSFFSVALLVILACVLWVKRIFY
QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS
QDCAGTPQGALEPCVQEATALLTCGPARPWKSVL
EEEQEGPGTRLPGNLSSDVLPAAGCTEWRVQTLAY
LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN
YCALGCYGGWHLSPGNTQSSGPIPALACGLSCD
HQGLETOQGVAWVLAGHCQRPGLHEDLQGMLLPSV
LSKARSWTF

IL2r-beta Ectodomain /IL9R/IL2RbTM
SEQ ID NO: 77
AVNGTSQFTCFYNSRANISCVWSQDQALQDTSCQV
HAWPDRRRWNQTCCELLPVSQASWACNLILGAPDSQ
KLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLR
LMAPIQLQVVHVETHRCNISWEISQASHYFERHLE
FEARTLSPGHTWEEAPLLTLKQKQEWICLETLPD
TQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAAL
GKDTIPWLGHLLVGLSGAFGFIIILVYLLIVKRIFY
QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS
QDCAGTPQGALEPCVQEATALLTCGPARPWKSVL
EEEQEGPGTRLPGNLSSDVLPAAGCTEWRVQTLAY
LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN
YCALGCYGGWHLSPGNTQSSGPIPALACGLSCD
HQGLETOQGVAWVLAGHCQRPGLHEDLQGMLLPSV
LSKARSWTF

IL2r-alpha Ectodomain/IL9R
SEQ ID NO: 78
ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFR
RIKSGSLYMLCTGNSSHSSWDNQCTSSATRNTT

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KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCR
EPPPWENEATERIYHFVVGQMVYYQCVQGYRALHR
GPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGE
EKPQASPEGRPESETSCLVTTTDFQIQTEMAATME
TSIFTTEYQLIPPWGWPGNTLVAVSIFLLLTGPTY
LLFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNF
QTMGAHGAGVLLSQDCAGTPQGALEPCVQEATAL
LTCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
PAAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEG
SRSSSSSSSSNNNNYCALGCYGGWHLSPGNTQS
SGPIPALACGLSCDHQGLETOQGVAWVLAGHCQRP
GLHEDLQGMLLPSVLSKARSWTF

IL2r-alpha Ectodomain/IL9R/IL7RaTM
SEQ ID NO: 79
ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFR
RIKSGSLYMLCTGNSSHSSWDNQCTSSATRNTT
KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCR
EPPPWENEATERIYHFVVGQMVYYQCVQGYRALHR
GPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGE
EKPQASPEGRPESETSCLVTTTDFQIQTEMAATME
TSIFTTEYQPILLTISILSFFSVALLVILACVLWV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS
SNNNNYCALGCYGGWHLSPGNTQSSGPIPALAC
GLSCDHQGLETOQGVAWVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTF

IL2r-alpha Ectodomain/IL9R/IL2RbTM
SEQ ID NO: 80
ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFR
RIKSGSLYMLCTGNSSHSSWDNQCTSSATRNTT
KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCR
EPPPWENEATERIYHFVVGQMVYYQCVQGYRALHR
GPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGE
EKPQASPEGRPESETSCLVTTTDFQIQTEMAATME
TSIFTTEYQIPWLGHLLVGLSGAFGFIIILVYLLIV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS

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SNNNNYCALGCYGGWHL SALPGNTQSSGPIPALAC

GLSCDHQGLETQQGVAWVL AGHCQRPGLHEDLQGM

LLPSVLSKARSWTF

ILT5/IL9R/cGC-F
SEQ ID NO: 81
GPFPKPTLWAEPGSVISWGSPVTIWCQGSQEAQEY

RLHKEGSPEPLDRNNPLEPKNKARFSIPSMTEHHA

GRYRCHYYSSAGWSEPSDPLEMVMTGAYSKPTLSA

LPSPVVASGGNMTLR CGSQKGYHHFVLMKEGEHQ
L
PRTLDSQQLHSRGFQALFPVGPVTPSHRWRFTCYY

YYTNPWVWSHPSDPLEILPSGVSRKPSLLTLQGP

VLAPGQSLTLQCGSDVGYNRFVLYKEGERDFLQRP

GQQPQAGLSQANFTLGPVSPSNGGQYRCYGAHNLS

SEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASG

ENVTLQCQSWWQFDTFLLTKEGAAHPPLRLRSMYG

AHKYQAEFPMSPV TSAHAGTYRCYGSYSSNPHLLS

HPSEPLELVVSGHSGGSSLPPTGPPSTPGLGRYLE

LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPRV

KRIFYQNVPS PAMFFQPLYSVHNGNFQTMGAHGA

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QTLAYLPQEDWAPTS LTRPAPPDSEGSRSSSSSSSS

SNNNNYCALGCYGGWHL SALPGNTQSSGPIPALAC

GLSCDHQGLETQQGVAWVL AGHCQRPGLHEDLQGM

LLPSVLSKARSWTFQPPQPQPQPQP PERTMPRIPT

LKNLEDLVTEYHG NFSAWSGVSKGLAESLQPDYSE

RLCLVSEIPPKGGALGEGPGASPCNQHS PYWAPPC

YTLKPET

ILT3/IL9R/cGC-F
SEQ ID NO: 82
GPFPKPTLWAEPGSVISWGSPVTIWCQGSQEAQEY

RLHKEGSPEPLDRNNPLEPKNKARFSIPSMTEHHA

GRYRCHYYSSAGWSEPSDPLEMVMTGAYSKPTLSA

LPSPVVASGGNMTLR CGSQKGYHHFVLMKEGEHQ
L
PRTLDSQQLHSRGFQALFPVGPVTPSHRWRFTCYY

YYTNPWVWSHPSDPLEILPSGVSRKPSLLTLQGP

VLAPGQSLTLQCGSDVGYNRFVLYKEGERDFLQRP

GQQPQAGLSQANFTLGPVSPSNGGQYRCYGAHNLS

SEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASG

ENVTLQCQSWWQFDTFLLTKEGAAHPPLRLRSMYG

AHKYQAEFPMSPV TSAHAGTYRCYGSYSSNPHLLS

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HPSEPLELVVSGHSGGSSLPPTGPPSTPGLGRYLE

LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPRV

KRIFYQNVPS PAMFFQPLYSVHNGNFQTMGAHGA

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KSVALEEEQEGPGTRLPGNLSS EDVLPAGCTEWRV

QTLAYLPQEDWAPTS LTRPAPPDSEGSRSSSSSSSS

SNNNNYCALGCYGGWHL SALPGNTQSSGPIPALAC

GLSCDHQGLETQQGVAWVL AGHCQRPGLHEDLQGM

LLPSVLSKARSWTFQPPQPQPQPQP PERTMPRIPT

LKNLEDLVTEYHG NFSAWSGVSKGLAESLQPDYSE

RLCLVSEIPPKGGALGEGPGASPCNQHS PYWAPPC

YTLKPET

ILT3/IL9R/cGC-F
SEQ ID NO: 83
QAGPLPKPTLWAEPGSVISWGNSVTIWCQGTLEAR

EYRLDKEESPAPWDRQNPLEPKNKARFSIPSMTE

YAGRYRCYRSPVGWSQPSDPLELVMTGAYSKPTL

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HPLLHLRSEHGAQQHQAEFPMSPVTSVHGGTYRCF

SSHGF SHYLLSHPSDPLELIVSGSLEDPRPSPTRS

VSTAAGPEDQPLMPTG SVPHSGLRRHWELIPPWG
W
PGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQ
N
VPSPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQ
D
CAGTPQGALEPCVQEATALLTCGPARPWKSVALEE

EQEGPGTRLPGNLSS EDVLPAGCTEWRVQTLAYLP

QEDWAPTS LTRPAPPDSEGSRSSSSSSSSSNNNNYC

ALGCYGGWHL SALPGNTQSSGPIPALACGLSCDHQ

GLETQQGVAWVL AGHCQRPGLHEDLQGM LPSVLS

KARSWTFGGGGSGGGSGGGGSERTMPRIPTLKNL

EDLVTEYHG NFSAWSGVSKGLAESLQPDYSERLCL

VSEIPPKGGALGEGPGASPCNQHS PYWAPPCYTLK

PET

ILT3/IL9R/cGC-S
SEQ ID NO: 84
QAGPLPKPTLWAEPGSVISWGNSVTIWCQGTLEAR

EYRLDKEESPAPWDRQNPLEPKNKARFSIPSMTE

YAGRYRCYRSPVGWSQPSDPLELVMTGAYSKPTL

SALPSPLVTSGKSVTLLCQSRSPMDTFLLIKERAA

HPLLHLRSEHGAQQHQAEFPMSPVTSVHGGTYRCF

SSHGF SHYLLSHPSDPLELIVSGSLEDPRPSPTRS

VSTAAGPEDQPLMPTG SVPHSGLRRHWELIPPWG
W

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PGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQN

VPSPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQD

CAGTPQGALEPCVQEATALLTCGPAPWKSVALEE

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QEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYC

ALGCYGGWHLSPGNTQSSGPIPALACGLSCDHQ

GLETQQGVAVVLAGHCQRPGLHEDLQGMLLPSVLS

KARSWTFQPPQPPQPPQPERTMPRIPTLKNLEDL

VTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSE

IPPKGALGEGPGASPCNQHSPYWAPPCYTLKPET

ILT4 IL9R/cGC-F

SEQ ID NO: 85

QTGTIPKPTLWAEPSVITQGSPVTLSCQGSLEAQ

EYRLYREKKSASWITRIRPELVKNGQFHIPSITWE

HTGRYGCQYYSRARWSELSDPLVLVMTGAYPKPTL

SAQSPVVTSGGRVTLQCESQVAFGGFILCKEGEE

EHPQCLNSQPHARGSSRAIFSVGPVSPNRRWSHRC

YGYDLNSPYVWSSPSDLLELLVPGVSKKPSLSVQP

GPVVAPGESLTLQCVSDVGYDRFVLYKEGERDLRQ

LPGRQPQAGLSQANFTLGPVSRSYGGQYRCYGAHN

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SGENVTLQCQSWRQFHTFLLTKAGAADAPLRLRSI

HEYPKYQAEFPMSPVTSAHAGTYRCYGSLSNDPYL

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QPLTPTGSDPQSGLGRHLGVLIIPPWGPNTLVAV

SIFLLLTGPTYLLFKLSPRVKRIFYQNVPSPAMFF

QPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQGA

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GNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKG

GALGEGPGASPCNQHSPYWAPPCYTLKPET

ILT4 IL9R/cGC-S

SEQ ID NO: 86

QTGTIPKPTLWAEPSVITQGSPVTLSCQGSLEAQ

EYRLYREKKSASWITRIRPELVKNGQFHIPS

ITWEHTGRYGCQYYSRARWSELSDPLVLV

MTGAYPKPTLSAQSPVVTSGGRVTLQCESQVAFG

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GFILCKEGEEHPQCLNSQPHARGSSRAIFSVGPV

SPNRRWSHRCYGYDLNSPYVWSSPSDLLELLVPGV

SKKPSLSVQPGPVVAPGESLTLQCVSDVGYDRFVL

YKEGERDLRQLPGRQPQAGLSQANFTLGPVSRSYG

GQYRCYGAHNLSSECSAPSDPLDILITGQIRGTPF

ISVQPGPTVASGENVTLLCQSWRQFHTFLLTKAGA

ADAPLRLRSIHEYPKYQAEFPMSPVTSAHAGTYRC

YGSLSNDPYLLSHPSEPLELVVSGPSMGSSPPPTG

PISTPAGEDQPLTPTGSDPQSGLGRHLGVLIIPPW

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HQGLETQQGVAVVLAGHCQRPGLHEDLQGMLLPSV

LSKARSWTFQPPQPPQPPQPERTMPRIPTLKNLE

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SEIPPKGALGEGPGASPCNQHSPYWAPPCYTLKP

ET

ILT2 IL9R/cGC-F

SEQ ID NO: 87

GHLPKPTLWAEPSVITQGSPVTLRCQGGQETQEY

RLYREKKTALWITRIPQELVKKGQFPIPSITWEHA

GRYRCYGSDTAGRSESSDPLELVVTGAYIKPTLS

AQSPVNVNNGNVILQCDQVAFDGFSLCKEGEDE

HPQCLNSQPHARGSSRAIFSVGPVSPSRWWYRCY

AYDSNSPYEWSLPSDLLELLVLGVSKKPSLSVQPG

PIVAPEETLTLQCGSDAGYNRFVLYKDGERDFLQL

AGAQPQAGLSQANFTLGPVSRSYGGQYRCYGAHN

SSEWSAPSDPLDILIAQGFYDRVSLSVQPGPTVAS

GENVTLLCQSQGWMQTFLLTKEGAADDPWRLRSTY

QSQKYQAEFPMGPVTSAHAGTYRCYGSQSSKPYLL

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LTPTGSDPQSGLGRHLGVLIIPPWGPNTLVAVSI

FLLLTGPTYLLFKLSPRVKRIFYQNVPSPAMFFQPP

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PCVQEATALLTCGPAPWKSVALEEEQEGPGTRLP

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RPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL

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SALPGNTQSSGPIPALACGLSCDHQGLETOQGVAV
VLAGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGG
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FSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGA
LGEGPGASPCNQHSPYWAPPCYTLKPET
ILT2 IL9R/cGC-S
SEQ ID NO: 88
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GRYRCYYGSDTAGRSESDPLELVVTGAYIKPTLS
AQPSPPVNSGGNVILQCDSQVAFDGFSLCKEGEDE
HPQCLNSQPHARGSSRAIFSVGPVSPSRRWWYRCY
AYDSNSPYEWSLPSDLLELLVLGVSKKPSLSVQPG
PIVAPEETLTLQCGSDAGYNRFVLYKDGERDFLQL
AGAQPQAGLSQANFTLGPVSRSYGGQYRCYGAHNL
SSEWSAPSDPLDILIAQGFYDRVLSVQPGPTVAS
GENVTLLCQSQGWMQTFLLTKEGAADDPWRLRSTY
QSQKYQAEFPMGPVTSAHAGTYRCYGSQSSKPYLL
THPSDPLELVVSGPSGGPSSPTTGPTSTSGPEDQP
LTPTGSDPQSGLGRHLGVLIPPWGWPGNTLVAVSI
FLLLTGPTYLLFKLSPRVKRIFYQNVPSPAMFFQP
LYSVHNGNFQTMGAHGAGVLLSQDCAGTPQGALE
PCVQEATALLTCGPARPWKSVALEEEQEGPGTRLP
GNLSSDVLPAAGCTEWRVQTLAYLPQEDWAPTSLT
RPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL
SALPGNTQSSGPIPALACGLSCDHQGLETOQGVAV
VLAGHCQRPGLHEDLQGMLLPSVLSKARSWTFQPP
PQPQPQPQPPTMPRIPTLKNLEDLVTEYHGNFSA
WSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGE
GPGASPCNQHSPYWAPPCYTLKPET
CTLA4 IL9R/cGC-F
SEQ ID NO: 89
KAMHVAQPAVVLASSRGIASFVCEYASPGKATEVR
VTVLRQADSQVTEVCAATYMMGNELTFLDDSICTG
TSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPY
LGIGNGTQIYVIDPEPCPDSDLIPWGWPGNTLVA
VSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSPAMF
FQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQG
ALEPCVQEATALLTCGPARPWKSVALEEEQEGPGT
RLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAPT
SLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGG

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WHLASALPGNTQSSGPIPALACGLSCDHQGLETOQG
VAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWTF
GGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTEY
HGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPK
GGALGEGPGASPCNQHSPYWAPPCYTLKPET
CTLA4 IL9R/cGC-S
SEQ ID NO: 90
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VTVLRQADSQVTEVCAATYMMGNELTFLDDSICTG
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LGIGNGTQIYVIDPEPCPDSDLIPWGWPGNTLVA
VSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSPAMF
FQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQG
ALEPCVQEATALLTCGPARPWKSVALEEEQEGPGT
RLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAPT
SLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGG
WHLASALPGNTQSSGPIPALACGLSCDHQGLETOQG
VAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWTF
QPQPQPQPQPPTMPRIPTLKNLEDLVTEYHGN
FSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGA
LGEGPGASPCNQHSPYWAPPCYTLKPET
TIM3/IL9R/cGC-F
SEQ ID NO: 91
SEVEYRAEVGNAYLPCFYTPAAPGNLVPVCWGKG
ACPVFECGNVLRDTERDVNYWTSRYWLNDFRKG
DVSLTIENVTLADSGIYCCRIQIPGIMNDEKFNLK
LVIKPAKVTPAPTRQORDFTAAPRMLTTRGHGPAE
TQTLGSLPDINLTQISTLANELRDSRLANDLRDSG
ATIRIGLIPWGWPGNTLVAVSIFLLLTGPTYLLF
KLSPRVKRIFYQNVPSPAMFFQPLYSVHNGNFQTM
GAHGAGVLLSQDCAGTPQGALEPCVQEATALLTC
GPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
CTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRS
SSSSSSNNNNYCALGCYGGWHLASALPGNTQSSGP
IPALACGLSCDHQGLETOQGVAVVLAGHCQRPGLH
EDLQGMLLPSVLSKARSWTFGGGGSGGGSGGGGS
ERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLA
ESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQ
HSPYWAPPCYTLKPET

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TIM3/IL9R/cGC-S
SEQ ID NO: 92
SEVEYRAEVGQNAYLPCFYTPAAPGNLVPVCWGKG
ACPVFECGNVVLRTDERDVNYWTSRYWLNNGDFR
KGDVSLTIENVTLADSGIYCCRIQIPG
IMNDEKFNLKLVIKPAKVTPAPTRQRDFTAAFPRM
LTTRGHGPAETQTLGSLPDINLTQISTLANELRDS
RLANDLRDSGATIRIGLIPPWGWPGNTLVAVSIFL
LLTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLY
SVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPC
VQEATALLTCGPARPWKSVALEEEQEGPGTRLPGN
LSSDVLPAAGCTEWRVQTLAYLPQEDWAPTSLTRP
APPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL
LPGNTQSSGPIPALACGLSCDHQGLETTQQGVAWVL
AGHCQRPGLHEDLQGMLLPSVLSKARSWTFQPPQ
PQPQPQPRTMPRIPTLKNLEDLVTEYHGNFSAWS
GVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGP
GASPCNQHSFYWAPPCYTLKPET
LAG3/IL9R/cGC-S
SEQ ID NO: 93
LQPGAEPVWVAQEGAPQLPCSTIPLQDLSLLR
RAGVTWQHQPDSGPPAAAPGHPLAPGPHPAAPSSW
GPRPRRYTVLSVGPGLRSGRLPLQPRVQLDERGR
QRGDFSLWLRPARRADAGEYRAAVHLRDRALSCRL
RLRLGQASMTASPPGSLRASDWVILNCSFSRPDRP
ASVHWFRNRGQGRVPVRESPPHHHLAESFLFLPQVS
PMDSGPWGCILTYRDGFNVSIMYNLTVLGLEPPTP
LTVYAGAGSRVGLPCRLPAGVGTRSFLLTAKWTPPG
GGPDLLVTGDNGDFTLRLEDVSSQAQAGTYTCHIHL
QEQQLNATVTLAIITVTPKSFSGPSLGKLLCEVT
PVSGQERFVWSSLDTPSQRSFSGPWLEAQEAQLLS
QPWQCQLYQGERLLGAAVYFTELSSPGAQSRGRAP
GALPAGHLLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFLKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
PAGCTEWRVQTLAYLPQEDWAPTSLTRPAPDSEGS
RSSSSSSSSNNNNYCALGCYGGWHL
SALPGNTQSS
GPIPALACGLSCDHQGLETTQQGVAWVL
AGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSFYWAPPCYTLKPET
PD1/IL9R/cGC-F
SEQ ID NO: 95
FTVTVPKDLVVEYGSNMTIECKFPVEKQLDLAAL
IVYWEMEDKNI IQFVHGEEDLKVQHSSYRQARLL
KDQLSLGNAALQITDVKLQDAGVYRCMISYGGADY
KRITVKVNAPYNKINQRI
LVDPVISEHELICOAE
GYPKAEVIWISSDHQVLSGKTTTTNSKREEKLFNV
ISILRINTTTNEIFYCTFRRLDPEENHTAELVIPE
LPLAHPNERLIPPWGWPGNTLVAVSIFLLLTGPT
YLLFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGN
FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA
LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
LPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPDSE
GSRSSSSSSSSNNNNYCALGCYGGWHL
SALPGNTQ

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SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQH
SPYWAPPCYTLKPET
LAG3/IL9R/cGC-F
SEQ ID NO: 94
LQPGAEPVWVAQEGAPQLPCSTIPLQDLSLLR
RAGVTWQHQPDSGPPAAAPGHPLAPGPHPAAPSSW
GPRPRRYTVLSVGPGLRSGRLPLQPRVQLDERGR
QRGDFSLWLRPARRADAGEYRAAVHLRDRALSCRL
RLRLGQASMTASPPGSLRASDWVILNCSFSRPDRP
ASVHWFRNRGQGRVPVRESPPHHHLAESFLFLPQVS
PMDSGPWGCILTYRDGFNVSIMYNLTVLGLEPPTP
LTVYAGAGSRVGLPCRLPAGVGTRSFLLTAKWTPPG
GGPDLLVTGDNGDFTLRLEDVSSQAQAGTYTCHIHL
QEQQLNATVTLAIITVTPKSFSGPSLGKLLCEVT
PVSGQERFVWSSLDTPSQRSFSGPWLEAQEAQLLS
QPWQCQLYQGERLLGAAVYFTELSSPGAQSRGRAP
GALPAGHLLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFLKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
PAGCTEWRVQTLAYLPQEDWAPTSLTRPAPDSEGS
RSSSSSSSSNNNNYCALGCYGGWHL
SALPGNTQSS
GPIPALACGLSCDHQGLETTQQGVAWVL
AGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSFYWAPPCYTLKPET
PD1/IL9R/cGC-F
SEQ ID NO: 95
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IVYWEMEDKNI IQFVHGEEDLKVQHSSYRQARLL
KDQLSLGNAALQITDVKLQDAGVYRCMISYGGADY
KRITVKVNAPYNKINQRI
LVDPVISEHELICOAE
GYPKAEVIWISSDHQVLSGKTTTTNSKREEKLFNV
ISILRINTTTNEIFYCTFRRLDPEENHTAELVIPE
LPLAHPNERLIPPWGWPGNTLVAVSIFLLLTGPT
YLLFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGN
FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA
LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSDVL
LPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPDSE
GSRSSSSSSSSNNNNYCALGCYGGWHL
SALPGNTQ

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SSGPIPALACGLSCDHQGLETOQGVAVWLAGHCQR

PGLHEDLQGMLLPSVLSKARSWTFGGGSGGGGSG

GGGSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVS

KGLAESLQPDYSERLCLVSEIPPKGGALGEGPGAS

PCNQHSPYWAPPCYTLKPET

PD1/IL9R/cGC-S

SEQ ID NO: 96

FTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAAL

IVYWEMEDKNI IQFVHGEEDLKVQHSSYRQARLL

KDQLSLGNAALQITDVKLQDAGVYRCMISYGGADY

KRITVKVNAPYNKINQRILVVDPVISEHELICOAE

GYPKAEVIWISSDHQVLSGKTTTTNSKREEKLFNV

ISILRINTTTNEIFYCTFRRLDPEENHTAELVIPE

LPLAHPPNERLIPPWGWPGNTLVAVSIFLLLTGPT

YLLFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGN

FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA

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LPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSE

GSRSSSSSSSSNNNYCALGCYGGWHL SALPGNTQ

SSGPIPALACGLSCDHQGLETOQGVAVWLAGHCQR

PGLHEDLQGMLLPSVLSKARSWTFQPPQPPQPPQ

PERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGL

AESLQPDYSERLCLVSEIPPKGGALGEGPGASPCN

QHSPYWAPPCYTLKPET

OPG/IL9R/cGC-F

SEQ ID NO: 97

ETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTA

KWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ

YVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPP

GFGVVQAGTPERN TVCKRCPDGGFSNETSSKAPCR

KHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCG

IDVTLCEEAFRRFAVPTKFTPNWLSVLVDNLPGTK

VNAESVERIKRQHSSQEQTQQLKLWKHQKNDQDI

VKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMES

LPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKN

GDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRF

LHSFTMYKLYQKLFLEMIGNQVQSVKISCLLIPPW

GWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFY

QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS

QDCAGTPQGALEPCVQEATALLTCGPARPWKSV

AL

EEQEGPGTRLPGNLSSDEVLPAGCTEWRVQTLAY

LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN

LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN

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HQGLETOQGVAVWLAGHCQRPGLHEDLQGMLLPSV

LSKARSWTFGGGSGGGGSGGGGSERTMPRIPTLK

NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL

CLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYT

LKPET

OPG/IL9R/cGC-S

SEQ ID NO: 98

ETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTA

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YVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPP

GFGVVQAGTPERN TVCKRCPDGGFSNETSSKAPCR

KHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCG

IDVTLCEEAFRRFAVPTKFTPNWLSVLVDNLPGTK

VNAESVERIKRQHSSQEQTQQLKLWKHQKNDQDI

VKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMES

LPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKN

GDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRF

LHSFTMYKLYQKLFLEMIGNQVQSVKISCLLIPPW

GWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFY

QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS

QDCAGTPQGALEPCVQEATALLTCGPARPWKSV

AL

EEQEGPGTRLPGNLSSDEVLPAGCTEWRVQTLAY

LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN

YCALGCYGGWHL SALPGNTQSSGPIPALACGLSCD

HQGLETOQGVAVWLAGHCQRPGLHEDLQGMLLPSV

LSKARSWTFQPPQPPQPPQPERTMPRIPTLKNLE

DLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLV

SEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKP

ET

TACI/IL9R/cGC-F

SEQ ID NO: 99

MSGLGRRRRGGRSRVDQEERFPQGLWTGVAMRSCP

EEQYWDPLLGTMSCKTICNHQSQR TCAAFCRSL

S

CRKEQGKFYDHLRDCISCASICGQHPKQ CAYFCE

NKL RSPVNLPPELRRQRSGEVENNSD NSGRYQGLE

HRGSEASPALPGLKLSADQVALVYSLIPPWGWPGN

TLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPS

PAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAG

TPQGALEPCVQEATALLTCGPARPWKSVALEEEQE

GPGTRLPGNLSSDEVLPAGCTEWRVQTLAYLPQED

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WAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALG
CYGGWHL SALPGNTQSSGPIPALACGLSCDHQGLE
TQQGVAWVL AGHCQRPGLHEDLQGM LLPSVLSKAR
SWTFGGGSGGGGSGGGGSERTMPRIPTLKNLEDL
VTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSE
IPPKGALGEGPGASPCNQHSPYWAPPCYTLKPET

TACI/IL9R/cGC-S
SEQ ID NO: 100
MSG LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCP
EEQYWDPLLGT CMSCKTICNHQSQRTCAAFCRS
LSCRKEQGKFYDHLRDCISCASICGQ
HPKQ CAYFCENKLRS PVNLPPELRRQRS GEVENNS
DNSGRYQGLEHRGSEASPALPGLKLSADQVALVYS
LIPPWGWP GNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPS PAMFFQPLYSVHNGNFQTWMAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSDVL PAGCTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSS
SNMNNYCALGCYGGWHL SALPGNTQSSGPIPALAC
GLSCDHQGLE TQQGVAWVL AGHCQRPGLHEDLQGM
LLPSVLSKARSWTFQPPQPPQPPQPPERTMPRIPT
LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE
RLCLVSEIPPKGALGEGPGASPCNQHSPYWAPPC
YTLKPET

BCMA/IL9R/cGC-F
SEQ ID NO: 101
MLQMAGQCSQNEYFDSL LHACIPCQLRCS SNTPL
TCQRYCNASVTNSVKGTNALIPPWGWP GNTLVAVS
IFLLLTGPTYLLFKLSPRVKRIFYQNVPS PAMFFQ
PLYSVHNGNFQTWMAHAGAGVLLSQDCAGTPQ GAL
EPCVQEATALLTCGPARPWKSVALEEEQEGPGTRL
PGNLSSDVL PAGCTEWRVQTLAYLPQEDWAPTS L
TRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWH
LSALPGNTQSSGPIPALACGLSCDHQGLE TQQGVA
WVL AGHCQRPGLHEDLQGM LLPSVLSKARSWTFGG
GGSGGGSGGGGSERTMPRIPTLKNLEDLVTEYHG
NFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKG
ALGEGPGASPCNQHSPYWAPPCYTLKPET

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BCMA/IL9R/cGC-S
SEQ ID NO: 102
MLQMAGQCSQNEYFDSL LHACIPCQLRCS SNTPL
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IFLLLTGPTYLLFKLSPRVKRIFYQNVPS PAMFFQ
PLYSVHNGNFQTWMAHAGAGVLLSQDCAGTPQ GAL
EPCVQEATALLTCGPARPWKSVALEEEQEGPGTRL
PGNLSSDVL PAGCTEWRVQTLAYLPQEDWAPTS L
TRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWH
LSALPGNTQSSGPIPALACGLSCDHQGLE TQQGVA
WVL AGHCQRPGLHEDLQGM LLPSVLSKARSWTFQ
PPQPPQPPPERTMPRIPTLKNLEDLVTEYHGNFS
AWSGVSKGLAESLQPDYSERLCLVSEIPPKGALG
EGPGASPCNQHSPYWAPPCYTLKPET

NGFR/IL9R/cGC-F
SEQ ID NO: 103
KEACPTGLYTHSGECKACNLGEGVAQPCGANQTV
CEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAP
CVEADDAVCRCAYGYQDETTGRCEACRVCEAGSG
LVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCT
VCEDTERQLRECTRWADAECEEIPGRWITRSTPPE
GSDSTAPSTQEPEAPPEQDLIASTVAGVVTTVMGS
SQPVVTRGTTDNLI PPWGWP GNTLVAVSIFLLLTG
PTYLLFKLSPRVKRIFYQNVPS PAMFFQPLYSVHN
GNFQTWMAHAGAGVLLSQDCAGTPQGALEPCVQEA
TALLTCGPARPWKSVALEEEQEGPGTRLPGNLSS
DVL PAGCTEWRVQTLAYLPQEDWAPTS LTRPAPPD
SEGSRSSSSSSSSNNNNYCALGCYGGWHL SALPGN
TQSSGPIPALACGLSCDHQGLE TQQGVAWVL AGHC
QRPGLHEDLQGM LLPSVLSKARSWTFGGGSGGGG
SGGGGSERTMPRIPTLKNLEDLVTEYHGNFSAWSG
VSKGLAESLQPDYSERLCLVSEIPPKGALGEGPG
ASPCNQHSPYWAPPCYTLKPET

NGFR/IL9R/cGC-S
SEQ ID NO: 104
KEACPTGLYTHSGECKACNLGEGVAQPCGANQTV
CEPCLDSVTFSDVVSATEPCKPCTECVGLQSM
SAPCVEADDAVCRCAYGYQDETTGRCE
ACRVCEAGSLVFSCQDKQNTVCEECPDGTYSDEA
NHVDPCLPCTVCEDTERQLRECTRWADAECEEIPG
RWITRSTPPEGSDSTAPSTQEPEAPPEQDLIASTV
AGVVTTVMGSSQPVVTRGTTDNLI PPWGWP GNTLV

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AVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSAM

FFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQ

GALEPCVQEATALLTCGPARPWKSVALEEEQEGPG

TRLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAP

TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCYG

GWHLSALPGNTQSSGPIPALACGLSCDHQGLETTQ

GVAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWT

FQPPQPPQPPQPPERTMPRIPTLKNLEDLVTEYHG

NFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGG

ALGEGPGASPCNQHSFYWAPPCTYTLKPET

EDAR/IL9R/cGC-F

SEQ ID NO: 105

EYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCG

YGTKDEDYGCVPKPAEKFSKGGYQICRRHKDCGEF

FRATVLTGDMENDAECGPCLPGYYMLENRPRNIY

GMVCYSCLLAPPNTKECVGATSGASANFPGTSGSS

TLSPFQHAHKELSGQGHLLATALLPPWGWPGNTLVA

VSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSAMFF

FQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQG

ALEPCVQEATALLTCGPARPWKSVALEEEQEGPGT

RLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAPT

SLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGG

WHLALPGNTQSSGPIPALACGLSCDHQGLETTQ

VAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWTF

GGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTEY

HGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPK

GGALGEGPGASPCNQHSFYWAPPCTYTLKPET

EDAR/IL9R/cGC-S

SEQ ID NO: 106

EYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCG

YGTKDEDYGCVPKPAEKFSKGGYQICRRHKDCGEF

FRATVLTGDMENDAECGPCLPGYYMLENRPRNIY

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TLSPFQHAHKELSGQGHLLATALLPPWGWPGNTLVA

VSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSAMFF

FQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQG

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SLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGG

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VAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWTF

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QPPQPPQPPQPPERTMPRIPTLKNLEDLVTEYHGN

FSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGA

LGEFGASPCNQHSFYWAPPCTYTLKPET

DCR2 (TNFRSF10D)/IL9R/cGC-F

SEQ ID NO: 107

ATIPRQDEVPPQTVAPQQQRRSLKEEECPAGSHRS

EYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQ

TNKSSCTTTRDTVQCEKGSFQDKNSPEMCRCTCT

GCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAA

EETVTTILGMLASPHYHLIPWGWPGNTLVAVSIFL

LLTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLY

SVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPC

VQEATALLTCGPARPWKSVALEEEQEGPGTRLPGN

LSSDVLPAAGCTEWRVQTLAYLPQEDWAPTSLTRP

APPDSEGSRSSSSSSSSNNNNYCALGCYGGWHLA

LPGNTQSSGPIPALACGLSCDHQGLETTQGVAVVL

AGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGGGS

GGGGSGGGGSERTMPRIPTLKNLEDLVTEYHGNFS

AWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALG

EGPGASPCNQHSFYWAPPCTYTLKPET

DCR2 (TNFRSF10D)/IL9R/cGC-S

SEQ ID NO: 108

ATIPRQDEVPPQTVAPQQQRRSLKEEECPAGSHRS

EYTGACNPCTEGVDYTIASNNLPSCLLCTVC

KSGQTNKSSCTTTRDTVQCEKGSFQDKN

SPEMCRCTCTGCPRGMVKVSNCTPRSDIKCKNESA

ASSTGKTPAAEETVTTILGMLASPHYHLIPWGWPG

NTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNV

SPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCA

GTPQGALEPCVQEATALLTCGPARPWKSVALEEEQ

EGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLPQE

DWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCAL

GCYGGWHLALPGNTQSSGPIPALACGLSCDHQGL

ETQQGVAVVLAGHCQRPGLHEDLQGMLLPSVLSKA

RSWTFQPPQPPQPPQPPERTMPRIPTLKNLEDLV

EYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIP

PKGGALGEGPGASPCNQHSFYWAPPCTYTLKPET

DCR1 (TNFRSF10C)/IL9R/cGC-F

SEQ ID NO: 109

ATTARQEEVPPQTVAPQQQRHSFKGEECPAGSHRS

EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQ

KHKSSCTMTRDTVQCEKGTFRNENSPEMCRKCSR

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CPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAE

ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTT

SPGTPAPAAEETMTTSPGTPAPAAEETMITSPGTP

ALIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPR

VKRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHG

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WKSVALEEEQEGPGTRLPGNLSSDVLPACTEWR

VQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS

SSNMNNYCALGCYGGWHLSPALPGNTQSSGPIPALA

CGLSCDHQGLETTQQGVAWVLAGHCQRPGLHEDLQG

MLLPSVLSKARSWTFGGGSGGGSGGGGSERTMP

RIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQP

DYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYW

APPCYTLKPET

DCR1 (TNFRSF10C) /IL9R/cGC-S

SEQ ID NO: 110

ATTARQEEVPQQTVPAPQQQRHSFKGEECPAGSHRS

EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQ

KHKSSCTMTRDTVQCCKEGTFRNENSPMCRKCSR

CPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAE

ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTT

SPGTPAPAAEETMTTSPGTPAPAAEETMITSPGTP

ALIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPR

VKRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHG

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WKSVALEEEQEGPGTRLPGNLSSDVLPACTEWR

VQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS

SSNMNNYCALGCYGGWHLSPALPGNTQSSGPIPALA

CGLSCDHQGLETTQQGVAWVLAGHCQRPGLHEDLQG

MLLPSVLSKARSWTFQPPQPQPQPQPPERTMPRIIP

TLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYS

ERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPP

CYTLKPET

CD40/IL9R/cGC-F

SEQ ID NO: 111

EPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFT

ETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLR

VQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC

SPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEK

CHPWTSCETKDLVVQAGTNKTDVVCQPQDRLRLI

PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR

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IFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGV

LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS

VALEEEQEGPGTRLPGNLSSDVLPACTEWRVQT

LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN

NNNYCALGCYGGWHLSPALPGNTQSSGPIPALACGL

SCDHQGLETTQQGVAWVLAGHCQRPGLHEDLQGMLL

PSVLSKARSWTFGGGSGGGSGGGGSERTMPRIIP

TLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYS

ERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPP

CYTLKPET

CD40/IL9R/cGC-S

SEQ ID NO: 112

EPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFT

ETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLR

VQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC

SPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEK

CHPWTSCETKDLVVQAGTNKTDVVCQPQDRLRLI

PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR

IFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGV

LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS

VALEEEQEGPGTRLPGNLSSDVLPACTEWRVQT

LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN

NNNYCALGCYGGWHLSPALPGNTQSSGPIPALACGL

SCDHQGLETTQQGVAWVLAGHCQRPGLHEDLQGMLL

PSVLSKARSWTFOPQPQPQPQPQPPERTMPRIPTLK

NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL

CLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYT

LKPET

FAS/IL9R/cGC-F

SEQ ID NO: 113

QVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH

KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA

HFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCK

PNFFCNSTVCEHCDPCTKCEHGIIKECTLTSTNTKC

KEEGSRSNLIPPWGWPGNTLVAVSIFLLLTGPTYL

LFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNFQ

TWGAHGAGVLLSQDCAGTPQGALEPCVQEATALL

TCGPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA

AGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS

RSSSSSSSSNMNNYCALGCYGGWHLSPALPGNTQSS

GPIPALACGLSCDHQGLETTQQGVAWVLAGHCQRP

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LHEDLQGMLLPVLSKARSWTFGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSPYWAPPCYTLKPET
FAS/IL9R/cGC-S
SEQ ID NO: 114
QVTDINSKGLELRKTVTTVETQNLLEGLHHDGQFCH
KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA
HFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCK
PNFFCNSTVCEHCDPCKCEHGIIKECTLTSTNKC
KEEGSRSNLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
GCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
RSSSSSSNNNNYCALGCYGGWHLALPGNTQSS
GPIPALACGLSCDHQGLETOQGVAVVLAGHCQRP
LHEDLQGMLLPVLSKARSWTFQPPQPPQPPQPE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAE
SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQ
SPYWAPPCYTLKPET
DR4/IL9R/cGC-F
SEQ ID NO: 115
ASGTEAAAATPSKVWSSAGRIEPRGGGRGALPTS
MGQHGPSARARAGRAPGPRPAREASPRLRVHKTFK
FVVVGVLQVVPSSAATIKLHDQSIGTQQWEHSPL
GELCPPGSHRSEHPGACNRCTEGVGYTNASNNLFA
CLPCTACKSDEEERSPCTTTRNTACQCKPGTFRND
NSAEMCRKCSRGCPRGMVKVDCTPWSDIECVHKE
SGNGHNLIPPWGWPGNTLVAVSIFLLLTGPTYLLF
KLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLTC
GPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
CTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
SSSSSSNNNNYCALGCYGGWHLALPGNTQSSGP
IPALACGLSCDHQGLETOQGVAVVLAGHCQRPGLH
EDLQGMLLPVLSKARSWTFGGGSGGGSGGGSGGG
ERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLA
ESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQ
HSPYWAPPCYTLKPET

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DR4/IL9R/cGC-S
SEQ ID NO: 116
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MGQHGPSARARAGRAPGPRPAREASPRLRVHKTFK
FVVVGVLQVVPSSAATIKLHDQSIGTQQWEHSPL
GELCPPGSHRSEHPGACNRCTEGVGYTNASNNLFA
CLPCTACKSDEEERSPCTTTRNTACQCKPGTFRND
NSAEMCRKCSRGCPRGMVKVDCTPWSDIECVHKE
SGNGHNLIPPWGWPGNTLVAVSIFLLLTGPTYLLF
KLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLTC
GPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
CTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
SSSSSSNNNNYCALGCYGGWHLALPGNTQSSGP
IPALACGLSCDHQGLETOQGVAVVLAGHCQRPGLH
EDLQGMLLPVLSKARSWTFQPPQPPQPPQPERT
MPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESL
QPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSP
YWAPPCYTLKPET
DR6/IL9R/cGC-F
SEQ ID NO: 117
QPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYV
SEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQ
PCPWPMEKLPALTDRECTCPPGMFQSNATCAP
HTVCPVGWVRKKGTETEDVRCKQCARGTFSDVPS
SVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPS
FSSSTSPSPGTAIFPRPEHMETHEVPSSTYVPKG
NSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKE
DVNKTLPNLQVNVHQQGPHRHILKLLPSMEATGG
EKSSTPIKGPKRGRHPRQNLKHFDINEHLIPPWGW
PGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQ
NVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLTC
GPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA
CTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
SSSSSSNNNNYCALGCYGGWHLALPGNTQSSGP
IPALACGLSCDHQGLETOQGVAVVLAGHCQRPGLH
EDLQGMLLPVLSKARSWTFGGGSGGGSGGGSGGG
ERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

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DR6/IL9R/cGC-S
SEQ ID NO: 118
QPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYV
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PCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAP
HTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPS
SVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLP
FSSSTSPSPGTAFPRPEHMETHEVPSSTYVPGM
NSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKE
DVNKTLPNLQVVNHQQGPHHRHILKLPSMEATGG
EKSSTPIKGPGRGHPRQNLHKHFDINEHLIPPGW
PGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQN
VPSPAMFFQPLYSVHNGNFQTMGAHGAGVLLSQD
CAGTPQGALEPCVQEATALLTCGPAPWKSVALEE
EQEGPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLP
QEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYC
ALGCYGGWHLALPGNTQSSGPIPALACGLSCDHQ
GLETQQGVAVVLAGHCQRPGLHEDLQGMLLPSVLS
KARSWTFQPPQPPQPPQPPERTMPRIPTLKNLEDL
VTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSE
IPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET
DR5/IL9R/cGC-F
SEQ ID NO: 119
ITQODLAPQORAAPQQRSSPSEGLCPPGHISED
GRDCISCKYQDYSTHWNLLFCLRCTRCDSGEVE
LSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGC
PRGMVKVGDCTPWSIDIECVHKESGTHSGEVP
ETVTSSPGTPASPCSLIPPGWPGNTLVAVSIFLL
LTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLYS
VHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPCV
QEATALLTCGPAPWKSVALEEEQEGPGTRLPGNL
SSDVLPAAGCTEWRVQTLAYLPQEDWAPTSLTRPA
PPDSEGSRSSSSSSSSNNNNYC
ALGCYGGWHLALPGNTQSSGPIPALACGLSCDHQ
GLETQQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGGSGGGGSGGGGSE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSK
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DR5/IL9R/cGC-S
SEQ ID NO: 120
ITQODLAPQORAAPQQRSSPSEGLCPPGHISED
GRDCISCKYQDYSTHWNLLFCLRCTRCDSGEVE

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LSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGC
PRGMVKVGDCTPWSIDIECVHKESGTHSGEVP
ETVTSSPGTPASPCSLIPPGWPGNTLVAVSIFLL
LTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLYS
VHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPCV
QEATALLTCGPAPWKSVALEEEQEGPGTRLPGNL
SSDVLPAAGCTEWRVQTLAYLPQEDWAPTSLTRPA
PPDSEGSRSSSSSSSSNNNNYC
ALGCYGGWHLALPGNTQSSGPIPALACGLSCDHQ
GLETQQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGGSGGGGSGGGGSE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSK
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ASPCNQHSPYWAPPCYTLKPET
DR3/IL9R/cGC-F
SEQ ID NO: 121
QGGTRSPRCDACAGDFHKKIGLFCCRCGPAGHYLKA
PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA
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SQCVSSSPFYCQPCLDGALHRHTRLLCSRRTDCGT
CLPGFYEHDGCVSCPTSTLGSCPERCAAVCGWRQ
LIPPGWPGNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPAPW
KSVALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRV
QTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS
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GLETQQGVAVVLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGGSGGGGSGGGGSE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSK
GLAESLQPDYSERLCLVSEIPPKGGALGEGPG
ASPCNQHSPYWA
PPCYTLKPET
DR3/IL9R/cGC-S
SEQ ID NO: 122
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SQCVSSSPFYCQPCLDGALHRHTRLLCSRRTDCGT
CLPGFYEHDGCVSCPTSTLGSCPERCAAVCGWRQ
LIPPGWPGNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPAPW

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KSVALEEEQEGPGTRLPGNLSSDVLPA GCTEWRV

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GLSCDHQGLETQQGVAWVL AGHCQRPGLHEDLQGM

LLPSVLSKARSWTFQPQPQPQPQP PERTMPRIPT

LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE

RLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPC

YTLKPET

TNFRSF1B/IL9R/cGC-F

SEQ ID NO: 123

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LSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCK

PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMD

AVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPE

PSTAPSTS FLLPMGPSPPAEGSTGDLIPPWGWPGN

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CYGGWHL SALPGNTQSSGPIPALACGLSCDHQGLE

TQQGVAWVL AGHCQRPGLHEDLQGM LPSVLSKAR

SWTFGGGSGGGGSGGGGSERTMPRIPTLKNLEDL

VTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSE

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TNFRSF1B/IL9R/cGC-S

SEQ ID NO: 124

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LSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCK

PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMD

AVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPE

PSTAPSTS FLLPMGPSPPAEGSTGDLIPPWGWPGN

TLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPS

PAMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAG

TPQGALEPCVQEATALLTCGPARPWKSVALEEEQE

GPGTRLPGNLSSDVLPA GCTEWRVQTLAYLPQED

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CYGGWHL SALPGNTQSSGPIPALACGLSCDHQGLE

TQQGVAWVL AGHCQRPGLHEDLQGM LPSVLSKAR

SWTFQPQPQPQPQPQP PERTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP

KGGALGEGPGASPCNQHSPYWAPPCYTLKPET

TNFRSF1/IL9R/cGC-F

SEQ ID NO: 125

LVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHK

GTLYNDCPGPGQD TDCRECESGSFTASENHLRHC

LSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRH

YWSENLFQCFNC SLCLNGTVHLSCQEKQNTVCTCH

AGFFLRENECVSCSNCKKSLECTKLCLPQIENVKG

TEDSGTTLIPPWGWPGN TLVAVSIFLLLTGPTYLL

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SSSSSSSSNNMNYCALGCYGGWHL SALPGNTQSSG

PIPALACGLSCDHQGLETQQGVAWVL AGHCQRPGL

HEDLQGM LPSVLSKARSWTFGGGSGGGGSGGGG

SERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGL

AESLQPDYSERLCLVSEIPPKGGALGEGPGASPCN

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TNFRSF1/IL9R/cGC-S

SEQ ID NO: 126

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LSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRH

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PIPALACGLSCDHQGLETQQGVAWVL AGHCQRPGL

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BMPR1B/IL9R/CGC-F
SEQ ID NO: 127
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TPIPHQRRSIECCTERNECNKDLHPTLPPLKNRDF
VDGPIHHRLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSDEVLP
AGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
RSSSSSSSSNNNNYCALGCGYGGWHL
SALPGNTQSS
GPIPALACGLSCDHQGLE
TQQGVAVWLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSPYWAPPCYTLKPET
BMPR1B/IL9R/CGC-S
SEQ ID NO: 128
KKEDGESTAPT
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TDGYCFTMIEEDDSGLPVVTSGCLGLEGSDFQCRD
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VDGPIHHRLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
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SALPGNTQSS
GPIPALACGLSCDHQGLE
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LLPSVLSKARSWTFQPPQPPQPPQPPQPE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAE
SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQH
SPYWAPPCYTLKPET
BMPR1A/IL9R/CGC-F
SEQ ID NO: 129
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SMLHGTGMKSDSDQK
KSENGVT
LAPEDTL
PF
LKCYCSGHC
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LCNQYLQPTLPPVIGPFFDGSIRLIPPWGWPGNT
LVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPS
PAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGT
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APTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGC
YGGWHL
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WTFGGGGSGGGSGGGGSERTMPRIPTLKNLEDLV
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PPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET
BMPR1A/IL9R/CGC-S
SEQ ID NO: 130
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KSENGVT
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LVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPS
PAMFFQPLYSVHNGNFQ
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PGTRLPGNLSSDEVLPAGCTEWRVQTLAYLPQEDW
APTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGC
YGGWHL
SALPGNTQSSGPIPALACGLSCDHQGLE
TQQGVAVWLAGHCQRPGLHEDLQGM
LLPSVLSKARS
WTFQPPQPPQPPQPPQPERTMPRIPTLKNLEDLVTEY
HGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPK
GGALGEGPGASPCNQHSPYWAPPCYTLKPET
BMPR2/IL9R/CGC-F
SEQ ID NO: 131
SQNQERLCAFKDPYQQDLGIGESRISHENG
TILCS
KGSTCYGLWEKSKGDINLVKQGCWSHIGDPQ
ECHY
EECVVTTTPPSIQNGTYRFCCCSTDLCNVNFTEN
F
PPPD
TTPLSPPHSFNRDET
LIPPWGWPGNTLVAVS
IFLLLTGPTYLLFKLSPRVKRIFYQNVSPAMFFQ
PLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGPARPWKSVALEEEQEGPGTRLPGNLSSDEVLPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCGYGGWHL
LSALPGNTQSSGPIPALACGLSCDHQGLE
TQQGVAVWLAGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET
BMPR2/IL9R/CGC-S
SEQ ID NO: 132
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TILCS
KGSTCYGLWEKSKGDINLVKQGCWSHIGDPQ
ECHY

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EECVVTTTPPSIQNGTYRFCCSTDL CNVNFTENF
PPPDTTPLSPPHSFNRDETLIPPWGWPGNTLVAVS
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LSALPGNTQSSGPIPALACGLSCDHQGLETQQGVA
WVLAGHCQRPG LHEDLQGMLLPSVLSKARSWTFQP
QPQPQPQPQP PERTMPRIPTLKNLEDLVTEYHG NFS
AWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALG
EGPGASPCNQHSPYWAPPCYTLKPET
CSF3R/IL9R/cGC-F
SEQ ID NO: 133
ECGHSVSAPIVHLGDPITASCIIKQNC SHLDPEP
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SCLMNLTSSSLICQWEPGPETHLPTSFTLKSFKSR
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WRPSGQAGAILPLCNTTELSCTFHLPSEAQ EVALV
AYNSAGTSRPTPVVFSESRGPALTRLHAMARDPHS
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SQHVYAYSQEMAPSHAPELHLKHIKGTWAQLEWVP
EPPELGKSPLTHYTI FWTNAQNQSFSAILNASSRG
FVLHGLEPASLYHIHLMAASQAGATNSTVLT LMTL
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LFKLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
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GPIPALACGLSCDHQGLETQQGVAVWLAGHCQRPG
LHEDLQGMLLPSVLSKARSWTFQPQPQPQPQPQPE
RTMPRIPTLKNLEDLVTEYHG NFSAWSGVSKGLAE
SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQH
SPYWAPPCYTLKPET
CSF1R/IL9R/cGC-F
SEQ ID NO: 135
IPVIEPSVP ELVVKPGATVTLRCVGNGSVEWDGPP
SPHWTLYSDGSSSILSTNNATFQNTGTYRCTEPGD
PLGGSAAIHLVYKDPARPWNVLAQE VVVFEQDAL
LPCLLTDPVLEAGVSLVRVRGRPLMRHTNYSFSPW
HGFTIHRAKFIQSQDYQCSALMGGRKVMSSISIRLK
VQKVI PGPPALTLVPAELVRIRGEAAQIVCSASSV
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LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
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CSF3R/IL9R/cGC-S
SEQ ID NO: 134
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QILWRLGAELQPGGRQQRLSDGTQESIITLPHLNH
TQAFLLSCCLNWGNSLQILDQVELRAGYPPAIPHNL
SCLMNLTSSSLICQWEPGPETHLPTSFTLKSFKSR
GNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNM
GIWVQAENALGTSMSPLCLDPMDVVKLEPPMLRT
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HKPQRGEASWALVGPLPLEALQYELCGLLPATAYT
LQIRCIRWPLPGHWSDWSPSLELRTERAPT VRLD
TWWRQRQLDPRTVQLFWKPVPLEEDSGRIQGYVVS
WRPSGQAGAILPLCNTTELSCTFHLPSEAQ EVALV
AYNSAGTSRPTPVVFSESRGPALTRLHAMARDPHS
LWVGWEPPNPWPQGYVIEWGLGPPSASNSNKTWRM
EQNGRATGFLLKENIRPFQLYEIIVTPLYQD TMGP
SQHVYAYSQEMAPSHAPELHLKHIKGTWAQLEWVP
EPPELGKSPLTHYTI FWTNAQNQSFSAILNASSRG
FVLHGLEPASLYHIHLMAASQAGATNSTVLT LMTL
TPEGSELHLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVSPAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSDVLP
AGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
RSSSSSSSSNNNNYCALGCYGGWHLSALPGNTQSS
GPIPALACGLSCDHQGLETQQGVAVWLAGHCQRPG
LHEDLQGMLLPSVLSKARSWTFQPQPQPQPQPQPE
RTMPRIPTLKNLEDLVTEYHG NFSAWSGVSKGLAE
SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQH
SPYWAPPCYTLKPET
CSF1R/IL9R/cGC-F
SEQ ID NO: 135
IPVIEPSVP ELVVKPGATVTLRCVGNGSVEWDGPP
SPHWTLYSDGSSSILSTNNATFQNTGTYRCTEPGD
PLGGSAAIHLVYKDPARPWNVLAQE VVVFEQDAL
LPCLLTDPVLEAGVSLVRVRGRPLMRHTNYSFSPW
HGFTIHRAKFIQSQDYQCSALMGGRKVMSSISIRLK
VQKVI PGPPALTLVPAELVRIRGEAAQIVCSASSV
DVNFDVFLQHNNTKLAIPQQSDFHNNRYQKVLT LN

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LDQVDFQHAGNYS CVASNVQGHSTSMFFRVVESA
YLNLSSEQNLIQEVTVGEGNLKVMVEAYPGLQGF
NWTYLGPFSDHQPEPKLANATTKDTYRHTFTLSLP
RLKPSEAGRYSFLARNPGWRALTFELTLRYPPEV
SVIWTFINGSGTLLCAASGYQPNTWLQCSGHTD
RCDEAQVLQVWDDPYPEVLSQEPFHKVTVQSLLTV
ETLEHNQTYECRAHNSVGSGSWAFIPISAGATHP
PDEFLFTPLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSADVLP
AGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
RSSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSS
GPIPALACGLSCDHQGLETTQQGVAVVLAGHCQRP
GHEDLQGMLLPSVLSKARSWTFGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSPYWAPPCYTLKPET
CSF1R/IL9R/cGC-S
IPVIEPSVPELVVKPGATVTLRCVGNSSVEWDGPP
SPHWTLYSDGSSSILSTNNATFQNTGTYRCTEPGD
PLGGSAAIHLYVKDPAWPVLAQEVVVFEDQDAL
LPCLLTDPVLEAGVSLVRVRGRPLMRHTNYSFSPW
HGFTIHRAKFIQSQDYQCSALMGRKVMSSISIRLK
VQKVI PGPPALTLVPAELVRIRGEAAQIVCSASSV
DVNFDVFLQHNNTKLAIPQQSDFHNNRYQKVLTLN
LDQVDFQHAGNYS CVASNVQGHSTSMFFRVVESA
YLNLSSEQNLIQEVTVGEGNLKVMVEAYPGLQGF
NWTYLGPFSDHQPEPKLANATTKDTYRHTFTLSLP
RLKPSEAGRYSFLARNPGWRALTFELTLRYPPEV
SVIWTFINGSGTLLCAASGYQPNTWLQCSGHTD
RCDEAQVLQVWDDPYPEVLSQEPFHKVTVQSLLTV
ETLEHNQTYECRAHNSVGSGSWAFIPISAGATHP
PDEFLFTPLIPPWGWPGNTLVAVSIFLLLTGPTYL
LFKLSPRVKRIFYQNVPSAMFFQPLYSVHNGNFQ
TWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSSADVLP
AGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGS
RSSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSS

SEQ ID NO: 136

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GPIPALACGLSCDHQGLETTQQGVAVVLAGHCQRP
GHEDLQGMLLPSVLSKARSWTFQQPQPQPQPQPE
RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAE
SLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQ
SPYWAPPCYTLKPET
VEGF Receptor 1/IL9R/cGC-F
SKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKW
SLPEMVSKESERLSITKSACGRNGKQFCSTLTNT
AQANHTGFYSCKYLAVPTSKKTESAIYIFISDT
GRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNIT
VTLKKFPLDTLIPDGKRIIWD SRKGFIISNATYKE
IGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQIST
PRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDE
KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDK
GLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQ
QVLETVAGKRSYRLSMKVKAFFSPEVVWLKDGLPA
TEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQ
SNVFNLTATLIVNVKQIYEKAVSSFPDPALYPL
GSRQILTCTAYGIPQPTIKFWHPCNHNHSEARCD
FCSNNEESFILDADSNMGNRIESITQRMALIEGKN
KMASTLVVADSRISGIYICIASNKVGTVGRNISFY
ITDVPNGFHVNLKMPTEGEDLKL SCTVNKFLYRD
VTWILLRTVNNRTMHYSISKQKMAITKEHSITLNL
TIMNVSLQDSGTYACRARNVYTGEIILQKEITIR
DQEAPYLLRNLSDH TVAISSSTLTDCHANGVPEPQ
ITWFKNNHKIQQEPGII LGPGSSSTLFIERVTEEDE
GVYHCKATNQKGSVESSAYLTVQGTSDKSNLELIP
PWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRI
FYQNVPSAMFFQPLYSVHNGNFQTWMGAHGAGVL
LSQDCAGTPQGALEPCVQEATALLTCGPARPWKSV
ALEEEQEGPGTRLPGNLSSADVLPAGCTEWRVQTL
AYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNN
NNYCALGCYGGWHL SALPGNTQSSGPIPALACGLS
CDHQGLETTQQGVAVVLAGHCQRPGLHEDLQGMLLP
SVLSKARSWTFGGGSGGGSGGGGSERTMPRIPT
LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE
RLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPC
YTLKPET

SEQ ID NO: 137

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VEGF Receptor 1/IL9R/cGC-S
SEQ ID NO: 138
SKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKW
SLPEMVSKESERLSITKSACGRNGKQFCSTLTLNT
AQANHTGFYSCKYLAVPTSKKKETESAIYIFISDT
GRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNIT
VTLKKFPLDTLIPDGKRIIWDSRKGFIIISNATYKE
IGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQIST
PRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDE
KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDK
GLYTCTVRSGPSFKSVNTSVHIYDKAFITVKHRKQ
QVLETVAGKRSYRLSMKVKAFPSPEVVWLKDGLPA
TEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQ
SNVFKNLTATLIVNVKPQIYEKAVSSFDPALYPL
GSRQILTCTAYGIPQPTIKFWHPCNHNHSEARCD
FCSNNEESFILDADSNMGNRIESITQORMAIEGKN
KMASTLVVADSRISGIYICIASNKVGTVGRNISFY
ITDVPNGFHVNLKMPTEGEDLKL SCTVNKFLYRD
VTWILLRTVNNRTMHYSISKQKMAITKEHSITLNL
TIMNVSLQDSGTYACRARNVYTGEEILQKKEITIR
DQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQ
ITWFKNNHKIQQEPGIILGPGSSTLFIERVTEEDE
GVYHCKATNQKGSVLESSAYLTVQGTSDKSNLELIP
PWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRI
FYQNVPS PAMFFQPLYSVHNGNFQ TWMGAHGAGVL
LSQDCAGTPQGALEPCVQEATALLTCGPARPWKSV
ALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQTL
AYLPQEDWAPTSLTRPAPPDSEGRSSSSSSSSSNN
NNYCALGCYGGWHL SALPGNTQSSGPIPALACGLS
CDHQGLETQQGVAVVL AGHCQR PGLHEDLQGM LLP
SVLSKARSWTFQPQPQPQPQP PERTMPRIPTLKN
LEDLVTEYHG NFSAWSGVSKGLAESLQPDY SERLC
LVSEIPPKGGALGEGPGASPCNQHSPYWAPP CYTL
KPET
VEGF Receptor 2/IL9R/cGC-F
SEQ ID NO: 139
ASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCR
GQRDLDWLWPNNQSGSEQRVEVTECSDGLFCKTLT
IPKVIGNDTGAYKCFYRETDLASVIYVYVQDYRSP
FIASVSDQHGVVYITENKNKTVVIPCLGSISNLNV
SLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISY

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AGMVFCEAKINDESYQSIMYIVVVVG YRIYDVVLS
PSHGIELSVGEKLV LNCTARTELVGIDFNWEYPS
SKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTR
SDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGS
GMESLVEATVGERVRIPAKYLGYPPEIKWYKNGI
PLESNHTIKAGHVLTIMEVSE RDTGNYTVILTNP I
SKEKQSHVVS LVVYVPPQIGEKSLISP VDSYQYGT
TQTLTCTVYAI PPPHHIHWYQLEEECANEPSQAV
SVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEG
KNKTVSTLV IQAANVSALYKCEAVNKVGRGERVIS
FHVTRGPEITLQPD MQPTEQESVSLWCTADRSTFE
NLTWYKLG PQPLPIHV GELPTPVCKNLDTLWKLNA
TMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKT
KKRHCVVRQLTVL ERVAPTITGNLENQTTSIGESI
EVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGN
RNLTI RVRKEDEGLYTCQACSVLGCAKVEAFFII
EGAQEKTNLELIPPWGWPGNTLVAVSIFLLLTGPT
YLLFKLSPRVKRIFYQNVPS PAMFFQPLYSVHNGN
FQ TWMGAHGAGVLLS QDCAGTPQGALEPCVQEATA
LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSEDV
LPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSE
GSRSSSSSSSSNNNYCALGCYGGWHL SALPGNTQ
SSGPIPALACGLSCDHQGLETQQGVAVVL AGHCQR
PGLHEDLQGM LLPSVLSKARSWTFGGGSGGGGSG
GGGSERTMPRIPTLKNLEDLVTEYHG NFSAWSGV S
KGLAESLQPDY SERLC LVSEIPPKGGALGEGPGAS
PCNQHSPYWAPP CYTLKPET
VEGF Receptor 2/IL9R/cGC-S
SEQ ID NO: 140
ASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCR
GQRDLDWLWPNNQSGSEQRVEVTECSDGLFCKTLT
IPKVIGNDTGAYKCFYRETDLASVIYVYVQDYRSP
FIASVSDQHGVVYITENKNKTVVIPCLGSISNLNV
SLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISY
AGMVFCEAKINDESYQSIMYIVVVVG YRIYDVVLS
PSHGIELSVGEKLV LNCTARTELVGIDFNWEYPS
SKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTR
SDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGS
GMESLVEATVGERVRIPAKYLGYPPEIKWYKNGI
PLESNHTIKAGHVLTIMEVSE RDTGNYTVILTNP I

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SKEKQSHVSVLVVYVPPQIGEKSLISPVDSYQYGT

TQTLTCTVYAI PPPHHIHWYQLEEECANEPSQAV

SVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEG

KNKTVSTLVIQAANVSALYKCEAVNKVGRGERVIS

FHVTRGPEITLQPDMPTEQESVSLWCTADRSTFE

NLTWYKLGPOPLPIHVGE LPTPVCKNLDTLWKLNA

TMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKT

KKRHCVVRQLTVLERVAPTITGNLENQTTSIGESI

EVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGN

RNLTIRVRKEDEGLYTCOACSVLGCAKVEAFFII

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FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA

LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSDEV

LPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSE

GSRSSSSSSSSNNNNYCALGCYGGWHL SALPGNTQ

SSGPIPALACGLSCDHQGLETQQGVAVVL AGHCQR

PGLHEDLQGMLLPSVLSKARSWTFQPQPQPQPQPQ

PERTMPRIPTLKNLEDLVTEYHG NFSAWSGVSKGL

AESLQPDYSERLCLVSEIPPKGGALGEGPGASPCN

QHSPYWAPPCYTLKPET

VEGF Receptor 3/IL9R/cGC-S

SEQ ID NO: 141

YSMTPTLNITEESHVIDTGDSL SISC RGQHPLEW

AWPGAQEAPATGDKDSED TG VVRDCEGTDARPYCK

VLLLHEVHANDTGSYVCYYKYI KARI EGTTAASSY

VFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPG

LNVT LRSQSSVLWPDGQEVVWDDRRGMLVSTPLLH

DALYLQCETTWDQDFLSNPFLVHITGNELYDIQL

LPRKSLELLVGEKLV LNCTVWAEFN SGVTFDWDYP

GKQAERGKWVPERRSQQTH TELSSILTIHNVSQHD

LGSYVCKANNGIQRFRESTEVI VHENPFISVEWLK

GPILEATAGDELVKLPVKLAAYPPPEFQWYKD GKA

LSGRHSPHALVLKEVTEASTGT YTLALWNSAAGLR

RNISLELVVNVPPQIHEKEASSPSIYSRHSRQALT

CTAYGVPLPLSIQWHWPWTPCKMFAQRSLRRRQQ

QDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGK

NKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYF

YVTTIPDGFTIESKPSEELLEGPVLLSCQADSYK

YEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATP

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LAASLEEVAPGARHATLSLSIPRVAPEHEGHYVCE

VQDRRSHDKHCHKKYL SVQALEAPRLTQNLTDLLV

NVSDSLEMQCLVAGAHAPSI VYKDERLLEEKSGV

DLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNS

SASVAVEGSEDKGSME LI PPWGWP GNTLVAVSIFL

LLTGPTYLLFKLSPRVKRIFYQNVPS PAMFFQPLY

SVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPC

VQEATALLTGPARPWKSVALEEEQEGPGTRLPGN

LSSDEVLPAGCTEWRVQTLAYLPQEDWAPTSLTRP

APPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL SA

LPGNTQSSGPIPALACGLSCDHQGLETQQGVAVVL

AGHCQRPGLHEDLQGMLLPSVLSKARSWTFQPQPQ

PQPQPQPERTMPRIPTLKNLEDLVTEYHG NFSAWS

GVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGP

GASPCNQHSPTYWAPPCYTLKPET

VEGF Receptor 3/IL9R/cGC-F

SEQ ID NO: 142

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VLLLHEVHANDTGSYVCYYKYI KARI EGTTAASSY

VFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPG

LNVT LRSQSSVLWPDGQEVVWDDRRGMLVSTPLLH

DALYLQCETTWDQDFLSNPFLVHITGNELYDIQL

LPRKSLELLVGEKLV LNCTVWAEFN SGVTFDWDYP

GKQAERGKWVPERRSQQTH TELSSILTIHNVSQHD

LGSYVCKANNGIQRFRESTEVI VHENPFISVEWLK

GPILEATAGDELVKLPVKLAAYPPPEFQWYKD GKA

LSGRHSPHALVLKEVTEASTGT YTLALWNSAAGLR

RNISLELVVNVPPQIHEKEASSPSIYSRHSRQALT

CTAYGVPLPLSIQWHWPWTPCKMFAQRSLRRRQQ

QDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGK

NKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYF

YVTTIPDGFTIESKPSEELLEGPVLLSCQADSYK

YEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATP

LAASLEEVAPGARHATLSLSIPRVAPEHEGHYVCE

VQDRRSHDKHCHKKYL SVQALEAPRLTQNLTDLLV

NVSDSLEMQCLVAGAHAPSI VYKDERLLEEKSGV

DLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNS

SASVAVEGSEDKGSME LI PPWGWP GNTLVAVSIFL

LLTGPTYLLFKLSPRVKRIFYQNVPS PAMFFQPLY

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SVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEPC
VQEATALLTCGPARPWKSVALEEEQEGPGTRLPGN
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LPGNTQSSGPIPALACGLSCDHQGLETTQQGVAVL
AGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGGS
GGGSGGGGSERTMPRIPTLKNLEDLVTEYHGNFS
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Activin R1A ectodomain/IL9R/cGC-F
SEQ ID NO: 143
MEDEKPKVNPPLYMCVCEGLSCGNEDHCEGQQCF
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PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
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LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS
VALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQQGVAVLAGHCQRPGLHEDLQGM
PSVLSKARSWTFGGGSGGGSGGGGSERTMPRI
TLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDY
ERLCLVSEIPPKGGALGEGPGASPCNQHSPYWA
CYTLKPET
Activin R1A ectodomain/IL9R/cGC-S
SEQ ID NO: 144
MEDEKPKVNPPLYMCVCEGLSCGNEDHCEGQQCF
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PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
IFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGV
LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS
VALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQQGVAVLAGHCQRPGLHEDLQGM
PSVLSKARSWTFQPPQPPQPPQPPERTMPRIPTL
NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSER
CLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCY
LKPET

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Activin R1B ectodomain/IL9R/cGC-F
SEQ ID NO: 145
SGPRGVQALLCACTSCLOANYTCETDGACMVSIFN
LDGMEHHVRTCIPKVELVPAGKPFYCLSSSEDLRNT
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PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
IFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGV
LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS
VALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQQGVAVLAGHCQRPGLHEDLQGM
PSVLSKARSWTFGGGSGGGSGGGGSERTMPRI
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ERLCLVSEIPPKGGALGEGPGASPCNQHSPYWA
CYTLKPET
Activin R1B ectodomain/IL9R/cGC-S
SEQ ID NO: 146
SGPRGVQALLCACTSCLOANYTCETDGACMVSIFN
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HCCYTDYCNRIDLRVPSGHLKEPEHPSMWGPVELI
PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
IFYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGV
LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS
VALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSN
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQQGVAVLAGHCQRPGLHEDLQGM
PSVLSKARSWTFQPPQPPQPPQPPERTMPRIPTL
NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL
CLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCY
LKPET
Activin R1C ectodomain/IL9R/cGC-F
SEQ ID NO: 147
LSPGLKCVCLLCDSSNFTCQTEGACWASVMLTNGK
EQVIKSCVSLPELNAQVFCHSSNNVTKTECCFTDF
CNNITLHLPTASPNAPKLGPMEIIPWGWPGNTLV
AVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSAM
FFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQ
GALEPCVQEATALLTCGPARPWKSVALEEEQEGPG
TRLPGNLSSSEDLVPAGCTEWRVQTLAYLPQEDWAP

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TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCGY
GWHLSALPGNTQSSGPIPALACGLSCDHQGLETOQ
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FGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTE
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KGGALGEGPGASPCNQHSPPYWAPPCYTLKPET
Activin RIC ectodomain/IL9R/cGC-S
SEQ ID NO: 148
LSPGLKCVCLLCDSSNFTCQTEGACWASVMLTNGK
EQVIKSCVSLPELNAQVFCSSNNVTKTECCFTDF
CNNITLHLPTASPNAPKLGPMEIIPPWGWPGNTLV
AVSIFLLLTGPTYLLFKLSPRVKRIFYQNVSPAM
FFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQ
GALEPCVQEATALLTCGPARPWKSVALEEEQEGPG
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TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCGY
GWHLSALPGNTQSSGPIPALACGLSCDHQGLETOQ
GVAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWT
FQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ
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ALGEGPGASPCNQHSPPYWAPPCYTLKPET
Activin R2B ectodomain/IL9R/cGC-F
SEQ ID NO: 149
SGRGEAETRECIYYNANWELERTNQGLERCEGEQ
DKRLHCYASWRNSSGTIELVKKGCWLDDFNCYDRQ
ECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPE
VTYEPPPTAPTLLTLIPPWGWPGNTLVAVSIFLLL
TGPTYLLFKLSPRVKRIFYQNVSPAMFFQPLYSV
HNGNFQTMGAHGAGVLLSQDCAGTPQGALEPCVQ
EATALLTCGPARPWKSVALEEEQEGPGTRLPGNLS
SEDVLPAGCTEWRVQTLAYLPQEDWAPTSLTRPAP
PDSEGSRSSSSSSSSNNNNYCALGCGYGGWHLALP
GNTQSSGPIPALACGLSCDHQGLETOQGVAVVL
HCQRPGLHEDLQGMLLPSVLSKARSWTFGGGSGG
GGSGGGGSERTMPRIPTLKNLEDLVTEYHGNFSAW
SGVSKGLAESLQPDYSERLCLVSEIPPKGALGEG
PGASPCNQHSPPYWAPPCYTLKPET
Activin R2B ectodomain/IL9R/cGC-S
SEQ ID NO: 150
SGRGEAETRECIYYNANWELERTNQGLERCEGEQ
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ECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPE

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VTYEPPPTAPTLLTLIPPWGWPGNTLVAVSIFLLL
TGPTYLLFKLSPRVKRIFYQNVSPAMFFQPLYSV
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EATALLTCGPARPWKSVALEEEQEGPGTRLPGNLS
SEDVLPAGCTEWRVQTLAYLPQEDWAPTSLTRPAP
PDSEGSRSSSSSSSSNNNNYCALGCGYGGWHLALP
GNTQSSGPIPALACGLSCDHQGLETOQGVAVVL
HCQRPGLHEDLQGMLLPSVLSKARSWTFQPFQPFQ
PQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ
SKGLAESLQPDYSERLCLVSEIPPKGALGEGPGA
SPCNQHSPPYWAPPCYTLKPET
Activin R2A ectodomain/IL9R/cGC-F
SEQ ID NO: 151
AILGRSETQECLFFNANWEKDRTNQTGVEPCYGD
DKRRHCFATWKNISGSIEIVKQGCWLDDINCYDR
DCVEKKDSPEVYFCCCEGNMCNEKFSYFPEMEVT
PTSNPVTPKPPLIPPWGWPGNTLVAVSIFLLLTGP
TYLLFKLSPRVKRIFYQNVSPAMFFQPLYSVHNG
NFQTMGAHGAGVLLSQDCAGTPQGALEPCVQEAT
ALLTCGPARPWKSVALEEEQEGPGTRLPGNLSSD
VLPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDS
EGSRSSSSSSSSNNNNYCALGCGYGGWHLALPGNT
QSSGPIPALACGLSCDHQGLETOQGVAVVL
RPGHEDLQGMLLPSVLSKARSWTFGGGSGGGGS
GGGGSERTMPRIPTLKNLEDLVTEYHGNFSAWSGV
SKGLAESLQPDYSERLCLVSEIPPKGALGEGPGA
SPCNQHSPPYWAPPCYTLKPET
Activin R2A ectodomain/IL9R/cGC-S
SEQ ID NO: 152
AILGRSETQECLFFNANWEKDRTNQTGVEPCYGD
DKRRHCFATWKNISGSIEIVKQGCWLDDINCYDR
DCVEKKDSPEVYFCCCEGNMCNEKFSYFPEMEVT
PTSNPVTPKPPLIPPWGWPGNTLVAVSIFLLLTGP
TYLLFKLSPRVKRIFYQNVSPAMFFQPLYSVHNG
NFQTMGAHGAGVLLSQDCAGTPQGALEPCVQEAT
ALLTCGPARPWKSVALEEEQEGPGTRLPGNLSSD
VLPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDS
EGSRSSSSSSSSNNNNYCALGCGYGGWHLALPGNT
QSSGPIPALACGLSCDHQGLETOQGVAVVL
RPGHEDLQGMLLPSVLSKARSWTFQPFQPFQPFQ
QPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ

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LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSPYWAPPCYTLKPET

IL10R-alpha/IL9R/cGC-F
SEQ ID NO: 153

HGTELPSPPSVWFEEFFHHILHWTPIPNOSESTC
YEVALLRYGIESWNSISNCSQTLSDLTAVTLDL
HSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLT
VGSVNLEIHNGFILGKIQLPRPKMAPANDTYESIF
SHFREYEIAIRKVPGNFTFTHKKVKHENFSLTSG
EVGEFCVQVKPSVASRSNKGMSKEECISLTRQYF
TVTNLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKL
SPRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMG
AHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
ALACGLSCDHQGLETOQGVAVVLAGHCQRPGLHED
LQGMLLPSVLSKARSWTFGGGSGGGGSGGGGSE
TMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAES
LQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHS
PYWAPPCYTLKPET

IL10R-alpha/IL9R/cGC-S
SEQ ID NO: 154

HGTELPSPPSVWFEEFFHHILHWTPIPNOSESTC
YEVALLRYGIESWNSISNCSQTLSDLTAVTLDL
HSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLT
VGSVNLEIHNGFILGKIQLPRPKMAPANDTYESIF
SHFREYEIAIRKVPGNFTFTHKKVKHENFSLTSG
EVGEFCVQVKPSVASRSNKGMSKEECISLTRQYF
TVTNLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKL
SPRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMG
AHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
ALACGLSCDHQGLETOQGVAVVLAGHCQRPGLHED
LQGMLLPSVLSKARSWTFQPPQPPQPPQPPERTMP
RIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQ
DYSERLCLVSEIPPKGGALGEGPGASPCNQHSPY
WAPPCYTLKPET

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TGFBR2 ectodomain/IL9R/cGC-F
SEQ ID NO: 155

TIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVR
FSTCDNQKSCMSNCSITSICEKPQEVCAVWRKND
ENITLETVCHDPKLPYHDFILEDAAASPKCIMKEKK
KPGETFFMCSCSSDECNDNHFSEEYNTSNPDLLL
IFQLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLS
PRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMGA
HGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
RPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
WRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
LACGLSCDHQGLETOQGVAVVLAGHCQRPGLHED
QGMLLPSVLSKARSWTFGGGSGGGGSGGGGSE
MPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAES
QPDYSERLCLVSEIPPKGGALGEGPGASPCNQHS
YWAPPCYTLKPET

TGFBR2 ectodomain/IL9R/cGC-S
SEQ ID NO: 156

TIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVR
FSTCDNQKSCMSNCSITSICEKPQEVCAVWRKND
ENITLETVCHDPKLPYHDFILEDAAASPKCIMKEKK
KPGETFFMCSCSSDECNDNHFSEEYNTSNPDLLL
IFQLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLS
PRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMGA
HGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
RPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
WRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
LACGLSCDHQGLETOQGVAVVLAGHCQRPGLHED
QGMLLPSVLSKARSWTFQPPQPPQPPQPPERTMP
IPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPD
YSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWA
PPCYTLKPET

TGFBR1 ectodomain/IL9R/cGC-F
SEQ ID NO: 157

LQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHN
SMCIAEIDLIPDRPFVFCAPSSKTGSVTTTYCCNQ
DHCNKIELPTTVKSSPGLGPVELLIPPWGWPGNTL
VAVSIFLLLTGPTYLLFKLS
PRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMGA
HGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS

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PTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCY
GGWHL₁SALPGNTQSSGPIPALACGLSCDHQGLE₁TQ
QGVAVVL₁AGHCQRPGLHEDLQGM₁LLPSVLSKAR₁SW
TFGGGSGGGGSGGGGSERTMPRIPTLKNLEDLVT
EYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIP
PKGGALGEGPGASPCNQHSPYWAPPCYTLKPET
TGFB₁R1 ectodomain/IL9R/cGC-S
LQCFC₁HLCTKDNFTCVTDGLCFVSVTETTDKVIHN
SMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQ
DHCNKIELPTTVKSSPGLGPVELLIPPWGWPGNTL
VAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPSPA
MFFQPLYSVHNGNFQ₁TWMGAHGAGVLLSQDCAGTP
QGALEPCVQEATALLTCGPARPWKSVALEEEQEGP
GTRLPGNLSSE₁DVLPAGCTEWRVQTLAYLPQEDWA
PTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCY
GGWHL₁SALPGNTQSSGPIPALACGLSCDHQGLE₁TQ
QGVAVVL₁AGHCQRPGLHEDLQGM₁LLPSVLSKAR₁SW
TFQ₁PQ₁PQ₁PQ₁PQ₁PQ₁PERTMPRIPTLKNLEDLVTEYH
GNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKG
GALGEGPGASPCNQHSPYWAPPCYTLKPET
TIGIT/IL9R/cGC-F
MMTGTIETTGNISA₁EKGGSII₁LQCHLSSTTAQVTQ
VNWEQ₁QDQLLAICNADLGWHISPSFKDRVAPGPGL
GLTLQSLTVNDTGEYFCIYHTYPDGYTGRI₁FLEV
LESSVAEHGARFQIPLIPPWGWPGNTLVAVSIFLL
LTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLY
VHNGNFQ₁TWMGAHGAGVLLSQDCAGTPQGALEPCV
QEATALLTCGPARPWKSVALEEEQEGPGTRLPGNL
SSE₁DVLPAGCTEWRVQTLAYLPQEDWAPTS₁LTRPA
PPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL₁SAL
PGNTQSSGPIPALACGLSCDHQGLE₁TQQGVAVVLA
GHCQRPGLHEDLQGM₁LLPSVLSKARSWTFGGGSG
GGGSGGGGSERTMPRIPTLKNLEDLVTEYHGNFSA
WSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGE
GPGASPCNQHSPYWAPPCYTLKPET
TIGIT/IL9R/cGC-S
MMTGTIETTGNISA₁EKGGSII₁LQCHLSSTTAQVTQ
VNWEQ₁QDQLLAICNADLGWHISPSFKDRVAPGPGL
GLTLQSLTVNDTGEYFCIYHTYPDGYTGRI₁FLEV

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LESSVAEHGARFQIPLIPPWGWPGNTLVAVSIFLL
LTGPTYLLFKLSPRVKRIFYQNVPSAMFFQPLY
VHNGNFQ₁TWMGAHGAGVLLSQDCAGTPQGALEPCV
QEATALLTCGPARPWKSVALEEEQEGPGTRLPGNL
SSE₁DVLPAGCTEWRVQTLAYLPQEDWAPTS₁LTRPA
PPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL₁SAL
PGNTQSSGPIPALACGLSCDHQGLE₁TQQGVAVVLA
GHCQRPGLHEDLQGM₁LLPSVLSKARSWTFQ₁PQ₁PQ
Q₁PQ₁PQ₁PERTMPRIPTLKNLEDLVTEYHGNFSAWSG
VSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPG
ASPCNQHSPYWAPPCYTLKPET
FCGR2B/IL9R/cGC-F
TPAAPKAVLKLEPQWINVLQEDSVTLTCRGTHSP
ESDSIQWFHNGNLIPTHTQPSYRFKANMNDSGEYT
CQTGQTSLSDPVHLTVLSEWLVLQTPHLEFQEGET
IVLRCHSWKDKPLVKV₁TFFQNGKSKKFSRSDPNFS
IPQANHSHSGDYHCTGNIGY₁TLYSSKPV₁TTVQAP
LIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPSAMFFQPLYSVHNGNFQ₁TWMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSE₁DVLPAGCTEWRV
QTLAYLPQEDWAPTS₁LTRPAPPDSEGSRSSSSSS
SNNNNYCALGCYGGWHL₁SALPGNTQSSGPIPALAC
GLSCDHQGLE₁TQQGVAVVL₁AGHCQRPGLHEDLQGM
LLPSVLSKARSWTFGGGSGGGGSGGGGSERTMPR
IPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPD
YSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWA
PPCYTLKPET
FCGR2B/IL9R/cGC-S
TPAAPKAVLKLEPQWINVLQEDSVTLTCRGTHSP
ESDSIQWFHNGNLIPTHTQPSYRFKANMNDSGEYT
CQTGQTSLSDPVHLTVLSEWLVLQTPHLEFQEGET
IVLRCHSWKDKPLVKV₁TFFQNGKSKKFSRSDPNFS
IPQANHSHSGDYHCTGNIGY₁TLYSSKPV₁TTVQAP
LIPPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRV
KRIFYQNVPSAMFFQPLYSVHNGNFQ₁TWMGAHGA
GVLLSQDCAGTPQGALEPCVQEATALLTCGPARPW
KSVALEEEQEGPGTRLPGNLSSE₁DVLPAGCTEWRV
QTLAYLPQEDWAPTS₁LTRPAPPDSEGSRSSSSSS

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SNMNNYCALGCGYGGWHL^SALPGNTQSSGPIPALAC

GLSCDHQGLE^TQQGVAWVL^AGH^CQRPGLHEDLQGM

LLPSVLSKARSWTFQPPQPPQPPQPPERTMPRIPT

LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE

RLCLVSEIPPKGGALGEGPGASPCNQHS^PYWAPPC

YTLKPET

FCGR1/IL9R/cGC-F

SEQ ID NO: 163

QVDTTKAVITLQPPWVS^VFQEETVTLHCEVLHLP^G

SSSTQWFLNGTATQTSTPSYRITSASVND^SGEYRC

QRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPL

ALRCHAWKDKLVYNVLYYRNGKAFKFFHWSNL^TI

LKTNI SHNGTYHCSGMGKHRYTSAGISVTVKELFP

APVLNASVTSPLLEG^NLVTLSCETKLLQRPGLQ^L

YFSFYMGSKTLRGRNTSSEYQILTARREDSGLYWC

EAATEDGNVLKRSPELELQVLGLQ^LPTPVWFHLIP

PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRI

FYQNVPS^PAMFFQPLYSVHNGNFQ^TWMGAHGAGVL

LSQDCAGTPQGALEPCVQEATALLTCGPARPWKS^V

ALEEEQEGPGTRLPGNLSSE^DVL^PPAGCTEWRVQ^TL

AYLPQEDWAPTS^LTRPAPPDSEGRSSSSSSSSNN

NNYCALGCGYGGWHL^SALPGNTQSSGPIPALACGL^S

CDHQGLE^TQQGVAWVL^AGH^CQRPGLHEDLQGM^LLP

SVLSKARSWTFGGGSGGGGSGGGGSERTMPRIPT

LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE

RLCLVSEIPPKGGALGEGPGASPCNQHS^PYWAPPC

YTLKPET

FCGR1/IL9R/cGC-S

SEQ ID NO: 164

QVDTTKAVITLQPPWVS^VFQEETVTLHCEVLHLP^G

SSSTQWFLNGTATQTSTPSYRITSASVND^SGEYRC

QRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPL

ALRCHAWKDKLVYNVLYYRNGKAFKFFHWSNL^TI

LKTNI SHNGTYHCSGMGKHRYTSAGISVTVKELFP

APVLNASVTSPLLEG^NLVTLSCETKLLQRPGLQ^L

YFSFYMGSKTLRGRNTSSEYQILTARREDSGLYWC

EAATEDG^TNVLKRSPELELQVLGLQ^LPTPVWFHLI

PPWGWPGN

TLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQNVPS

PAMFFQPLYSVHNGNFQ^TWMGAHGAGVLLSQDCAG

TPQGALEPCVQEATALLTCGPARPWKSVALEEEQE

-continued

GPGTRLPGNLSSE^DVL^PPAGCTEWRVQ^TLAYLPQED

WAPTS^LTRPAPPDSEGRSSSSSSSSSNMNNYCALG

CYGGWHL^SALPGNTQSSGPIPALACGLSCDHQGLE

TQQGVAWVL^AGH^CQRPGLHEDLQGM^LLP^SVLSKAR

SWTFQPPQPPQPPQPPERTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSE^RLCLVSEIPP

KGGALGEGPGASPCNQHS^PYWAPPCYTLKPET

2B4/IL9R/cCG-F

SEQ ID NO: 165

CQGSADHVVSISGVPLQLQPN^SIQTKVDSIAWKKL

LPSQNGFHHILKWENGSLPSNTSND^RFSFIVKNLS

LLIKAAQQQDSGLYCLEVTSISGKVQTATFQV^FVF

ESLLPDKVEKPRLQGGKILDRGRCQVALSCLVSR

DGNVSYAWYRGSKLIQTAGNLTYLDEEVDING^THT

YTCNVSNPVS^WESHTLNL^TQDCQNAHQEF^RFWPLI

PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR

IFYQNVPS^PAMFFQPLYSVHNGNFQ^TWMGAHGAGV

LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS

VALEEEQEGPGTRLPGNLSSE^DVL^PPAGCTEWRVQ^T

LAYLPQEDWAPTS^LTRPAPPDSEGRSSSSSSSSNN

NNYCALGCGYGGWHL^SALPGNTQSSGPIPALACGL^S

SCDHQGLE^TQQGVAWVL^AGH^CQRPGLHEDLQGM^LLP

PSVLSKARSWTFGGGSGGGGSGGGGSERTMPRI^P

TLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDY^S

ERLCLVSEIPPKGGALGEGPGASPCNQHS^PYWAPP

CYTLKPET

2B4/IL9R/cCG-S

SEQ ID NO: 166

CQGSADHVVSISGVPLQLQPN^SIQTKVDSIAWKKL

LPSQNGFHHILKWENGSLPSNTSND^RFSFIVKNLS

LLIKAAQQQDSGLYCLEVTSISGKVQTATFQV^FVF

ESLLPDKVEKPRLQGGKILDRGRCQVALSCLVSR

DGNVSYAWYRGSKLIQTAGNLTYLDEEVDING^THT

YTCNVSNPVS^WESHTLNL^TQDCQNAHQEF^RFWPLI

PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR

IFYQNVPS^PAMFFQPLYSVHNGNFQ^TWMGAHGAGV

LLSQDCAGTPQGALEPCVQEATALLTCGPARPWKS

VALEEEQEGPGTRLPGNLSSE^DVL^PPAGCTEWRVQ^T

LAYLPQEDWAPTS^LTRPAPPDSEGRSSSSSSSSNN

NNYCALGCGYGGWHL^SALPGNTQSSGPIPALACGL^S

SCDHQGLE^TQQGVAWVL^AGH^CQRPGLHEDLQGM^LLP

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PSVLSKARSWTFQPQPQPQPQPPERTMPRIPTLK
NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL
CLVSEIPPKGGALGEGPGASPCNQHSPLYWAPPCYT
LKPET
LAIR1/IL9R/cGC-F
SEQ ID NO: 167
QEEDLPRPSISAEPGTVIPLGSHVTFVCRGPVGVQ
TFRLERESRSTYNDTEDVSQASPSESEARFRIDSV
SEGNAGPYRCIYYKPPKWSEQSDYLELLVKETSGG
PDSPDTEPGSSAGPTQRPSDNSHNEHAPASQGLKA
EHLYLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKL
SPRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMWG
AHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
ALACGLSCDHQGLETTQGVAVVLAGHCQRPGLHED
LQGMLLPSVLSKARSWTFGGGSGGGSGGGGSE
TMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAES
LQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHS
PLYWAPPCYTLKPET
LAIR1/IL9R/cGC-S
SEQ ID NO: 168
QEEDLPRPSISAEPGTVIPLGSHVTFVCRGPVGVQ
TFRLERESRSTYNDTEDVSQASPSESEARFRIDSV
SEGNAGPYRCIYYKPPKWSEQSDYLELLVKETSGG
PDSPDTEPGSSAGPTQRPSDNSHNEHAPASQGLKA
EHLYLIPPWGWPGNTLVAVSIFLLLTGPTYLLFKL
SPRVKRIFYQNVPSAMFFQPLYSVHNGNFQTMWG
AHGAGVLLSQDCAGTPQGALEPCVQEATALLTCGP
ARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGCT
EWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS
SSSSNNNNYCALGCYGGWHLALPGNTQSSGPI
ALACGLSCDHQGLETTQGVAVVLAGHCQRPGLHED
LQGMLLPSVLSKARSWTFQPQPQPQPQPQPPERTMP
RIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQ
PDYSERLCLVSEIPPKGGALGEGPGASPCNQHS
PLYWAPPCYTLKPET
CD5/IL-9R/cGC-F
SEQ ID NO: 169
RLSWYDPDFQARLTRSNSKCQGQLEVYLDGWHMV
CSQSWGRSSKQWEDPSQASKVCQRLNCGVPLSLGP

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FLVITYTPQSSIICYGQLGSFSNCSHSRNDMCHSLG
LTCLEPQKTPPTTRPPPTTTPEPTAPPRLQLVAQ
SGGQHCAGVVEFYSGSLGGTISYEAQDKTDLENF
LCNNLQCGSFLKHLPETEAGRAQDPGEPREHQPLP
IQWKIQNSSCTSLHCFRKIKPKQSGRVLALLCSG
FQPKVQSRLVGGSSICEGTVEVRQGAQWAALCDSS
SARSSLRWEEVCREQQCGSVNSYRVLDAGDPTSRG
LFCPHQKLSQCHELWERNASYCKKVFTCQDPNPLI
PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
IFYQNVPSAMFFQPLYSVHNGNFQTMGAHAGV
LLSQDCAGTPQGALEPCVQEATALLTCGPAPRWKS
VALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSS
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQGVAVVLAGHCQRPGLHEDLQGMLL
PSVLSKARSWTFGGGSGGGSGGGGSERTMPRI
TLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYS
ERLCLVSEIPPKGGALGEGPGASPCNQHS
PLYWAPPCYTLKPET
CD5/IL-9R/cGC-S
SEQ ID NO: 170
RLSWYDPDFQARLTRSNSKCQGQLEVYLDGWHMV
CSQSWGRSSKQWEDPSQASKVCQRLNCGVPLSLGP
FLVITYTPQSSIICYGQLGSFSNCSHSRNDMCHSLG
LTCLEPQKTPPTTRPPPTTTPEPTAPPRLQLVAQ
SGGQHCAGVVEFYSGSLGGTISYEAQDKTDLENF
LCNNLQCGSFLKHLPETEAGRAQDPGEPREHQPLP
IQWKIQNSSCTSLHCFRKIKPKQSGRVLALLCSG
FQPKVQSRLVGGSSICEGTVEVRQGAQWAALCDSS
SARSSLRWEEVCREQQCGSVNSYRVLDAGDPTSRG
LFCPHQKLSQCHELWERNASYCKKVFTCQDPNPLI
PPWGWPGNTLVAVSIFLLLTGPTYLLFKLSPRVKR
IFYQNVPSAMFFQPLYSVHNGNFQTMGAHAGV
LLSQDCAGTPQGALEPCVQEATALLTCGPAPRWKS
VALEEEQEGPGTRLPGNLSSDVLPAAGCTEWRVQ
LAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSS
NNNYCALGCYGGWHLALPGNTQSSGPIPALACGL
SCDHQGLETTQGVAVVLAGHCQRPGLHEDLQGMLL
PSVLSKARSWTFQPQPQPQPQPQPPERTMPRIPTLK
NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL

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CLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYT
LKPET

TWEAKR/IL9R/cGC-F

SEQ ID NO: 171

EQAPGTAPCSRGSWSADLDKCMDASCRRARPHSD

FCLGCAAAPPAPFRLLWPLIPPWGWPGNTLVAVSI

FLLLTGPTYLLFKLSPRVKRIFYQNVSPAMFFQP

LYSVHNGNFQTMGAHGAGVLLSQDCAGTPQGALE

PCVQEATALLTGCPARPWKSVALEEEQEGPGTRLP

GNLSSDVLPA GCTEWRVQTLAYLPQEDWAPTSLT

RPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL

SALPGNTQSSGPIPALACGLSCDHQGLETOQGVAW

VLAGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGG

GGGGGGGGGGSSERTMPRIPTLKNLEDLVTEYHGN

FSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGA

LGEGPGASPCNQHSPYWAPPCYTLKPET

TWEAKR/IL9R/cGC-S

SEQ ID NO: 172

EQAPGTAPCSRGSWSADLDKCMDASCRRARPHSD

FCLGCAAAPPAPFRLLWPLIPPWGWPGNTLVAVSI

FLLLTGPTYLLFKLSPRVKRIFYQNVSPAMFFQP

LYSVHNGNFQTMGAHGAGVLLSQDCAGTPQGALE

PCVQEATALLTGCPARPWKSVALEEEQEGPGTRLP

GNLSSDVLPA GCTEWRVQTLAYLPQEDWAPTSLT

RPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWHL

SALPGNTQSSGPIPALACGLSCDHQGLETOQGVAW

VLAGHCQRPGLHEDLQGMLLPSVLSKARSWTFQPQ

PQPQPQPQPERTMPRIPTLKNLEDLVTEYHGNFSA

WSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGE

GPGASPCNQHSPYWAPPCYTLKPET

TWEAKR/IL9R/cGC-F/TNFR1-TM

SEQ ID NO: 173

EQAPGTAPCSRGSWSADLDKCMDASCRRARPHSD

FCLGCAAAPPAPFRLLWPVLLPLVIFFGLCLLSLL

FIGLMYVKRIFYQNVSPAMFFQPLYSVHNGNFQT

WMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLT

CGPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA

GCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSR

SSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSSG

PIPALACGLSCDHQGLETOQGVAWVLAGHCQRPGL

HEDLQGMLLPSVLSKARSWTFGGGGGGGGGGGG

SERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGL

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AESLQPDYSERLCLVSEIPPKGGALGEGPGASPCN

QHSPYWAPPCYTLKPET

TWEAKR/IL9R/cGC-S/TNFR1-TM

SEQ ID NO: 174

EQAPGTAPCSRGSWSADLDKCMDASCRRARPHSD

FCLGCAAAPPAPFRLLWPVLLPLVIFFGLCLLSLL

FIGLMYVKRIFYQNVSPAMFFQPLYSVHNGNFQT

WMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLT

CGPARPWKSVALEEEQEGPGTRLPGNLSSDVLPA

GCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSR

SSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSSG

PIPALACGLSCDHQGLETOQGVAWVLAGHCQRPGL

HEDLQGMLLPSVLSKARSWTFQPQPQPQPQPER

TMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAES

LQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHS

PYWAPPCYTLKPET

OPG/IL9R/cGC-F/TNFR1-TM

SEQ ID NO: 175

ETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTA

KWKTVCAPCPDHYTDSWHTSDECLYCSVPCKELQ

YVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPP

GFGVVQAGTPERN TVCKRCPDGGFFSNETSSKAPCR

KHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCG

IDVTLCEEAFRFAVPTKFTPNWLSVLVDNLPGTK

VNAESVERIKRQHSSEQTFQLLKLWKHQNKDQDI

VKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMES

LPGKKVGAEDIEKTIKACKPSDQILKL LSLWRIKN

GDQDTLKGLMHALKH SKTYHFPKTVTQSLKKTIRF

LHSFTMYKLYQKLFLEMIGNQVQSVKISCLVLLPL

VIFFGLCLLSLLFIGLMYVKRIFYQNVSPAMFFQ

PLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQGAL

EPCVQEATALLTGCPARPWKSVALEEEQEGPGTRL

PGNLSSDVLPA GCTEWRVQTLAYLPQEDWAPTSL

TRPAPPDSEGSRSSSSSSSSNNNNYCALGCYGGWH

LSALPGNTQSSGPIPALACGLSCDHQGLETOQGV

WVLAGHCQRPGLHEDLQGMLLPSVLSKARSWTFGG

GGGGGGGGGGSSERTMPRIPTLKNLEDLVTEYHG

NFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGG

ALGEGPGASPCNQHSPYWAPPCYTLKPET

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OPG/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 176
ETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTA
KWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQ
YVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPP
GFGVVQAGTPERN TVCKRCPDGFFSNETSSKAPCR
KHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCG
IDVTLC EEAFRRFAVPTKFTPNWLSVLVDNLPGTK
VNAESVERIKRQHSSQEQTQQLLKLWKHQNKDQDI
VKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMES
LPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKN
GDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRF
LHSFTMYKLYQKLFLEMIGNQVQSVKISCLVLLPL
VIFFGLCLLSLLFIGLMYVKRIFYQNVPS PAMFFQ
PLYSVHNGNFQ TWMGAGAGVLLSQDCAGTPQGAL
EPCVQEATALLTCGPARPWKSVALEEEQEGPGTRL
PGNLSS EDVLPAGCTEWRVQTLAYLPQEDWAPTS
L TRPAPPDSEGRSSSSSSSSNNNNYCALGCYGGWH
LSALPGNTQSSGPIPALACGLSCDHQGLETOQGVA
WVLAGHCQRPG LHEDLQGM LPSVLSKARSWTFQP
QPQPQPQPQP PERTMPRIPTLKNLEDLVTEYHGNFS
AWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALG
EGPGASPCNQHSPYWAPPCYTLKPET
TACI/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 177
MSG LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCP
EEQYWDPLLGT CMSCKTICNHQSQRTCAAFCRSL
CRKEQGKFYDHLLRDCISCASICGQ
HPKQ CAYFCENKLRSPVNLPPELRRQRSGEVENNS
DNSGRYQGLEHRGSEASPALPGLKLSADQVALVYS
VLLPLVIFFG LCLLSLLFIGLMYVKRIFYQNVPS
AMFFQPLYSVHNGNFQ TWMGAGAGVLLSQDCAGT
PQGALEPCVQEATALLTCGPARPWKSVALEEEQEG
PGTRLPGNLSS EDVLPAGCTEWRVQTLAYLPQEDW
APTSLTRPAPPDSEGRSSSSSSSSNNNNYCALGC
YGGWHL SALPGNTQSSGPIPALACGLSCDHQGLE
TOQGVAVVLAGHCQRPG LHEDLQGM LPSVLSKARS
WTFGGGSGGGSGGGG SERTMPRIPTLKNLEDLV
TEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEI
PPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

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TACI/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 178
MSG LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCP
EEQYWDPLLGT CMSCKTICNHQSQRTCAAFCRSL
CRKEQGKFYDHLLRDCISCASICGQHPKQ CAYFCE
NKLRS PVNLPPELRRQRSGEVENNSDNSGRYQGLE
HRGSEASPALPGLKLSADQVALVYSVLLPLVIFFG
LCLLSLLFIGLMYVKRIFYQNVPS PAMFFQPLYSV
HNGNFQ TWMGAGAGVLLSQDCAGTPQGALEPCVQ
EATALLTCGPARPWKSVALEEEQEGPGTRLPGNL
SEDVLPAGCTEWRVQTLAYLPQEDWAPTS LTRPAP
PDSEGRSSSSSSSSNNNNYCALGCYGGWHL SALP
GNTQSSGPIPALACGLSCDHQGLETOQGVAVVL
AGHCQRPG LHEDLQGM LPSVLSKARSWTFQPQPQP
QPQP PERTMPRIPTLKNLEDLVTEYHGNFSAWSGV
SKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGA
SPCNQHSPYWAPPCYTLKPET
BCMA/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 179
MLQ MAGQCSQNEYFDSL LHACIPQLRCSSNTPL
TCQRYCNASVTNSVKGTNAVLLPLVIFFG LCLLSL
LFIGLMYVKRIFYQNVPS PAMFFQPLYSVHNGNFQ
TWMGAGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSS EDVLP
AGCTEWRVQTLAYLPQEDWAPTS LTRPAPPDSEGR
SSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSS
GPIPALACGLSCDHQGLETOQGVAVVLAGHCQRPG
LHEDLQGM LPSVLSKARSWTFGGGSGGGSGGG
GSERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKG
LAESLQPDYSERLCLVSEIPPKGGALGEGPGASPC
NQHSPYWAPPCYTLKPET
BCMA/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 180
MLQ MAGQCSQNEYFDSL LHACIPQLRCSSNTPL
CQRYCNASVTNSVKGTNAVLLPLVIFFG LCLLSL
FIGLMYVKRIFYQNVPS PAMFFQPLYSVHNGNFQ
TWMGAGAGVLLSQDCAGTPQGALEPCVQEATALL
TCGPARPWKSVALEEEQEGPGTRLPGNLSS EDVLP
AGCTEWRVQTLAYLPQEDWAPTS LTRPAPPDSEGR
SSSSSSSSNNNNYCALGCYGGWHL SALPGNTQSS
GPIPALACGLSCDHQGLETOQGVAVVLAGHCQRPG
LHEDLQGM LPSVLSKARSWTFQPQPQPQPQP

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TMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAES
LQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHS
PYWAPPCYTLKPET
NGFR/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 181
KEACPTGLYTHSGECKACNLGEGVAQPCGANQTV
CEPCLDSVTFSADVVSATEPCKPCTECVGLQMSAP
CVEADDAVCRCAYGYQDETGTGRCEACRVCEAGSG
LVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCT
VCEDTERQLRECTRWADAEECEIPGRWITRSTPPE
GSDSTAPSTQEPPEAPPEQDLIASTVAGVVTVMGS
SQPVVTRGTTDNVLLPLVIFFGLCLLSLLFIGLMY
VKRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHG
AGVLLSQDCAGTPQGALEPCVQEATALLTCGPARP
WKSVALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWR
VQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS
SSNMNNYCALGCYGGWHL SALPGNTQSSGPIPALA
CGLSCDHQGLETTQQGVAVVL AGHCQR PGLHEDLQG
MLLPSVLSKARSWTFGGGSGGGGSGGGGSERTMP
RIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQP
DYSERLCLVSEIPPKGGALGEGPGASPCNQHS
PYWAPPCYTLKPET
NGFR/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 182
KEACPTGLYTHSGECKACNLGEGVAQPCGANQTV
CEPCLDSVTFSADVVSATEPCKPCTECVGLQMSAP
CVEADDAVCRCAYGYQDETGTGRCEACRVCEAGSG
LVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCT
VCEDTERQLRECTRWADAEECEIPGRWITRSTPPE
GSDSTAPSTQEPPEAPPEQDLIASTVAGVVTVMGS
SQPVVTRGTTDNVLLPLVIFFGLCLLSLLFIGLMY
VKRIFYQNVPSAMFFQPLYSVHNGNFQTMGAHG
AGVLLSQDCAGTPQGALEPCVQEATALLTCGPARP
WKSVALEEEQEGPGTRLPGNLSSSEDLVPAGCTEWR
VQTLAYLPQEDWAPTSLTRPAPPDSEGSRSSSSSS
SSNMNNYCALGCYGGWHL SALPGNTQSSGPIPALA
CGLSCDHQGLETTQQGVAVVL AGHCQR PGLHEDLQG
MLLPSVLSKARSWTFQPPQPPQPPQPPPERTMPRI
PTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYS
ERLCLVSEIPPKGGALGEGPGASPCNQHS
PYWAPPCYTLKPET

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EDAR/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 183
EYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCG
YGTKDEEDYGCVP CPAEKFSKGGYQICRRHKDCEGF
FRATVLT PGDMENDAECGPCLPGYYMLENRPRNIY
GMVCYSCLLAPPNTKECVGATSGASANFPGTSGSS
TLSPFQHAHKELSGQGH LATAVLLPLVIFFGLCLL
SLLFIGLMYVKRIFYQNVPSAMFFQPLYSVHNGN
FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA
LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSSEDL
VPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSE
GSRSSSSSSSSNMNNYCALGCYGGWHL SALPGNTQ
SSGPIPALACGLSCDHQGLETTQQGVAVVL AGHCQR
PGLHEDLQGM LPSVLSKARSWTFGGGSGGGGSG
GGGSERTMPRIPTLKNLEDLVTEYHGNFSAWSGV
SKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGAS
PCNQHS
PYWAPPCYTLKPET
EDAR/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 184
EYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCG
YGTKDEEDYGCVP CPAEKFSKGGYQICRRHKDCEGF
FRATVLT PGDMENDAECGPCLPGYYMLENRPRNIY
GMVCYSCLLAPPNTKECVGATSGASANFPGTSGSS
TLSPFQHAHKELSGQGH LATAVLLPLVIFFGLCLL
SLLFIGLMYVKRIFYQNVPSAMFFQPLYSVHNGN
FQTMGAHGAGVLLSQDCAGTPQGALEPCVQEATA
LLTCGPARPWKSVALEEEQEGPGTRLPGNLSSSEDL
VPAGCTEWRVQTLAYLPQEDWAPTSLTRPAPPDSE
GSRSSSSSSSSNMNNYCALGCYGGWHL SALPGNTQ
SSGPIPALACGLSCDHQGLETTQQGVAVVL AGHCQR
PGLHEDLQGM LPSVLSKARSWTFQPPQPPQPPQPP
PERTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGL
AESLQPDYSERLCLVSEIPPKGGALGEGPGASPCN
QHSPYWAPPCYTLKPET
DCR2 (TNFRSF10D)/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 185
ATIPRQDEVPPQQT VAPQQRRSLKEEECPAGSHRS
EYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQ
TNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRCTCRT
GCPRGMVKVSNCTPRSDIKCKNES AASSTGKTPAA
EETVT TILGMLASPYHVLLPLVIFFGLCLLSLLFI
GLMYVKRIFYQNVPSAMFFQPLYSVHNGNFQTM

-continued
GAHGAGVLLSQDCAGTPQGALEPCVQEATALTCG

PARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGC

TEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS

SSSSSSNNNNYCALGCYGGWHL SALPGNTQSSGPI

PALACGLSCDHQGLETTQQGVAWVL AGHCQRPGLHE

DLQGM LLPSVLSKARSWTFGGGSGGGSGGGGSE

RTMPRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAE

SLQPDYSERLCLVSEI PPKGGALGEGPGASPCNQH

SPYWAPPCYTLKPET

DCR2 (TNFRSF10D) / IL9R / cGC - S / TNFR1 - TM
SEQ ID NO: 186
ATIPRQDEVPPQQT VAPQQQRSLKEEECPAGSHRS

EYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQ

TNKSSCTTTRD TVCQCEKGSFQDKNSPEMCR TCRT

GCPRG MVKVS NCTPRSDI KCKNESAASSTGKTPAA

EETVT TILGMLASPYHVLPLVIFFGLC LLSLLFI

GLMYVKRIFYQNVPS PAMFFQPLYSVHNGNFQ TW

GAHGAGVLLSQDCAGTPQGALEPCVQEATALTCG

PARPWKSVALEEEQEGPGTRLPGNLSSDVLPAAGC

TEWRVQTLAYLPQEDWAPTSLTRPAPPDSEGSRSS

SSSSSSNNNNYCALGCYGGWHL SALPGNTQSSGPI

PALACGLSCDHQGLETTQQGVAWVL AGHCQRPGLHE

DLQGM LLPSVLSKARSWTFQPPQPQPQPQPPTM

PRIPTLKNLEDLVTEYHGNFSAWSGVSKGLAESLQ

PDYSERLCLVSEI PPKGGALGEGPGASPCNQHSPY

WAPPCYTLKPET

DCR1 (TNFRSF10C) / IL9R / cGC - F / TNFR1 - TM
SEQ ID NO: 187
ATTARQEEVPQQT VAPQQQRHSFKGEECPAGSHRS

EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQ

KHKSSCTMTRD TVCQCKEGTFRNENSPEMCRKCSR

CPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAE

ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTT

SPGTPAPAAEETMTTSPGTPAPAAEETMITSPGTP

AVLLPLVIFFGLC LLSLLFIGLMYVKRIFYQNVPS

PAMFFQPLYSVHNGNFQ TWGAHGAGVLLSQDCAG

TPQGALEPCVQEATALTCGP ARPWKSVALEEEQEGPG

GPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAP

WAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALG

CYGGWHL SALPGNTQSSGPI PALACGLSCDHQGLE

TQQGVAWVL AGHCQRPGLHEDLQGM LLPSVLSKAR

SWTFOPQPQPQPQPQPPTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP

KGGALGEGPGASPCNQHSPYWAPPCYTLKPET

CD40 / IL9R / cGC - F / TNFR1 - TM
SEQ ID NO: 189
EPPTACREKQYLINSQCCSLCQPGQKLVS DCTEFT

ETECPCGESEFLDTWNRETHCHQH KYCDPNLGLR

VQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC

SPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEK

CHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRVL

LPLVIFFGLC LLSLLFIGLMYVKRIFYQNVPS PAM

FFQPLYSVHNGNFQ TWGAHGAGVLLSQDCAGTPQ

GALEPCVQEATALTCGP ARPWKSVALEEEQEGPG

TRLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAP

TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCY

GWHL SALPGNTQSSGPI PALACGLSCDHQGLETTQ

GVAWVL AGHCQRPGLHEDLQGM LLPSVLSKARSW

FGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP

KGGALGEGPGASPCNQHSPYWAPPCYTLKPET

CD40 / IL9R / cGC - S / TNFR1 - TM
SEQ ID NO: 190
EPPTACREKQYLINSQCCSLCQPGQKLVS DCTEFT

ETECPCGESEFLDTWNRETHCHQH KYCDPNLGLR

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SWTFGGGSGGGSGGGGSERTMPRIPTLKNLEDL

VTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSE

IPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

DCR1 (TNFRSF10C) / IL9R / cGC - S / TNFR1 - TM
SEQ ID NO: 188
ATTARQEEVPQQT VAPQQQRHSFKGEECPAGSHRS

EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQ

KHKSSCTMTRD TVCQCKEGTFRNENSPEMCRKCSR

CPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAE

ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTT

SPGTPAPAAEETMTTSPGTPAPAAEETMITSPGTP

AVLLPLVIFFGLC LLSLLFIGLMYVKRIFYQNVPS

PAMFFQPLYSVHNGNFQ TWGAHGAGVLLSQDCAG

TPQGALEPCVQEATALTCGP ARPWKSVALEEEQEGPG

GPGTRLPGNLSSDVLPAAGCTEWRVQTLAYLPQED

WAPTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALG

CYGGWHL SALPGNTQSSGPI PALACGLSCDHQGLE

TQQGVAWVL AGHCQRPGLHEDLQGM LLPSVLSKAR

SWTFOPQPQPQPQPQPPTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP

KGGALGEGPGASPCNQHSPYWAPPCYTLKPET

CD40 / IL9R / cGC - F / TNFR1 - TM
SEQ ID NO: 189
EPPTACREKQYLINSQCCSLCQPGQKLVS DCTEFT

ETECPCGESEFLDTWNRETHCHQH KYCDPNLGLR

VQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC

SPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEK

CHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRVL

LPLVIFFGLC LLSLLFIGLMYVKRIFYQNVPS PAM

FFQPLYSVHNGNFQ TWGAHGAGVLLSQDCAGTPQ

GALEPCVQEATALTCGP ARPWKSVALEEEQEGPG

TRLPGNLSSDVLPAAGCTEWRVQTLAYLPQEDWAP

TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCY

GWHL SALPGNTQSSGPI PALACGLSCDHQGLETTQ

GVAWVL AGHCQRPGLHEDLQGM LLPSVLSKARSW

FGGGSGGGSGGGGSERTMPRIPTLKNLEDLVTE

YHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP

KGGALGEGPGASPCNQHSPYWAPPCYTLKPET

CD40 / IL9R / cGC - S / TNFR1 - TM
SEQ ID NO: 190
EPPTACREKQYLINSQCCSLCQPGQKLVS DCTEFT

ETECPCGESEFLDTWNRETHCHQH KYCDPNLGLR

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VQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC
SPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEK
CHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRVL
LPLVIFFGLCLLSLLFIGLMYVKRIFYQNVPSAM
FFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTPQ
GALEPCVQEATALLTCGPARPWKSVALEEEQEGPG
TRLPGNLSSDVLPACTEWRVQTLAYLPQEDWAP
TSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGCY
GWHLSALPGNTQSSGPIPALACGLSCDHQGLETTQ
GVAWVLAGHCQRPGLHEDLQGMLLPSVLSKARSWT
FQPPQPPQPPQPPQPPERTMPRIPTLKNLEDLVTEYHG
NFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGG
ALGEGPGASPCNQHSFYWAPPCTYTLKPET
FAS/IL9 R/cGC-F/TN FR1-TM
SEQ ID NO: 191
QVTDINSKGLELRKTVTTVETQNLGLHHDGQFCH
KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA
HFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCK
PNFFCNSTVCEHCDPCTKCEHGIIKECTLTSTNTKC
KEEGSRSNVLLPLVIFFGLCLLSLLFIGLMYVKRI
FYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGVL
LSQDCAGTPQGALEPCVQEATALLTCGPARPWKSV
ALEEEQEGPGTRLPGNLSSDVLPACTEWRVQTL
AYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNN
NNYCALGCYGGWHLALPGNTQSSGPIPALACGLS
CDHQGLETTQGVAVVLAGHCQRPGLHEDLQGMLLP
SVLSKARSWTFGGGSGGGGSGGGGSERTMPRIPT
LKNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSE
RLCLVSEIPPKGGALGEGPGASPCNQHSFYWAPP
YTLKPET
FAS/IL9R/cGC-S/TN FR1-TM
SEQ ID NO: 192
QVTDINSKGLELRKTVTTVETQNLGLHHDGQFCH
KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA
HFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCK
PNFFCNSTVCEHCDPCTKCEHGIIKECTLTSTNTKC
KEEGSRSNVLLPLVIFFGLCLLSLLFIGLMYVKRI
FYQNVPSAMFFQPLYSVHNGNFQTMGAHGAGVL
LSQDCAGTPQGALEPCVQEATALLTCGPARPWKSV
ALEEEQEGPGTRLPGNLSSDVLPACTEWRVQTL
AYLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNN

-continued
NNYCALGCYGGWHLALPGNTQSSGPIPALACGLS
CDHQGLETTQGVAVVLAGHCQRPGLHEDLQGMLLP
SVLSKARSWTFQPPQPPQPPQPPERTMPRIPTLKN
LEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERLC
LVSEIPPKGGALGEGPGASPCNQHSFYWAPPCTYTL
KPET
DR4/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 193
ASGTEAAAATPSKVGSSAGRIEPRGGGRGALPTS
MGQHGPSARARAGRAPGPRPAREASPRLRVHKTFK
FVVVGVLQVVPSSAATIKLHDQSIGTQQWEHSPL
GELCPPGSHRSEHPGACNRCTEGVGYTNASNNLFA
CLPCTACKSDEEERSPCTTTRNTACQCKPGTFRND
NSAEMCRKCSRGCPRGMVKVDCTPWSDIECVHKE
SGNGHNVLLPLVIFFGLCLLSLLFIGLMYVKRIFY
QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS
QDCAGTPQGALEPCVQEATALLTCGPARPWKSV
EEEQEGPGTRLPGNLSSDVLPACTEWRVQTLAY
LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN
YCALGCYGGWHLALPGNTQSSGPIPALACGLSCD
HQGLETTQGVAVVLAGHCQRPGLHEDLQGMLLPSV
LSKARSWTFGGGSGGGGSGGGGSERTMPRIPTLK
NLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSERL
CLVSEIPPKGGALGEGPGASPCNQHSFYWAPPCTY
LKPET
DR4/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 194
ASGTEAAAATPSKVGSSAGRIEPRGGGRGALPTS
MGQHGPSARARAGRAPGPRPAREASPRLRVHKTFK
FVVVGVLQVVPSSAATIKLHDQSIGTQQWEHSPL
GELCPPGSHRSEHPGACNRCTEGVGYTNASNNLFA
CLPCTACKSDEEERSPCTTTRNTACQCKPGTFRND
NSAEMCRKCSRGCPRGMVKVDCTPWSDIECVHKE
SGNGHNVLLPLVIFFGLCLLSLLFIGLMYVKRIFY
QNVPSAMFFQPLYSVHNGNFQTMGAHGAGVLLS
QDCAGTPQGALEPCVQEATALLTCGPARPWKSV
EEEQEGPGTRLPGNLSSDVLPACTEWRVQTLAY
LPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNNN
YCALGCYGGWHLALPGNTQSSGPIPALACGLSCD
HQGLETTQGVAVVLAGHCQRPGLHEDLQGMLLPSV
LSKARSWTFQPPQPPQPPQPPERTMPRIPTLKNLE

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DLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLV

SEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKP

ET

DR6/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 194
QPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYV
SEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQ
PCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAP
HTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPS
SVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPS
FSSSTSPSPGTAFPRPEHMETHEVPSSTYVPGKM
NSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKE
DVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGG
EKSSTPIKGPKRGHPRQNLHKHFDINEHVLLPLVI
FFGLCLLSLLFIGLMYVKRIFYQNVPSAMFFQPL
YSVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEP
CVQEATALLTCGPAPWKSVALEEEQEGPGTRLPG
NLSSSEDVLPAGCTEWRVQTLAYLPQEDWAPTSLTR
PAPPDSEGSRSSSSSSSSNNMNYCALGCYGGWHL
ALPGNTQSSGPIPALACGLSCDHQGLETOQGVAVW
LAGHCQRPGLHEDLQGMLLPSVLSKARSWTFGGGG
SGGGGSGGGGSERTMPRIPTLKNLEDLVTEYHGNF
SAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGAL
GEGPGASPCNQHSPYWAPPCYTLKPET

DR6/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 195
QPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYV
SEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQ
PCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAP
HTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPS
SVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPS
FSSSTSPSPGTAFPRPEHMETHEVPSSTYVPGKM
NSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKE
DVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGG
EKSSTPIKGPKRGHPRQNLHKHFDINEHVLLPLVI
FFGLCLLSLLFIGLMYVKRIFYQNVPSAMFFQPL
YSVHNGNFQTMGAHGAGVLLSQDCAGTPQGALEP
CVQEATALLTCGPAPWKSVALEEEQEGPGTRLPG
NLSSSEDVLPAGCTEWRVQTLAYLPQEDWAPTSLTR
PAPPDSEGSRSSSSSSSSNNMNYCALGCYGGWHL
ALPGNTQSSGPIPALACGLSCDHQGLETOQGVAVW

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LAGHCQRPGLHEDLQGMLLPSVLSKARSWTFQPOP

QPOPPOPPERTMPRIPTLKNLEDLVTEYHGNFSAW

SGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEG

PGASPCNQHSPYWAPPCYTLKPET

DR5/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 196
ITQODLAPQQRAPQQRSSPSEGLCPPGHHISED
GRDCISCKYQDYSTHWNDLLFCLRCTRCDSGEVE
LSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGC
PRGMVKVGDCPTWSDIECVHKESGTKHSGEVPAVE
ETVTSSPGTPASPCSV

LLPLVIFFGCLLSLLFIGLMYVKRIFYQNVPSPA
MFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTP
QGALEPCVQEATALLTCGPAPWKSVALEEEQEGP
GTRLPGNLSSSEDVLPAGCTEWRVQTLAYLPQEDWA
PTSLTRPAPPDSEGSRSSSSSSSSNNMNYCALGCY
GGWHL
SALPGNTQSSGPIPALACGLSCDHQGLETO
QGVAVWLAGHCQRPGLHEDLQGMLLPSVLSKARSW
TFGGGGSGGGGSGGGGSERTMPRIPTLKNLEDLV
TEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIP
PKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

DR5/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 197
ITQODLAPQQRAPQQRSSPSEGLCPPGHHISED
GRDCISCKYQDYSTHWNDLLFCLRCTRCDSGEVE
LSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGC
PRGMVKVGDCPTWSDIECVHKESGTKHSGEVPAVEE
TVTSSPGTPASPCSV

LLPLVIFFGCLLSLLFIGLMYVKRIFYQNVPSPA
MFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGTP
QGALEPCVQEATALLTCGPAPWKSVALEEEQEGP
GTRLPGNLSSSEDVLPAGCTEWRVQTLAYLPQEDWA
PTSLTRPAPPDSEGSRSSSSSSSSNNMNYCALGCY
GGWHL
SALPGNTQSSGPIPALACGLSCDHQGLETO
QGVAVWLAGHCQRPGLHEDLQGMLLPSVLSKARSW
TFQPOPPOPPOPPERTMPRIPTLKNLEDLVTEYH
GNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKG
GALGEGPGASPCNQHSPYWAPPCYTLKPET

DR3/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 198
QGGTRSPRCDACAGDFHKKIGLFCCRGCPAGHYLKA
PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA

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CDEQASQVALENC SAVADTRCGCKPGWFVECQVSQ
CVSSSPFYCQPCLDCGALHRHTRL LCSRDTDCGT
CLPGFYEHDGCVSCPTSTLGSCPERCAAVCGWRQ
VLLPLVIFFGLCLLSLLFIGLMYVKRIFYQNVPS
AMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGT
PQGALEPCVQEATALLTCGPARPWKSVALEEEQEG
PGTRLPGNLSSDVLPA GCTEWRVQTLAYLPQEDW
APTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGC
YGGWHL SALPGNTQSSGPIPALACGLSCDHQGLET
QQGVAVVL AGHCQRPGLHEDLQGM L LPSVLSKARS
WTFGGGSGGGSGGGGSERTMPRIPTLKNLEDLV
TEYHG NFSAWSGVSKGLAESLQPDYSERLCLVSEI
PPKGGALGEGPGASPCNQHS PYWAPPCYTLKPET
DR3/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 199
QGGTRSPRCD CAGDFHKKIGLFCCRGCPAGHYLKA
PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA
CDEQASQVALENC SAVADTRCGCKPGWFVECQVSQ
CVSSSPFYCQPCLDCGALHRHTRL LCSRDTDCGT
CLPGFYEHDGCVSCPTSTLGSCPERCAAVCGWRQ
VLLPLVIFFGLCLLSLLFIGLMYVKRIFYQNVPS
AMFFQPLYSVHNGNFQTMGAHGAGVLLSQDCAGT
PQGALEPCVQEATALLTCGPARPWKSVALEEEQEG
PGTRLPGNLSSDVLPA GCTEWRVQTLAYLPQEDW
APTSLTRPAPPDSEGSRSSSSSSSSNNNNYCALGC
YGGWHL SALPGNTQSSGPIPALACGLSCDHQGLET
QQGVAVVL AGHCQRPGLHEDLQGM L LPSVLSKARS
WTFQPPQPPQPPQPPERTMPRIPTLKNLEDLVTEY
HGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPK
GGALGEGPGASPCNQHS PYWAPPCYTLKPET
TNFRSF1B/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 200
LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKC
SPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPE
CLSCGSRCS SDQVETQACTREQNR ICTCRPGWYCA
LSKQEGCRLCAPLRKCRPGFGVARPGTETSDV VCK
PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMD
AVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPE
PSTAPSTS FLLPMGPSPPAEGSTGDVLLPLVIFFG
LCLLSLLFIGLMYVKRIFYQNVPS PAMFFQPLYSV
HNGNFQTMGAHGAGVLLSQDCAGTPQGALEPCVQ

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EATALLTCGPARPWKSVALEEEQEGPGTRLPGNLS
SEDVLPAGCTEWRVQTLAYLPQEDWAPTS LTRPAP
PDSEGSRSSSSSSSSNNNNYCALGCYGGWHL SALP
GNTQSSGPIPALACGLSCDHQGLETQQGVAVVL AG
HCQRPGLHEDLQGM L LPSVLSKARSWTFGGGSGG
GGSGGGGSERTMPRIPTLKNLEDLVTEYHG NFSAW
SGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEG
PGASPCNQHS PYWAPPCYTLKPET
TNFRSF1B/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 201
LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKC
SPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPE
CLSCGSRCS SDQVETQACTREQNR ICTCRPGWYCA
LSKQEGCRLCAPLRKCRPGFGVARPGTETSDV VCK
PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMD
AVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPE
PSTAPSTS FLLPMGPSPPAEGSTGDVLLPLVIFFG
LCLLSLLFIGLMYVKRIFYQNVPS PAMFFQPLYSV
HNGNFQTMGAHGAGVLLSQDCAGTPQGALEPCVQ
EATALLTCGPARPWKSVALEEEQEGPGTRLPGNLS
SEDVLPAGCTEWRVQTLAYLPQEDWAPTS LTRPAP
PDSEGSRSSSSSSSSNNNNYCALGCYGGWHL SALP
GNTQSSGPIPALACGLSCDHQGLETQQGVAVVL AG
HCQRPGLHEDLQGM L LPSVLSKARSWTFQPPQPPQ
PQPQPERTMPRIPTLKNLEDLVTEYHG NFSAWSGV
SKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGA
SPCNQHS PYWAPPCYTLKPET
TNFRSF1/IL9R/cGC-F/TNFR1-TM
SEQ ID NO: 202
LVPHLG DREKRDSVCPQGKYIHPQNNSICCTKCHK
GTLYNDCPGPGQD TDCRECESGFTASENHLRHC
LSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRH
YWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCH
AGFFLRENECVSCSNCKKSELECTKLCLPQIENVKG
TEDSGTTVLLPLVIFFGLCLLSLLFIGLMYVKRIF
YQNVPS PAMFFQPLYSVHNGNFQTMGAHGAGVLL
SQDCAGTPQGALEPCVQEATALLTCGPARPWKSV A
LEEEQEGPGTRLPGNLSSDVLPA GCTEWRVQTLA
YLPQEDWAPTS LTRPAPPDSEGSRSSSSSSSSNNN
NYCALGCYGGWHL SALPGNTQSSGPIPALACGLSC
DHQGLETQQGVAVVL AGHCQRPGLHEDLQGM L LPS

-continued
VLSKARSWTFGGGSGGGGSGGGGSERTMPRIPTL
KNLEDLVTEYHGNFSAWSGVSKGLAESLQPDYSER
LCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCY
TLKPET
TNFRSF1/IL9R/cGC-S/TNFR1-TM
SEQ ID NO: 203
LVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHK
GTLYLNDPCPGPGQDTCRECESGSFTASENHLRHC
LSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRH
YWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCH
AGFFLRENECVSCSNCKKSLECTKLCLPQIENVKG
TEDSGTTVLLPLVIFFGLCLLSLLFIGHLMYVKRIF

-continued
YQNVPSPAMFFQPLYSVHNGNFQTMGAHGAGVLL
SQDCAGTPQGALEPCVQEATALLTCGPARPWKSVA
LEEEQEGPGTRLPGNLSSSEDLVPAGCTEWRVQTLA
YLPQEDWAPTSLTRPAPPDSEGSRSSSSSSSSNNN
NYCALGCGYGGWHLSPGNTQSSGPIPALACGLSC
DHQGLETTQQGVAWVLAGHCQRPGLHEDLQGMLLPS
VLSKARSWTFOPQPQPQPQPQPPTMPRIPTLKNL
EDLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCL
VSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLK
PET

SEQUENCE LISTING

Sequence total quantity: 205
SEQ ID NO: 1 moltype = AA length = 214
FEATURE Location/Qualifiers
REGION 1..214
 note = MISC_FEATURE - IL-2rb
source 1..214
 mol_type = protein
 organism = synthetic construct
SEQUENCE: 1
AVNGTSQFTC FYNSTRANISC VWSQDQALQD TSCQVHAWPD RRRWNQTCEL LPVSQASWAC 60
NLILGAPDSQ KLTTVDIVTL RVLCREGVRW RVMAIQDFKP FENLRMAPI SLQVVHVETH 120
RCNISWEISQ ASHYFERHLE FEARTLSPGH TWEEAPLLTL KQKQEWICLE TLTPDTQYEF 180
QVRVKPLQGE FTTWSPWSQP LAFRTKPAAL GKDT 214

SEQ ID NO: 2 moltype = AA length = 219
FEATURE Location/Qualifiers
REGION 1..219
 note = MISC_FEATURE - IL-2ra
source 1..219
 mol_type = protein
 organism = synthetic construct
SEQUENCE: 2
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCO 60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH 120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTGEMETS QFPGEEKPQA 180
SPEGRPESET SCLVTTTDFQ IQTEMAATME TSIFTTEYQ 219

SEQ ID NO: 3 moltype = AA length = 207
FEATURE Location/Qualifiers
REGION 1..207
 note = MISC_FEATURE - IL-4
source 1..207
 mol_type = protein
 organism = synthetic construct
SEQUENCE: 3
MKVLQEPTCV SDYMSISTCE WKMNGPTNCS TELRLLYQLV FLLSEAHTCI PENNGGAGCV 60
CHLLMDDVVS ADNYTDLWA GQQLLWKGSF KPSEHVKPRA PGNLTVHTNV SDTLLLTWSN 120
PYPPDNYLYN HLTAVNIWS ENDPADFRIY NVTYLEPSLR IAASTLKSGI SYRARVRAWA 180
QCYNTTWSEW SPSTKWHNSY REPFEQH 207

SEQ ID NO: 4 moltype = AA length = 219
FEATURE Location/Qualifiers
REGION 1..219
 note = MISC_FEATURE - IL-7ra
source 1..219
 mol_type = protein
 organism = synthetic construct
SEQUENCE: 4
ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE DPDVNITNLE FEICGALVEV 60
KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK IDLTTIVKPE APFDLSVVYR 120

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EGANDFVVTF	NTSHLQKKYV	KVLMHDVAYR	QEKDENKWITH	VNLSSTKLTL	LQRKLQPAAM	180
YEIKVRSIPD	HYFKGFWSEW	SPSYFRTPE	INNSSGEMD			219
SEQ ID NO: 5	moltype = AA length = 175					
FEATURE	Location/Qualifiers					
REGION	1..175					
	note = MISC_FEATURE - IL-15ra					
source	1..175					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 5						
ITCPPPMSVE	HADIWVKSYS	LYSRERYICN	SGFKRKAGTS	SLTECVLNKA	TNVAHWTTTPS	60
LKCIRDPALV	HQRPAPPSTV	TTAGVTPQPE	SLSPSGKEPA	ASSPSSNNTA	ATTAAIVPGS	120
QLMPKSPST	GTTEISSHES	SHGTPSQTTA	KNWELTASAS	HQPPGVYPQG	HSDTT	175
SEQ ID NO: 6	moltype = AA length = 213					
FEATURE	Location/Qualifiers					
REGION	1..213					
	note = MISC_FEATURE - IL-21ra					
source	1..213					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 6						
CPDLVCYTDY	LQTVICILEM	WNLHPSTLTL	TWQDQYEELK	DEATSCSLHR	SAHNATHATY	60
TCHMDVFHFM	ADDIFSVNIT	DQSGNYSQEC	GSFLLAESIK	PAPPFNVTVT	FSGQYNISWR	120
SDYEDPAFYM	LKGKLYELQ	YRNRGDPWAV	SPRKRLISVD	SRSVSLPLE	FRKDSSYELQ	180
VRAGPMPGSS	YQGTWSEWSD	PVIFQTQSEE	LKE			213
SEQ ID NO: 7	moltype = AA length = 93					
FEATURE	Location/Qualifiers					
REGION	1..93					
	note = MISC_FEATURE - TGFBR1					
source	1..93					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 7						
LQCFCHLCTK	DNFTCVTDGL	CFVSVTETTD	KVIHNSMCIA	EIDLIPRDRP	FVCAPSSKTG	60
SVTTYCCNQ	DHCNKIELPT	TVKSSPGLGP	VEL			93
SEQ ID NO: 8	moltype = AA length = 144					
FEATURE	Location/Qualifiers					
REGION	1..144					
	note = MISC_FEATURE - TGFBR2					
source	1..144					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 8						
TIPPHVQKSV	NNDMIVTDNN	GAVKFPQLCK	FCDVRFSTCD	NQKSCMSNCS	ITSICEKPQE	60
VCVAVWRKND	ENITLETVCH	DPKLPYHDFI	LEDAASPKCI	MKEKKKPGET	FFMCSCSSDE	120
CNDNIIFSEE	YNTSNPDLLL	VIFQ				144
SEQ ID NO: 9	moltype = AA length = 214					
FEATURE	Location/Qualifiers					
REGION	1..214					
	note = MISC_FEATURE - IL-10ra					
source	1..214					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 9						
HGTELPSPPS	VWFEAFFHH	ILHWTPIPNQ	SESTCYEVAL	LRYGIESWNS	ISNCSQTLSTY	60
DLTAVTLDLY	HSNGYRARVR	AVDGSRHSNW	TVTNTFRSVD	EVTLTVGSVN	LEIHNGFILG	120
KIQLPRPKMA	PANDTYESIF	SHFREYEIAI	RKVPGNFTFT	HKKVKHENFS	LLTSGEVGEF	180
CVQVKPSVAS	RSNKGWWSKE	ECISLTRQYF	TVTN			214
SEQ ID NO: 10	moltype = AA length = 148					
FEATURE	Location/Qualifiers					
REGION	1..148					
	note = MISC_FEATURE - FAS					
source	1..148					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 10						
QVTDINSKGL	ELRKTVTTVE	TQNLEGLHHD	GQFCHKPCPP	GERKARDCTV	NGDEPDCVPC	60
QEGKEYTDKA	HFSSKCRRCR	LCDEGHGLEV	EINCTRQTNT	KCRCKPNFFC	NSTVCEHCDP	120
CTKCEHGIK	ECTLTSNTKC	KEEGSRSN				148

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SEQ ID NO: 11	moltype = AA length = 126				
FEATURE	Location/Qualifiers				
REGION	1..126				
	note = MISC_FEATURE - CTLA4				
source	1..126				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 11					
KAMHVAQPAV	VCLASSRGIAS	FVCEYASPGK	ATEVRVTVLR	QADSQVTEVC	AATYMMGNEL 60
TFLDDSICTG	TSSGNQVNLT	IQGLRAMDTG	LYICKVELMY	PPPYLGGIGN	GTQIYVIDPE 120
PCPDSD					126
SEQ ID NO: 12	moltype = AA length = 428				
FEATURE	Location/Qualifiers				
REGION	1..428				
	note = MISC_FEATURE - LAG3				
source	1..428				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 12					
LQPGAEPVAV	WAQEGAPAQL	PCSPTIPLQD	LSLLRRAGVT	WQHQPDSGPP	AAAPGHPLAP 60
GPHPAAPSSW	GPRPRRYTVL	SVGPGGLRSG	RLPLQPRVQL	DERGRQRGDF	SLWLRPARRA 120
DAGEYRAAVH	LRDRALSCRL	RLRLGQASMT	ASPPGSLRAS	DWVILNCSFS	RPDRPASVHW 180
FRNRGQGRVP	VRESPHHHLA	ESFLFLPQVS	PMDSGPWGCI	LTYRDGFNVS	IMYNLTVLGL 240
EPPTPLTVYA	GAGSRVGLPC	RLPAGVGTRS	FLTAKWTPPG	GGPDLLVTGD	NGDFTLRLED 300
VSQAQAGTYT	CHIHLEQQQL	NATVTLAIIT	VTPKSFGSPG	SLGKLLCEVT	PVSGQERFVW 360
SSLDTPSQRS	FSGPWLEAQE	AQLLSQPWQC	QLYQGERLLG	AAVYFTELSS	PGAQRSGRAP 420
GALPAGHL					428
SEQ ID NO: 13	moltype = AA length = 181				
FEATURE	Location/Qualifiers				
REGION	1..181				
	note = MISC_FEATURE - TIM3				
source	1..181				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 13					
SSEVEYRAEVG	QNAYLPCFYT	PAAPGNLVPV	CWGKGACPVF	ECGNVVLRTD	ERDVNYWTSR 60
YWLNGDFRKG	DVSLTIENVT	LADSGIYCCR	IQIPGIMNDE	KFNCLKLVIKP	AKVTPAPTRQ 120
RDFTAAAFPRM	LTTRGHGPAE	TQTLGSLPDI	NLTQISTLAN	ELRDSRLAND	LRDSGATIRI 180
G					181
SEQ ID NO: 14	moltype = AA length = 220				
FEATURE	Location/Qualifiers				
REGION	1..220				
	note = MISC_FEATURE - PD1				
source	1..220				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 14					
FTVTVPKDLY	VVEYGSNMTI	ECKFPVEKQL	DLAALIVYWE	MEDKNIIQFV	HGEEDLKVQH 60
SSSYRQRARLL	KDQLSLGNAA	LQITDVKLQD	AGVYRCMISY	GGADYKRITV	KVNAPYNKIN 120
QRILVVDVPT	SEHELTCQAE	GYPKAEVIWT	SSDHQVLSGK	TTTTNSKREE	KLFNVTSTLR 180
INTTTNEIFY	CTFRRLDPEE	NHTAELVIPE	LPLAHPNER		220
SEQ ID NO: 15	moltype = AA length = 438				
FEATURE	Location/Qualifiers				
REGION	1..438				
	note = MISC_FEATURE - ILT2				
source	1..438				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 15					
GHLPKPTLWA	EPGSVITQGS	PVTLRCQGGQ	ETQEYRLYRE	KKTALWITRI	PQELVKKGQF 60
PIPSITWEHA	GRYRCYGS	TAGRSESSDP	LELVVTGAYI	KPTLSAQSP	VVNSGGNVIL 120
QCDSQVAFDG	FSLCKEGEDE	HPQCLNSQPH	ARGSSRAIFS	VGPVSPSRW	WYRCYAYDSN 180
SPYEWSLPSD	LLELLVLGVS	KKPSLSVQPG	PIVAPEETLT	LQCGSDAGYN	RFVLYKDGER 240
DFLQLAGAP	QAGLSQANFT	LGPVRSYGG	QYRCYGAHNL	SSEWSAPSDP	LDILIAGQFY 300
DRVLSVQPG	PTVASGENVT	LLCQSQGMQ	TFLLTKEGAA	DDPWRLRSTY	QSQYQAEFP 360
MGPVTSAHAG	TYRCYGSQSS	KPYLLTHPSD	PLELVVSGPS	GGPSSPTTGP	TSTSGPEDQP 420
LTPTGSDPQS	GLGRHLGV				438
SEQ ID NO: 16	moltype = AA length = 238				
FEATURE	Location/Qualifiers				
REGION	1..238				
	note = MISC_FEATURE - ILT3				

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source	1..238					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 16						
QAGPLPKPTL	WAEPGSVISW	GNSVTIWCQG	TLEAREYRLD	KEESPAPWDR	QNPLEPKNKA	60
RFSIPSMTED	YAGRYRCYYR	SPVGWSQPSD	PLELVMTGAY	SKPTLSALPS	PLVTSGKSVT	120
LLCQSRSPMD	TFLLIKERAA	HPLLHLRSEH	GAQQHQAEFP	MSPVTSVHGG	TYRCFSSHGF	180
SHYLLSHPSD	PLELIVSGSL	EDPRPSPTRS	VSTAAGPEDQ	PLMPTGSVPH	SGLRRHWE	238
SEQ ID NO: 17	moltype = AA length = 440					
FEATURE	Location/Qualifiers					
REGION	1..440					
	note = MISC_FEATURE - ILT4					
source	1..440					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 17						
QTGTIPKPTL	WAEPDSVITQ	GSPVTLSCQG	SLEAQEYRLY	REKKSASWIT	RIRPELVKNG	60
QFHIPSITWE	HTGRYGCQYY	SRARWSELSD	PLVLVMTGAY	PKPTLSAQPS	PVVTSGGRVT	120
LQCESQVAFG	GFILCKEGEE	EHPQCLNSQP	HARGSSRAIF	SVGPVSPNRR	WSHRCYGYDL	180
NSSPYVWSSPS	DLLELLVPGV	SKKPSLSVQP	GPVVAPGESL	TLQCVSDVGY	DRFVLYKEGE	240
RDLRQLPGRQ	PQAGLSQANF	TLGPVSRSYG	GQYRCYGAHN	LSSECSAPSD	PLDILITGQI	300
RGTPFISVQP	GPTVASGENV	TLLCQSWRQF	HTFLLTKAGA	ADAPLRLRSI	HEYPKYQAEF	360
PMSPV TSAHA	GTYRCYGSLN	SDPYLLSHPS	EPLELVVSGP	SMGSSPPPTG	PISTPAGPED	420
QPLTPTGSDP	QSGLGRHLGV					440
SEQ ID NO: 18	moltype = AA length = 420					
FEATURE	Location/Qualifiers					
REGION	1..420					
	note = MISC_FEATURE - ILT5					
source	1..420					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 18						
GPFPKPTLWA	EPGSVISWGS	PVTIWCQGSQ	EAQEYRLHKE	GSPEPLDRNN	PLEPKNKARF	60
SIPSMTEHHA	GRYRCHYYSS	AGWSEPSDPL	EMVMTGAYSK	PTLSALPSPV	VASGGNMTLR	120
CGSQKGYYHF	VLMKEGEHQL	PRTLDSQQLH	SRGFQALFPV	GPVTPSHRWR	FTCYYYTNT	180
PWVWSHPSDP	LEILPSGVSR	KPSLLTLQGP	VLAPGQSLTL	QCGSDVGYNR	FVLYKEGERD	240
FLQRPGQQPQ	AGLSQANFTL	GPVSPSNGGQ	YRCYGAHNLS	SEWSAPSDPL	NILMAGQIYD	300
TVLSAQPGP	TVASGENVTL	LCQSWWQFDT	FLLTKEGAAH	PPLRLRSMYG	AHKYQAEFPM	360
SPV TSAHAGT	YRCYGSYSSN	PHLLSHPSEP	LELVVSGHSG	GSSLPPTGPP	STPGLGRYLE	420
SEQ ID NO: 19	moltype = AA length = 732					
FEATURE	Location/Qualifiers					
REGION	1..732					
	note = MISC_FEATURE - VEGFR1					
source	1..732					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 19						
SKLKDPELSL	KGTQHIMQAG	QTLHLQCRGE	AAHKWSLP	PEMVS	KESERLSI	TKSACGRNGK
QFCSTLTLNT	AQANHTGFYS	CKYLAVPTSK	KKETESAIYI	FISDTGRPFV	EMYSEIPEII	120
HMTGRELVI	PCRVTSPNIT	VTLKKFPLDT	LIPDGKRIIW	DSRKGFIISN	ATYKEIGLLT	180
CEATVNGHLY	KTNYLTHRQT	NTIIDVQIST	PRPVKLLRGH	TLVLNCTATT	PLNTRVQMTW	240
SYPDEKNKRA	SVRRRIDQSN	SHANIFYSVL	TIDKMQNKDK	GLYTCRVRSG	PSFKSVNTSV	300
HIYDKAFITV	KHRKQQVLET	VAGKRSYRLS	MKVKAFFSPE	VVWLKDGLPA	TEKSARYLTR	360
GYSLIIKDVT	EEDAGNYTIL	LSIKQSNVFK	NLTATLIVNV	KPQIYEKAVS	SFPDPALYPL	420
GSRQILTCTA	YGIPQPTIKW	FWHPCNHNHS	EARCDFCSNN	EESFILDADS	NMGNRIESIT	480
QRMAIEGKN	KMASTLVVAD	SRISGIYICI	ASNKVGTVGR	NISFYITDVP	NGFHVNLKEM	540
PTEGEDLKLS	CTVNKFLYRD	VTWILLRTVN	NRTMHYSISK	QKMAITKEHS	ITLNLTIMNV	600
SLQDSGTYAC	RARNVYTGE	ILQKKEITIR	DQEAPYLLRN	LSDHTVAISS	STTLDCHANG	660
VPEPQITWFK	NNHKIQQEPG	IILGPGSSTL	FIERVTEEDE	GVYHCKATNQ	KGSVESSAYL	720
TVQGTSDKSN	LE					732
SEQ ID NO: 20	moltype = AA length = 745					
FEATURE	Location/Qualifiers					
REGION	1..745					
	note = MISC_FEATURE - VEGFR2					
source	1..745					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 20						
ASVGLPSVSL	DLPRLSIQKD	ILTIKANTTL	QITCRGQRDL	DWLWPNNQSG	SEQRVEVTEC	60
SDGLFCKTLT	IPKVIGNDTG	AYKCFYRETD	LASVIYVYVQ	DYRSPFIASV	SDQHGVVYIT	120
ENKNKTVVIP	CLGSISNLNV	SLCARYPEKR	FVPDGNRISW	DSKKGFTIPS	YMISYAGMVF	180
CEAKINDESY	QSIMYIVVVV	GYRIYDVVLS	PSHGIELSVG	EKLVLNCTAR	TELNVGIDFN	240

WEYPSSKHQH	KKLVNRDLKT	QSGSEMKKFL	STLTIDGVTR	SDQGLYTCAA	SSGLMTKKNS	300
TFVRVHEKPF	VAFGSGMESL	VEATVGERVR	IPAKYLGYP	PEIKWYKNGI	PLESNHTIKA	360
GHVLTIMEVS	ERDTGNYTVI	LTNPISEKQ	SHVSVLVVYV	PPQIGEKSLI	SPVDSYQYGT	420
TQTLTCTVYA	IPPPHHIHWY	WQLEEECANE	PSQAVSVTNP	YPCEEWRSVE	DFQGGNKIEV	480
NKNQFALIEG	KNKTVSTLVI	QAANVSALYK	CEAVNKGVRG	ERVISFHVTR	GPEITLQPDM	540
QPTQESVSL	WCTADRSTFE	NLTWYKLGPO	PLPIHVGELP	TPVCKNLDTL	WKLNATMFSN	600
STNDILIMEL	KNASLQDQGD	YVCLAQDRKT	KKRHCVVVRQL	TVLERVAPT	TGNLENQTTT	660
IGESIEVSCT	ASGNPPPQIM	WFKDNETLVE	DSGIVLKDGN	RNLTIRRVRK	EDEGLYTCQA	720
CSVLGCAKVE	AFFIIEGAQE	KTNLE				745
SEQ ID NO: 21	moltype = AA length = 751					
FEATURE	Location/Qualifiers					
REGION	1..751					
	note = MISC_FEATURE - VEGFR3					
source	1..751					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 21						
YSMTPTLNI	TEESHVIDTG	DSLSISCRGQ	HPLEWAWPGA	QEAPATGDKD	SEDTGVRDC	60
EGTDARPYCK	VLLLHEVHAN	DTGSYVCYK	YIKARIEGTT	AASSYVFVRD	FEQPFINKPD	120
TLLVNRKDAM	WVPCLVSIPG	LNVTLSQSS	VLWPDGQEVV	WDDRRGMLVS	TPLLHDALYL	180
QCETTWGDQD	FLSNPFLVHI	TGNELYDIQL	LPRKSLELLV	GEKLVLNCTV	WAEFNSGVTF	240
DWDYPGKQAE	RGKWVPERRS	QQTHTELSSI	LTIHNVSQHD	LGSYVCKANN	GIQRFRESTE	300
VIVHENPFIS	VEWLKGPIL	ATAGDELVKL	PVKLAAYPPP	EFQWYKDGKA	LSGRHSPHAL	360
VLKEVTEAST	GTYTALWNS	AAGLRNLSL	ELVVNVPPQI	HEKEASSPSI	YSRHSRQALT	420
CTAYGVPLPL	SIQWHRPWT	PCKMFAQRSL	RRRQQDLMP	QCRDWRVTT	QDAVNPIESL	480
DTWTEFVEGK	NKTVSKLVIQ	NANVSAMYKC	VVSNKVGQDE	RLIYFYVTI	PDGFTIESKP	540
SEELLEGPV	LLSCQADSYK	YEHLRWYRLN	LSTLHDAHGN	PLLLDCKNVH	LFATPLAASL	600
EEVAPGARHA	TLSLSIPRVA	PEHEGHYVCE	VQDRRSHDKH	CHKKYLSVQA	LEAPRLTQNL	660
TDLLVNVSDS	LEMQCLVAGA	HAPSIWVYKD	ERLLEEKSGV	DLADSNQKLS	IQRVREEDAG	720
RYLCSVCNAK	GCVNSSASVA	VEGSEDKGSM	E			751
SEQ ID NO: 22	moltype = AA length = 380					
FEATURE	Location/Qualifiers					
REGION	1..380					
	note = MISC_FEATURE - OPG					
source	1..380					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 22						
ETFPKYLHY	DEETSHQLLC	DKCPPGTLYK	QHCTAKWKT	CAPCPDHYYT	DSWHTSDECL	60
YCSPVCKELQ	YVKQECNRTH	NRVCECKEGR	YLEIEFCLKH	RSCPPGFGVV	QAGTPERNVT	120
CKRCPDGFPS	NETSSKAPCR	KHTNCSVFG	LLTQKGNATH	DNICSGNSES	TQKCGIDVT	180
CEEAFFRFAV	PTKFTPNWLS	VLVDNLPGTK	VNAESVERIK	RQHSSQEQT	QLLKLWKHQ	240
KDQDIVKKII	QDIDLCEVSV	QRHIGHANLT	FEQLRSLMES	LPQKKVGAED	IEKTIKACKP	300
SDQILKLLSL	WRIKNGDQDT	LKGLMHALKH	SKTYHFPKTV	TQSLKKTIRF	LHSFTMYKLY	360
QKLFLEMIGN	QVQSVKISCL					380
SEQ ID NO: 23	moltype = AA length = 165					
FEATURE	Location/Qualifiers					
REGION	1..165					
	note = MISC_FEATURE - TACI					
source	1..165					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 23						
MSGLGRSRRG	GRSRVDQEE	FPQGLWTGVA	MRSCEPEQYW	DPLLGTCSMC	KTICNHQSQR	60
TCAAFCSRSL	CRKEQGKFYD	HLLRDCISCA	SICGQHPKQC	AYFCENKLRS	PVNLPPELRR	120
QRSGEVENNS	DNSGRYQGLE	HRGSEASPAL	PGLKLSADQV	ALVYS		165
SEQ ID NO: 24	moltype = AA length = 54					
FEATURE	Location/Qualifiers					
REGION	1..54					
	note = MISC_FEATURE - BCM4					
source	1..54					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 24						
MLQMAGQCSQ	NEYFDSLHA	CIPCQLRCSS	NTPPLTCQRY	CNASVTNSVK	GTNA	54
SEQ ID NO: 25	moltype = AA length = 222					
FEATURE	Location/Qualifiers					
REGION	1..222					
	note = MISC_FEATURE - NGFR					
source	1..222					
	mol_type = protein					

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organism = synthetic construct	
SEQUENCE: 25	
KEACPTGLYT HSGECCKACN LGEGVAQPCG ANQTVCEPCL DSVTFSDVVS ATEPCKPCTE	60
CVGLQSMSAP CVEADDAVCR CAYGYYQDET TGRCEACRVC EAGSGLVFSC QDKQNTVCEE	120
CPDGTYSDEA NHVDPCLPCT VCEDTERQLR ECTRWADAEC EEIPGRWITR STPPEGSDST	180
APSTQEPEAP PEQDLIASTV AGVVTTVMGS SQPVVTRGTT DN	222
SEQ ID NO: 26	
moltype = AA length = 161	
FEATURE	
Location/Qualifiers	
REGION	
1..161	
note = MISC_FEATURE - EDAR	
source	
1..161	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 26	
EYSNCGENEY YNQTGLCQE CPPCGPGEEP YLSCGYGTKD EDYGCVPCPA EKFSKGGYQI	60
CRRHKDCEGF FRATVLTPGD MENDAECGPC LPGYMLENR PRNIYGMVCY SCLLAPPNTK	120
ECVGATSGAS ANFPGTSGSS TLPSPQHAHK ELSGQGHLAT A	161
SEQ ID NO: 27	
moltype = AA length = 156	
FEATURE	
Location/Qualifiers	
REGION	
1..156	
note = MISC_FEATURE - DCR2 (TNFRSF10D)	
source	
1..156	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 27	
ATIPRQDEVP QQTVAPQQQR RSLKEEECPA GSHRSEYTGA CNPCTEGVDY TIASNNLPSC	60
LLCTVCKSGQ TNKSSCTTTR DTVCQCEKGS FQDKNSPEMC RTCRTGCPRG MVKVSNCTPR	120
SDIKCKNESA ASSTGKTPAA EETVTTILGM LASPYH	156
SEQ ID NO: 28	
moltype = AA length = 211	
FEATURE	
Location/Qualifiers	
REGION	
1..211	
note = MISC_FEATURE - DCR1 (TNFRSF10C)	
source	
1..211	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 28	
ATTARQEEVP QQTVAPQQQR HSFKGEECPA GSHRSEHTGA CNPCTEGVDY TNASNNEPSC	60
FPCTVCKSDQ KHKSSCTMTR DTVCQCKEGT FRNENSP EMC RKCSRCPSGE VQVSNCTSWD	120
DIQCVVEEFGA NATVETPAAE ETMNTSPGTP APAAEETMNT SPGTPAPAAE ETMTTSPGTP	180
APAAEETMTT SPGTPAPAAE ETMITSPGTP A	211
SEQ ID NO: 29	
moltype = AA length = 173	
FEATURE	
Location/Qualifiers	
REGION	
1..173	
note = MISC_FEATURE - CD40	
source	
1..173	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 29	
EPPTACREKQ YLINSQCCSL CQPGQKLVS D CTEFTETECL PCGESEFLDT WNRETHCHQH	60
KYCDPNLGLR VQQKGTS ETD TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD	120
TICEPCPVGF FSNVSSAFEK CHPWTSCETK DLVVQQAGTN KTDVVCGPQD RLR	173
SEQ ID NO: 30	
moltype = AA length = 216	
FEATURE	
Location/Qualifiers	
REGION	
1..216	
note = MISC_FEATURE - DR4	
source	
1..216	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 30	
ASGTEAAAAT PSKVWGSSAG RIEPRGGGRG ALPTSMGQHG PSARARAGRA PGPRPAREAS	60
PRLRVHKTFK FVVVGVLQV VPSSAATIKL HDQSIGTQOW EHSPLGELCP PGSHRSEHPG	120
ACNRCTEGVG YTNASNNLFA CLPCTACKSD EEERSPCTTT RNTACQCKPG TFRNDNSAEM	180
CRKCSRGCPR GMVKVKDCTP WSDIECVHKE SGNHGN	216
SEQ ID NO: 31	
moltype = AA length = 308	
FEATURE	
Location/Qualifiers	
REGION	
1..308	
note = MISC_FEATURE - DR6	
source	
1..308	
mol_type = protein	
organism = synthetic construct	

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SEQUENCE: 31					
QPEQKASNLI	GTYRHVD RAT	GQVLTCDKCP	AGTYVSEHCT	NTSLRVCSSC	PVGTFTRHEN 60
GIEKCHDCSQ	PCPWPMIEKL	PCAAALTDREC	TCPPGMFQSN	ATCAPHTVCP	VGWGVRRKGT 120
ETEDVRCKQC	ARGTFSDVPS	SVMKCKAYTD	CLSQNLVVIK	PGTKETDNVC	GTLPSFSSST 180
SPSPGTAIFP	RPEHMETHEV	PSSTYVPKGM	NSTESNSSAS	VRPKVLSSIQ	EGTVPDNTSS 240
ARGKEDVNKT	LPNLQVVNHQ	QGP HHRHILK	LLPSMEATGG	EKSSTPIKGP	KRGHPRQNLH 300
KHFDINEH					308
SEQ ID NO: 32					
FEATURE		moltype = AA length = 155			
REGION		Location/Qualifiers			
		1..155			
		note = MISC_FEATURE - DR5			
source		1..155			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 32					
ITQQDLAPQQ	RAAPQQKRSS	PSEGLCPPGH	HISEDGRDCI	SCKYGQDYST	HWNDLLFCLR 60
CTRCDSGEVE	LSPCTTTRNT	VCQCEEGTFR	EEDSPEMCRK	CRTGCPRGMV	KVGDCPTWSD 120
IECVHKESGT	KHSGEVP AVE	ETVTSSPGTP	ASPCS		155
SEQ ID NO: 33					
FEATURE		moltype = AA length = 175			
REGION		Location/Qualifiers			
		1..175			
		note = MISC_FEATURE - DR3			
source		1..175			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 33					
QGGTRSPRCD	CAGDFHKKIG	LFCCRGCPAG	HYLKAPCTEP	CGNSTCLVCP	QDTFLAWENH 60
HNSECARCQA	CDEQASQVAL	ENCSAVADTR	CGCKPGWFVE	CQVSQCVSSS	PFYCQPCLDC 120
GALHRHTRL L	CSRRD TDCGT	CLPGFYE HGD	GCVSCTPSTL	GSCPERCAAV	CGWRQ 175
SEQ ID NO: 34					
FEATURE		moltype = AA length = 235			
REGION		Location/Qualifiers			
		1..235			
		note = MISC_FEATURE - TNFRSF1B			
source		1..235			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 34					
LPAQVAFTPY	APEPGSTCRL	REYYDQTAQM	CCSKCSPGQH	AKVFCTKTS D	TVCDSCEDST 60
YTQLWNWVPE	CLSCGSRCSS	DQVETQACTR	EQNRICTCRP	GWYCALSKQE	GCRLCAPLRK 120
CRPGFGVARP	GTETSDVVCK	PCAPGTFSNT	TSSTDICRPH	QICNVVAIPG	NASMDAVCTS 180
TSPTRSMAPG	AVHLPQPVST	RSQHTQPTPE	PSTAPSTSFL	LPMGPSPPAE	GSTGD 235
SEQ ID NO: 35					
FEATURE		moltype = AA length = 182			
REGION		Location/Qualifiers			
		1..182			
		note = MISC_FEATURE - TNFRSF1			
source		1..182			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 35					
LVP HLG DREK	RDSVCPQGKY	IHPQNN SICC	TKCHKGT YLY	NDCPGPGQDT	DCRECESGSF 60
TASENHLRHC	LSCSKCRKEM	GQVEISSCTV	DRDTVCGCRK	NQYRHYWSEN	LFQCFNCSLC 120
LNQTVHLSCQ	EKQNTVCTCH	AGFFLRENEC	VSCSNCKKSL	ECTKLCLPQI	ENVKGTEDSG 180
TT					182
SEQ ID NO: 36					
FEATURE		moltype = AA length = 113			
REGION		Location/Qualifiers			
		1..113			
		note = MISC_FEATURE - BMPR1B			
source		1..113			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 36					
KKEDGESTAP	TPRPKVL RCK	CHH HCPEDSV	NNICSTDGYC	FTMIEEDDSG	LPVVTSGCLG 60
LEGSDFQCRD	TPIPHQRRSI	ECCTERNECN	KDLHPTLPPL	KNRDFVDGPI	HHR 113
SEQ ID NO: 37					
FEATURE		moltype = AA length = 129			
REGION		Location/Qualifiers			
		1..129			
		note = MISC_FEATURE - BMPR1A			
source		1..129			
		mol_type = protein			
		organism = synthetic construct			

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SEQUENCE: 37					
QNLD SMLHGT	GMKSDSDQKK	SENGVTLAPE	DTLPFLKCYC	SGHCPDDAIN	NTCITNGHCF 60
AIIEEDDQGE	TTLASGCMKY	EGSDFQCKDS	PKAQLRRTIE	CCRTNLCNQY	LQPTLPPVVI 120
GPFFDGSIR					129
SEQ ID NO: 38					
		moltype = AA length = 124			
FEATURE		Location/Qualifiers			
REGION		1..124			
		note = MISC_FEATURE - BMPR2			
source		1..124			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 38					
SSQNQERLCAF	KDPYQQDLGI	GESRISHENG	TILCSKGSTC	YGLWEKSKGD	INLVKQGCWS 60
HIGDPQECHY	EECVVTTTPP	SIQNGTYRFC	CCSTDLCNVN	FTENFPPPD	TPLSPPHSFN 120
RDET					124
SEQ ID NO: 39					
		moltype = AA length = 603			
FEATURE		Location/Qualifiers			
REGION		1..603			
		note = MISC_FEATURE - CSF3R			
source		1..603			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 39					
ECGHISVSAP	IVHLGDPITA	SCIIKQNC SH	LDPEPQILWR	LGAELQPGGR	QQR LSDGTQE 60
SIITLPHLNH	TQAF LSCCLN	WGNSLQILDQ	VELRAGYPPA	IPHNLSCLMN	LTTSSLICQW 120
EPGPETHLPT	SFTLKSFKSR	GNCQTQGDSI	LDCVPKDGQS	HCCIPRKHLL	LYQNMGIWVQ 180
AENALGTSMS	PQLCLDPM DV	VKLEPPMLRT	MDPSPEAAPP	QAGCLQLCWE	PWQPGLHINQ 240
KCELRHKPQR	GEASWALVGP	LPLEALQYEL	CGLLPATAYT	LQIRCIRWPL	PGHWSDWSPS 300
LELR TTERAP	TVRLDTWWRQ	RQLDPRTVQL	FWKVPVLEED	SGRIQGYVVS	WRPSGQAGAI 360
LPLCNTTELS	CTFHLPSEAQ	EVALVAYNSA	GTSRPTPVVF	SES RGPALTR	LHAMARDPHS 420
LWVGWEPPNP	WPQGYVIEWG	LGPPSASNSN	KTWRMEQNGR	ATGFLLKENI	RPFQLYEIIV 480
TPLYQDTMGP	SQHVYAYSQE	MAPSHAPELH	LKHIGKTWAQ	LEWVPEPPEL	GKSPLTHYTI 540
FWTNAQNQSF	SAILNASSRG	FVLHGLEPAS	LYHIHLMAAS	QAGATNSTVL	TLMTLTPEGS 600
ELH					603
SEQ ID NO: 40					
		moltype = AA length = 498			
FEATURE		Location/Qualifiers			
REGION		1..498			
		note = MISC_FEATURE - CSF1R			
source		1..498			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 40					
IPVIEPSVPE	LVVKPGATVT	LRCVGN GSVE	WDGPPSPHWT	LYSDGSSSIL	STNNATFQNT 60
GTYRCTEPGD	PLGGSAAIHL	YVKD PARPWN	VLAQEVVVFE	DQDALLPCLL	TDPVLEAGVS 120
LVRVRGRPLM	RHTNYSFSPW	HGFTIHRAKF	IQSQDYQCSA	LMGGRKVMSI	SIRLKVQKVI 180
PGPPALTLPV	AELVRIRGEA	AQIVCSASSV	DVNFDVFLQH	NNTKLAIPQQ	SDFHNNRYQK 240
VLTLNLDQVD	FQHAGNYSCV	ASNVOGKHST	SMFFRVVESA	YLNLSSEQNL	IQEVTVGEGL 300
NLKVMVEAYP	GLQGFNWTYL	GPFS DHQPEP	KLANATTKDT	YRHTFTLSLP	RLKPSEAGRY 360
SFLARNPGGW	RALTFELTLR	YPPEVSVIWT	FINGSGTLLC	AASGYPPQPNV	TWLQCSGHTD 420
RCDEAQVLQV	WDDPYPEVLS	QEPFHKVTVQ	SLLTVETLEH	NQTYECRAHN	SVGSGSWAFI 480
PISAGATHTP	PDEFLEFTP				498
SEQ ID NO: 41					
		moltype = AA length = 103			
FEATURE		Location/Qualifiers			
REGION		1..103			
		note = MISC_FEATURE - Activin R1A			
source		1..103			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 41					
MEDEKPKVNP	KLYMCVCEGL	SCGNEDHCEG	QQCFSSLSIN	DGFHVYQKGC	FQVYEQGKMT 60
CKTPPSPGQA	VECCQGDWCN	RNITAQLPTK	GKSFPGTQNF	HLE	103
SEQ ID NO: 42					
		moltype = AA length = 103			
FEATURE		Location/Qualifiers			
REGION		1..103			
		note = MISC_FEATURE - Activin R1B			
source		1..103			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 42					
SGPRGVQALL	CACTSCLOAN	YTCETDGACM	VSIFNLDGME	HHVRTCIPKV	ELVPAGKPFY 60
CLSS EDLRNT	HCCYTDYCNR	IDLRVPSGHL	KEPEHPSMWG	PVE	103

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SEQ ID NO: 43		moltype = AA length = 92	
FEATURE		Location/Qualifiers	
REGION		1..92	
		note = MISC_FEATURE - Activin R1C	
source		1..92	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 43			
LSPGLKCVCL	LCDSSNFTCQ	TEGACWASVM LTNGKEQVIK SCVSLPELNA QVFC	60
TKTECCFTDF	CNNITLHLPT	ASNAPKLGP ME	92
SEQ ID NO: 44		moltype = AA length = 119	
FEATURE		Location/Qualifiers	
REGION		1..119	
		note = MISC_FEATURE - Activin R2B	
source		1..119	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 44			
SGRGEAETRE	CIYYNANWEL	ERTNQSGLER CEQEQDKRLH CYASWRNSSG TIELVKKGCW	60
LDDFNCYDRQ	ECVATEENPQ	VYFCCCEGNF CNERFTHLPE AGGPEVTYEP PPTAPTLT	119
SEQ ID NO: 45		moltype = AA length = 116	
FEATURE		Location/Qualifiers	
REGION		1..116	
		note = MISC_FEATURE - Activin R2A	
source		1..116	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 45			
AILGRSETQE	CLFFNANWEK	DRTNQTGVEP CYGDKDKRRH CFATWKNISG SIEIVKQGCW	60
LDDINCYDRT	DCVEKKDSPE	VYFCCCEGNM CNEKFSYFPE MEVTQPTSNP VTPKPP	116
SEQ ID NO: 46		moltype = AA length = 120	
FEATURE		Location/Qualifiers	
REGION		1..120	
		note = MISC_FEATURE - TIGIT	
source		1..120	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 46			
MMTGTIETTG	NISAEKGGSI	ILQCHLSSTT AQVTQVNWEQ QDQLLAICNA DLGWHISPSF	60
KDRVAPGPGL	GLTLQSLTVN	DTGEYFCIYH TYPDGYTGR IFLEVLESSV AEHGARFQIP	120
SEQ ID NO: 47		moltype = AA length = 175	
FEATURE		Location/Qualifiers	
REGION		1..175	
		note = MISC_FEATURE - FCGR2B	
source		1..175	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 47			
TPAAPPKAVL	KLEPQWINVL	QEDSVTLTCR GTHSPESDSI QWFHNGNLIP THTQPSYRFK	60
ANNNDSGEYT	CQTGQTSLS	PVHLTVLSEW LVLQTPHLEF QEGETIVLRC HSWKDKPLVK	120
VTFFQNGKSK	KFSRSDPNFS	IPQANHSHSG DYHCTGNIGY TLYSSKPVTI TVQAP	175
SEQ ID NO: 48		moltype = AA length = 277	
FEATURE		Location/Qualifiers	
REGION		1..277	
		note = MISC_FEATURE - FCGR1	
source		1..277	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 48			
QVDTTKAVIT	LQPPWVS	EETVTLHCEV LHLPGSSSTQ WFLNGTATQT STPSYRITSA	60
SVNDSGEYRC	QRGLSGRSDP	IQLEIHRGWL LLQVSSRVFT EGEPLALRCH AWKDKLVYNV	120
LYYRNGKAFK	FFHWNSNLTI	LKTNISHNGT YHCSGMGKHR YTSAGISVTV KELFPAPVLN	180
ASVTSPLLEG	NLVTLSCE	LLLQRPGLQL YFSFYMGSKT LRGRNTSSEY QILTARREDS	240
GLYWCEAAATE	DGNVLKRSPE	LELQVLGLQL PTPVWFH	277
SEQ ID NO: 49		moltype = AA length = 208	
FEATURE		Location/Qualifiers	
REGION		1..208	
		note = MISC_FEATURE - 2B4	
source		1..208	

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	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 49		
CQGSADHVVS	ISGVPLQLQP NSIQTKVDSI AWKKLLPSQN GFHHILKWEN GSLPSNTSND	60
RFSFIVKNLS	LLIKAAQQQD SGLYCLEVTS ISGKVQTATF QVVFVESLLP DKVEKPRLQG	120
QGKILDRGRC	QVALSCLVSR DGNVSYAWYR GSKLIQTAGN LTYLDEEVDI NGTHTYTCNV	180
SNPVSWESHT	LNLTQDCQNA HQEFRFWP	208
SEQ ID NO: 50	moltype = AA length = 144	
FEATURE	Location/Qualifiers	
REGION	1..144	
	note = MISC_FEATURE - LAIR1	
source	1..144	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 50		
QEEDLPRPSI	SAEPGTVIPL GSHVTFVCRG PVGVQTFRLE RESRSTYNDT EDVSQASPSE	60
SEARFRIDSV	SEGNAGPYRC IYYKPPKWSE QSDYLELLVK ETSGGPDSPD TEPGSSAGPT	120
QRPSDNSHNE	HAPASQGLKA EHLV	144
SEQ ID NO: 51	moltype = AA length = 348	
FEATURE	Location/Qualifiers	
REGION	1..348	
	note = MISC_FEATURE - CD5	
source	1..348	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 51		
RLSWYDPDFQ	ARLTRSNSKC QGQLEVYLKD GWHMVCSQSW GRSSKQWEDP SQASKVCQRL	60
NCGVPLSLGP	FLVTYTPQSS IICYGQLGSF SNCSHSRNDM CHSLGLTCLE PQKTTPTTTR	120
PPPTTTPEPT	APPRQLVAQ SGGQHCAGVV EFYSGSLGGT ISYEAQDKTQ DLENFLCNNL	180
QCGSFLKHLF	ETEAGRAQDP GEPREHQPLP IQWKIQNSSC TSLEHCFRKI KPQKSGRVLA	240
LLCSGFQPKV	QSRLVGGSSI CEGTVEVRQG AQWAALCDSS SARSSLRWEE VCREQQCGSV	300
NSYRVLDAGD	PTSRGLFCPH QKLSQCHELW ERNSYCKKVF VTCQDPNP	348
SEQ ID NO: 52	moltype = AA length = 53	
FEATURE	Location/Qualifiers	
REGION	1..53	
	note = MISC_FEATURE - TWEAKR	
source	1..53	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 52		
EQAPGTAPCS	RGSSWSADLD KCMDCASCRA RPHSDFCLGC AAAPPAPFRL LWP	53
SEQ ID NO: 53	moltype = AA length = 34	
FEATURE	Location/Qualifiers	
REGION	1..34	
	note = MISC_FEATURE - IL-9	
source	1..34	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 53		
LIPPWGWPGN	TLVAVSIFLL LTGPTYLLFK LSPR	34
SEQ ID NO: 54	moltype = AA length = 25	
FEATURE	Location/Qualifiers	
REGION	1..25	
	note = MISC_FEATURE - IL-7ra	
source	1..25	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 54		
PILLTISILS	FFSVALLVIL ACVLW	25
SEQ ID NO: 55	moltype = AA length = 25	
FEATURE	Location/Qualifiers	
REGION	1..25	
	note = MISC_FEATURE - IL-2rb	
source	1..25	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 55		
IPWLGHLLVG	LSGAFGFIIIL VYLLI	25
SEQ ID NO: 56	moltype = AA length = 23	

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FEATURE	Location/Qualifiers	
REGION	1..23	
	note = MISC_FEATURE - TNFR1	
source	1..23	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 56		
VLLPLVIFFG LCLLSLLFIG LMY		23
SEQ ID NO: 57	moltype = AA length = 225	
FEATURE	Location/Qualifiers	
REGION	1..225	
	note = MISC_FEATURE - IL-9	
source	1..225	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 57		
VKRIFYQNVP SPAMFFQPLY SVHNGNFQTW MGAHGAGVLL SQDCAGTPQG ALEPCVQEAT		60
ALLTCGPARP WKSVALEEEQ EGPGRRLPGN LSSEDVLPAG CTEWRVQTLA YLPQEDWAPT		120
SLTRPAPPDS EGSRSSSSSS SSNNNNYCAL GCYGGWHLA LPGNTQSSGP IPALACGLSC		180
DHQGLETTQQG VAWVLGHQC RPGLHEDLQG MLLPSVLSKA RSWTF		225
SEQ ID NO: 58	moltype = AA length = 86	
FEATURE	Location/Qualifiers	
REGION	1..86	
	note = MISC_FEATURE - BOX1/2	
source	1..86	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 58		
ERTMPRIPTL KNLEDLVTEY HGNFSAWSGV SKGLAESLQP DYSERLCLVS EIPPKGGALG		60
EGPGASPCNQ HSPYWAPPCY TLKPET		86
SEQ ID NO: 59	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
	note = MISC_FEATURE - Gly Ser Linker	
source	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 59		
GGGSGGGGS GGGGS		15
SEQ ID NO: 60	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
	note = MISC_FEATURE - Q-Pro Linker	
source	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 60		
QPQPQPQPQP QP		12
SEQ ID NO: 61	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
	note = MISC_FEATURE - K-Pro Linker	
source	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 61		
KPKPKPKPKP KP		12
SEQ ID NO: 62	moltype = AA length = 26	
FEATURE	Location/Qualifiers	
REGION	1..26	
	note = MISC_FEATURE - Exemplary signal sequence	
source	1..26	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 62		
MAAPALSWRL PLLLLLLPLA TSWASA		26
SEQ ID NO: 63	moltype = AA length = 472	
FEATURE	Location/Qualifiers	
REGION	1..472	

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	note = MISC_FEATURE - IL21r/IL9R				
source	1..472				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 63					
CPDLVCYTDY	LQTVICILEM	WNLHPSTLTL	TWQDQYEELK	DEATSCSLHR	SAHNATHATY 60
TCHMDVFHFM	ADDIFSVNIT	DQSGNYSQEC	GSFLLAESIK	PAPPFNVTVT	FSGQYNISWR 120
SDYEDPAFYM	LKGKLQYELQ	YRNRGDPWAV	SPRRKLISVD	SRSVSLPLE	FRKDSSYELQ 180
VRAGPMPGSS	YQGTWSEWSD	PVIFQTQSEE	LKELIPPWGW	PGNTLVAVSI	FLLLTGPTYL 240
LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMWGA	HGAGVLLSQD	CAGTPQGALE 300
PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	WRVQTLAYLP 360
QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHLSPALPG	NTQSSGPIPA 420
LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGMML	PSVLSKARSW	TF 472
SEQ ID NO: 64	moltype = AA length = 463				
FEATURE	Location/Qualifiers				
REGION	1..463				
	note = MISC_FEATURE - IL21r/IL9R/IL7RaTM				
source	1..463				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 64					
CPDLVCYTDY	LQTVICILEM	WNLHPSTLTL	TWQDQYEELK	DEATSCSLHR	SAHNATHATY 60
TCHMDVFHFM	ADDIFSVNIT	DQSGNYSQEC	GSFLLAESIK	PAPPFNVTVT	FSGQYNISWR 120
SDYEDPAFYM	LKGKLQYELQ	YRNRGDPWAV	SPRRKLISVD	SRSVSLPLE	FRKDSSYELQ 180
VRAGPMPGSS	YQGTWSEWSD	PVIFQTQSEE	LKEPILLTIS	ILSFFSVALL	VILACVLWVK 240
RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL 300
LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTSL 360
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLSPALP	GNTQSSGPIP	ALACGLSCDH 420
QGLETQQGVA	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTF	463
SEQ ID NO: 65	moltype = AA length = 463				
FEATURE	Location/Qualifiers				
REGION	1..463				
	note = MISC_FEATURE - IL21r/IL9R/IL2RbTM				
source	1..463				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 65					
CPDLVCYTDY	LQTVICILEM	WNLHPSTLTL	TWQDQYEELK	DEATSCSLHR	SAHNATHATY 60
TCHMDVFHFM	ADDIFSVNIT	DQSGNYSQEC	GSFLLAESIK	PAPPFNVTVT	FSGQYNISWR 120
SDYEDPAFYM	LKGKLQYELQ	YRNRGDPWAV	SPRRKLISVD	SRSVSLPLE	FRKDSSYELQ 180
VRAGPMPGSS	YQGTWSEWSD	PVIFQTQSEE	LKEIPWLGH	LVGLSGAFGF	IILVYLLIVK 240
RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL 300
LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTSL 360
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLSPALP	GNTQSSGPIP	ALACGLSCDH 420
QGLETQQGVA	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTF	463
SEQ ID NO: 66	moltype = AA length = 434				
FEATURE	Location/Qualifiers				
REGION	1..434				
	note = MISC_FEATURE - IL15r-alpha/IL9R				
source	1..434				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 66					
IITCPPMSVE	HADIWVKSYS	LYSRERYICN	SGFKRKAGTS	SLTECVLNKA	TNVAHWTTTPS 60
LKCIKDPALV	HQRPAPPSTV	TTAGVTPQPE	SLSPSGKEPA	ASSPSSNNTA	ATTAAIVPGS 120
QLMPKSPST	GTTEISSHES	SHGTPSQTTA	KNWELTASAS	HQPPGVYPQG	HSDTTLIPPW 180
GWPGNTLVAV	SIFLLLTGPT	YLLFKLSPRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTMW 240
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPTRLPGNL 300
SSSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG 360
CYGGWHLSPAL	PGNTQSSGPI	PALACGLSCD	HQGLETQQGV	AWVLAGHCQR	PGLHEDLQGM 420
LLPSVLSKAR	SWTF				434
SEQ ID NO: 67	moltype = AA length = 425				
FEATURE	Location/Qualifiers				
REGION	1..425				
	note = MISC_FEATURE - IL15r-alpha/IL9R/IL7RaTM				
source	1..425				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 67					
IITCPPMSVE	HADIWVKSYS	LYSRERYICN	SGFKRKAGTS	SLTECVLNKA	TNVAHWTTTPS 60
LKCIKDPALV	HQRPAPPSTV	TTAGVTPQPE	SLSPSGKEPA	ASSPSSNNTA	ATTAAIVPGS 120
QLMPKSPST	GTTEISSHES	SHGTPSQTTA	KNWELTASAS	HQPPGVYPQG	HSDTTPILLT 180

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ISILSFFSVA	LLVILACVLW	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW	MGAHGAGVLL	240
SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN	LSSEDEVLPAG	300
CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNNYCAL	GCGYGGWHLA	360
LPGNTQSSGP	IPALACGLSC	DHQGLETTQQG	VAWVLAGHCQ	RPGLHEDLQG	MLLPSVLSCA	420
RSWTF						425
SEQ ID NO: 68	moltype = AA length = 425					
FEATURE	Location/Qualifiers					
REGION	1..425					
	note = MISC_FEATURE - IL15r-alpha/IL9R/IL2RbTM					
source	1..425					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 68						
ITCPPPMSVE	HADIWVKSYS	LYSRERYICN	SGFKRKAGTS	SLTECVLNKA	TNVAHWTTTPS	60
LKCIRDPALV	HQRPAAPPSTV	TTAGVTPQPE	SLSPSGKEPA	ASSPSSNNTA	ATTAAIVPGS	120
QLMPKSPST	GTTEISSHES	SHGTPSQTTA	KNWELTASAS	HQPPGVYPQG	HSDDTIPWLG	180
HLLVGLSGAF	GFIILVYLLI	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW	MGAHGAGVLL	240
SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN	LSSEDEVLPAG	300
CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNNYCAL	GCGYGGWHLA	360
LPGNTQSSGP	IPALACGLSC	DHQGLETTQQG	VAWVLAGHCQ	RPGLHEDLQG	MLLPSVLSCA	420
RSWTF						425
SEQ ID NO: 69	moltype = AA length = 478					
FEATURE	Location/Qualifiers					
REGION	1..478					
	note = MISC_FEATURE - IL7r-alpha /IL9R					
source	1..478					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 69						
ESGYAQNGDL	EDAELDDYSF	SCYSQLEVNG	SQHSLTCAFE	DPDVNITNLE	FEICGALVEV	60
KCLNFRKLQE	IYFIETKKFL	LIGKSNICVK	VGEKSLTCKK	IDLTTIVKPE	APFDLSVVYR	120
EGANDFVVTF	NTSHLQKKYV	KVLMHDAVAY	QEKDENKWTH	VNLSSTKLTL	LQRKLQPAAM	180
YEIKVRSIPD	HYFKGFWEW	SPSYFRTPE	INNSSGEMDL	IPPWGWPGNT	LVAVSIFLLL	240
TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ	PLYSVHNGNF	QTMWGAHGAG	VLLSQDCAGT	300
PQGALEPCVQ	EATALLTCGP	ARPWKSVALE	EEQEGPGTRL	PGNLSSSEVL	PAGCTEWRVQ	360
TLAYLPQEDW	APTSLTRPAP	PDSEGRSSSS	SSSSNNNNNY	CALGCGYGGW	LSALPGNTQS	420
SGPIPALACG	LSCDHQGLET	QQGVAVVLAG	HCQRPGLHED	LQGMMLPSVL	SKARSWTF	478
SEQ ID NO: 70	moltype = AA length = 469					
FEATURE	Location/Qualifiers					
REGION	1..469					
	note = MISC_FEATURE - IL7r-alpha /IL9R/IL7RaTM					
source	1..469					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 70						
ESGYAQNGDL	EDAELDDYSF	SCYSQLEVNG	SQHSLTCAFE	DPDVNITNLE	FEICGALVEV	60
KCLNFRKLQE	IYFIETKKFL	LIGKSNICVK	VGEKSLTCKK	IDLTTIVKPE	APFDLSVVYR	120
EGANDFVVTF	NTSHLQKKYV	KVLMHDAVAY	QEKDENKWTH	VNLSSTKLTL	LQRKLQPAAM	180
YEIKVRSIPD	HYFKGFWEW	SPSYFRTPE	INNSSGEMDP	ILLTISILSF	FSVALLVILA	240
CVLWVKRIFY	QNVSPAMFF	QPLYSVHNGN	FQTMWGAHGA	GVLLSQDCAG	TPQGALEPCV	300
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSSEVL	LPAGCTEWRV	QTLAYLPQED	360
WAPTSLTRPA	PPDSEGRSS	SSSSNNNNN	YCALGCGYGGW	HLSALPGNTQ	SSGPIPALAC	420
GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	DLQGMMLPSV	LSKARSWTF		469
SEQ ID NO: 71	moltype = AA length = 469					
FEATURE	Location/Qualifiers					
REGION	1..469					
	note = MISC_FEATURE - IL7r-alpha /IL9R/IL2RbTM					
source	1..469					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 71						
ESGYAQNGDL	EDAELDDYSF	SCYSQLEVNG	SQHSLTCAFE	DPDVNITNLE	FEICGALVEV	60
KCLNFRKLQE	IYFIETKKFL	LIGKSNICVK	VGEKSLTCKK	IDLTTIVKPE	APFDLSVVYR	120
EGANDFVVTF	NTSHLQKKYV	KVLMHDAVAY	QEKDENKWTH	VNLSSTKLTL	LQRKLQPAAM	180
YEIKVRSIPD	HYFKGFWEW	SPSYFRTPE	INNSSGEMDI	PWLGHLLVGL	SGAFGFIIIV	240
YLLIVKRIFY	QNVSPAMFF	QPLYSVHNGN	FQTMWGAHGA	GVLLSQDCAG	TPQGALEPCV	300
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSSEVL	LPAGCTEWRV	QTLAYLPQED	360
WAPTSLTRPA	PPDSEGRSS	SSSSNNNNN	YCALGCGYGGW	HLSALPGNTQ	SSGPIPALAC	420
GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	DLQGMMLPSV	LSKARSWTF		469
SEQ ID NO: 72	moltype = AA length = 466					
FEATURE	Location/Qualifiers					

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REGION	1..466	note = MISC_FEATURE - IL4r-alpha/IL9R				
source	1..466	mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 72						
MKVLQEPTCV	SDYMSISTCE	WKMNGPTNCS	TELRLLYQLV	FLLSEAHTCI	PENNGGAGCV	60
CHLLMDDVVS	ADNYTLDLWA	GQQLLWKGSF	KPSEHVKPRA	PGNLTVHTNV	SDTLLLTWSN	120
PYPDPNYLYN	HLTYAVNIWS	ENDPADFRIY	NVTYLEPSLR	IAASTLKSGI	SYRARVRAWA	180
QCYNTTWSEW	SPSTKWHNSY	REPFEQHLIP	PWGWPGNTLV	AVSIFLLLTG	PTYLLFKLSP	240
RVKRIFYQNV	PSPAMFFQPL	YSVHNGNFQT	WMGAHGAGVL	LSQDCAGTPQ	GALEPCVQEA	300
TALLTCGPAR	PWKSVALEEE	QEGPGTRLPG	NLSSEDLVLP	GCTEWRVQTL	AYLPQEDWAP	360
TSLTRPAPPD	SEGSRSSSSS	SSSNNNNYCA	LGCGYGGWHL	ALPGNTQSSG	PIPALACGLS	420
CDHQGLETQQ	GVAWVLAGHC	QRPGLHEDLQ	GMLLPSVLSK	ARSWTF		466
SEQ ID NO: 73	moltype = AA length = 457					
FEATURE	Location/Qualifiers					
REGION	1..457	note = MISC_FEATURE - IL4r-alpha/IL9R/IL7RaTM				
source	1..457	mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 73						
MKVLQEPTCV	SDYMSISTCE	WKMNGPTNCS	TELRLLYQLV	FLLSEAHTCI	PENNGGAGCV	60
CHLLMDDVVS	ADNYTLDLWA	GQQLLWKGSF	KPSEHVKPRA	PGNLTVHTNV	SDTLLLTWSN	120
PYPDPNYLYN	HLTYAVNIWS	ENDPADFRIY	NVTYLEPSLR	IAASTLKSGI	SYRARVRAWA	180
QCYNTTWSEW	SPSTKWHNSY	REPFEQHPIL	LTISILSFFS	VALLVILACV	LWVKRIFYQN	240
VVPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	300
RPWKSVALEE	EQEGPGTRLP	GNLSSSEDLV	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	360
DSEGSRSSSS	SSSSNNNNYC	ALGCGYGGWH	SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	420
QGVAVVLAGH	CQRPGLHEDL	QGMLLPSVLS	KARSWTF			457
SEQ ID NO: 74	moltype = AA length = 457					
FEATURE	Location/Qualifiers					
REGION	1..457	note = MISC_FEATURE - IL4r-alpha/IL9R/IL2RbTM				
source	1..457	mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 74						
MKVLQEPTCV	SDYMSISTCE	WKMNGPTNCS	TELRLLYQLV	FLLSEAHTCI	PENNGGAGCV	60
CHLLMDDVVS	ADNYTLDLWA	GQQLLWKGSF	KPSEHVKPRA	PGNLTVHTNV	SDTLLLTWSN	120
PYPDPNYLYN	HLTYAVNIWS	ENDPADFRIY	NVTYLEPSLR	IAASTLKSGI	SYRARVRAWA	180
QCYNTTWSEW	SPSTKWHNSY	REPFEQHPIW	LGHLLVGLSG	AFGFIIILVYL	LIVKRIFYQN	240
VVPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	300
RPWKSVALEE	EQEGPGTRLP	GNLSSSEDLV	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	360
DSEGSRSSSS	SSSSNNNNYC	ALGCGYGGWH	SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	420
QGVAVVLAGH	CQRPGLHEDL	QGMLLPSVLS	KARSWTF			457
SEQ ID NO: 75	moltype = AA length = 473					
FEATURE	Location/Qualifiers					
REGION	1..473	note = MISC_FEATURE - IL2r-beta Ectodomain /IL9R				
source	1..473	mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 75						
AVNGTSQFTC	FYNSTRANISC	VVSQDQALQD	TSCQVHAWPD	RRRWNTCEL	LPVSQASWAC	60
NLILGAPDSQ	KLTTVDIVTL	RVLCREGVRW	RVMAIQDFKP	FENLRMAPI	SLQVVHVETH	120
RCNISWEISQ	ASHYFERHLE	FEARTLSPGH	TWEEAPLLTL	KQKEWICLE	TLTPDTQYEF	180
QVRVKPLQGE	FTTWSPWSQP	LAFRTKPAAL	GKDTLIPPWG	WPGNTLVAVS	IFLLLTGPTY	240
LLFKLSPRVK	RIFYQNVPSP	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	300
EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	EWRVQTLAYL	360
PQEDWAPTSL	TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLSALP	GNTQSSGPIP	420
ALACGLSCDH	QGLETQQGVA	WVLAGHCQRP	GLHEDLQGML	LPSVLSKARS	WTF	473
SEQ ID NO: 76	moltype = AA length = 464					
FEATURE	Location/Qualifiers					
REGION	1..464	note = MISC_FEATURE - IL2r-beta Ectodomain /IL9R/IL7RaTM				
source	1..464	mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 76						
AVNGTSQFTC	FYNSTRANISC	VVSQDQALQD	TSCQVHAWPD	RRRWNTCEL	LPVSQASWAC	60
NLILGAPDSQ	KLTTVDIVTL	RVLCREGVRW	RVMAIQDFKP	FENLRMAPI	SLQVVHVETH	120

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RCNISWEISQ	ASHYFERHLE	FEARTLSPGH	TWEEAPLLTL	KQKQEWICLE	TLTPDTQYEF	180
QVRVKPLQGE	FTTWSPWSQP	LAFRTKPAAL	GKDTPIILLTI	SILSFFSVAL	LVILACVLWV	240
KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	300
LLTCGPAPRW	KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	360
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHL SAL	PGNTQSSGPI	PALACGLSCD	420
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVL SKAR	SWTF		464
SEQ ID NO: 77	moltype = AA length = 464					
FEATURE	Location/Qualifiers					
REGION	1..464					
	note = MISC_FEATURE - IL2r-beta Ectodomain /IL9R/IL2RbTM					
source	1..464					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 77						
AVNGTSQFTC	FYNSTRANISC	VWSQD GALQD	TSCQVHAWPD	RRRWNTCEL	LPVSQASWAC	60
NLILGAPDSQ	KLTTVDIVTL	RVLCREGVRW	RVMAIQDFKP	FENLR LMAPI	SLQVVHVETH	120
RCNISWEISQ	ASHYFERHLE	FEARTLSPGH	TWEEAPLLTL	KQKQEWICLE	TLTPDTQYEF	180
QVRVKPLQGE	FTTWSPWSQP	LAFRTKPAAL	GKDTIPWLGH	LLVGLSGAFG	FIILVYLLIV	240
KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	300
LLTCGPAPRW	KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	360
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHL SAL	PGNTQSSGPI	PALACGLSCD	420
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVL SKAR	SWTF		464
SEQ ID NO: 78	moltype = AA length = 478					
FEATURE	Location/Qualifiers					
REGION	1..478					
	note = MISC_FEATURE - IL2r-alpha Ectodomain/IL9R					
source	1..478					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 78						
ELCDDDPPEI	PHATFKAMAY	KEGTMLNCEC	KRGFRRIKSG	SLYMLCTGNS	SHSSWDNQCQ	60
CTSSATRNTT	KQVTPQPEEQ	KERKTTEMQS	PMQPV DQASL	PGHCREPPPW	ENEATERIYH	120
FVVGQMVYYQ	CVQGYRALHR	GPAESVCKMT	HGKTRWTQPQ	LICTGEMETS	QFPGEEKPQA	180
SPEGRPESET	SCLVTTTDFQ	IQTEMAATME	TSIFTTEYQL	IPPWGWPGNT	LVAVSIFLLL	240
TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ	PLYSVHNGNF	QTMGAHGAG	VLLSQDCAGT	300
PQGALEPCVQ	EATALLTCGP	ARPWKSVALE	EEQEGPGTRL	PGNLSSEDVL	PAGCTEWRVQ	360
TLAYLPQEDW	APTSLTRPAP	PDSEGSRSSS	SSSSNNNNNY	CALGCYGGWH	LSALPGNTQS	420
SGPIPALACG	LSCDHQGLET	QQGVAWVL AG	HCQRPGLHED	LQGM L LPSVL	SKARSWTF	478
SEQ ID NO: 79	moltype = AA length = 469					
FEATURE	Location/Qualifiers					
REGION	1..469					
	note = MISC_FEATURE - IL2r-alpha Ectodomain/IL9R/IL7RaTM					
source	1..469					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 79						
ELCDDDPPEI	PHATFKAMAY	KEGTMLNCEC	KRGFRRIKSG	SLYMLCTGNS	SHSSWDNQCQ	60
CTSSATRNTT	KQVTPQPEEQ	KERKTTEMQS	PMQPV DQASL	PGHCREPPPW	ENEATERIYH	120
FVVGQMVYYQ	CVQGYRALHR	GPAESVCKMT	HGKTRWTQPQ	LICTGEMETS	QFPGEEKPQA	180
SPEGRPESET	SCLVTTTDFQ	IQTEMAATME	TSIFTTEYQP	ILLTISILSF	FSVALLVILA	240
CVLWVKRIFY	QNVSPAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	300
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSEDV	LPAGCTEWRV	QTLAYLPQED	360
WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	420
GLSCDHQGLE	TQQGVAWVLA	GHCQRPGLHE	DLQGM L LPSV	LSKARSWTF		469
SEQ ID NO: 80	moltype = AA length = 469					
FEATURE	Location/Qualifiers					
REGION	1..469					
	note = MISC_FEATURE - IL2r-alpha Ectodomain/IL9R/IL2RbTM					
source	1..469					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 80						
ELCDDDPPEI	PHATFKAMAY	KEGTMLNCEC	KRGFRRIKSG	SLYMLCTGNS	SHSSWDNQCQ	60
CTSSATRNTT	KQVTPQPEEQ	KERKTTEMQS	PMQPV DQASL	PGHCREPPPW	ENEATERIYH	120
FVVGQMVYYQ	CVQGYRALHR	GPAESVCKMT	HGKTRWTQPQ	LICTGEMETS	QFPGEEKPQA	180
SPEGRPESET	SCLVTTTDFQ	IQTEMAATME	TSIFTTEYQI	PWLGHLLVGL	SGAFGFIIIV	240
YLLIVKRIFY	QNVSPAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	300
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSEDV	LPAGCTEWRV	QTLAYLPQED	360
WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	420
GLSCDHQGLE	TQQGVAWVLA	GHCQRPGLHE	DLQGM L LPSV	LSKARSWTF		469
SEQ ID NO: 81	moltype = AA length = 780					

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FEATURE		Location/Qualifiers				
REGION		1..780				
		note = MISC_FEATURE - ILT5/IL9R/cGC-F				
source		1..780				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 81						
GPFPPKPTLWA	EPGSVISWGS	PVTIWCQGSQ	EAQEYRLHKE	GSPEPLDRNN	PLEPKNKARF	60
SIPSMTEHHA	GRYRCHYYSS	AGWSEPSDPL	EMVMTGAYSK	PTLSALPSPV	VASGGNMTLR	120
CGSQKGYHHF	VLMKEGEHQL	PRTLDSQQLH	SRGFQALFPV	GPVTPSHRWR	FTCYYYTNT	180
PWVWSHPSDP	LEILPSGVSR	KPSLLTLQGP	VLAPGQSLTL	QCGSDVGYNR	FVLYKEGERD	240
FLQRPQGQQPQ	AGLSQANFTL	GPVSPSNGGQ	YRCYGAHNLS	SEWSAPSDPL	NILMAGQIYD	300
TVSLSAQPGP	TVASGENVTL	LCQSWWQFDT	FLLTKEGAAH	PPLRLRSMYG	AHKYQAEFPM	360
SSPVTSAHAGT	YRCYGSYSSN	PHLLSHPSEP	LELVVSGHSG	GSSLPPTGPP	STPGLGRYLE	420
LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	QNVSPAMFF	QPLYSVHNGN	480
FQFTWMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	540
LPGNLSSSDV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	600
YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	660
DLQGMMLPSV	LSKARSWTFG	GGSGGGGSG	GGGSERTMPR	IPTLKNLEDL	VTEYHGNFSA	720
WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET	780
SEQ ID NO: 82		moltype = AA length = 777				
FEATURE		Location/Qualifiers				
REGION		1..777				
		note = MISC_FEATURE - ILT5/IL9R/cGC-S				
source		1..777				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 82						
GPFPPKPTLWA	EPGSVISWGS	PVTIWCQGSQ	EAQEYRLHKE	GSPEPLDRNN	PLEPKNKARF	60
SIPSMTEHHA	GRYRCHYYSS	AGWSEPSDPL	EMVMTGAYSK	PTLSALPSPV	VASGGNMTLR	120
CGSQKGYHHF	VLMKEGEHQL	PRTLDSQQLH	SRGFQALFPV	GPVTPSHRWR	FTCYYYTNT	180
PWVWSHPSDP	LEILPSGVSR	KPSLLTLQGP	VLAPGQSLTL	QCGSDVGYNR	FVLYKEGERD	240
FLQRPQGQQPQ	AGLSQANFTL	GPVSPSNGGQ	YRCYGAHNLS	SEWSAPSDPL	NILMAGQIYD	300
TVSLSAQPGP	TVASGENVTL	LCQSWWQFDT	FLLTKEGAAH	PPLRLRSMYG	AHKYQAEFPM	360
SSPVTSAHAGT	YRCYGSYSSN	PHLLSHPSEP	LELVVSGHSG	GSSLPPTGPP	STPGLGRYLE	420
LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	QNVSPAMFF	QPLYSVHNGN	480
FQFTWMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	540
LPGNLSSSDV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	600
YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	660
DLQGMMLPSV	LSKARSWTFQ	PQPQPQPQPQ	PERTMPRIPT	LKNLEDLVE	YHGNFSAWSG	720
VSKGLAESLQ	PDYSERLCLV	SEIPPKGGAL	GEGPGASPCN	QHSPYWAPP	YTLKPET	777
SEQ ID NO: 83		moltype = AA length = 598				
FEATURE		Location/Qualifiers				
REGION		1..598				
		note = MISC_FEATURE - ILT3/IL9R/cGC-F				
source		1..598				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 83						
QAGPLPKPTL	WAEPGSVISW	GNSVTIWCQG	TLEAREYRLD	KEESPAPWDR	QNPLEPKNKA	60
RFSIPSMTE	YAGRYRCYR	SPVGWSQPSD	PLELVMTGAY	SKPTLSALPS	PLVTSGKSVT	120
LLCQSRSPMD	TFLLIKERAA	HPLLHLRSEH	GAQQHQAEFP	MSPVTSVHGG	TYRCFSSHGF	180
SHYLLSHPSD	PLELIVSGSL	EDPRPSPTRS	VSTAAGPEDQ	PLMPTGSVPH	SGLRRHWELI	240
PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ	300
TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP	360
GNLSSSDVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGSRSSSS	SSSSNNNNYC	420
ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	QGVAVVLAGH	CQRPGLHEDL	480
QGMMLPSVLS	KARSWTFGGG	GSGGGGSGGG	GSERTMPRIP	TLKNLEDLVT	EYHGNFSAWS	540
GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEFGASPCN	NQHSPYWAPP	CYTLKPET	598
SEQ ID NO: 84		moltype = AA length = 595				
FEATURE		Location/Qualifiers				
REGION		1..595				
		note = MISC_FEATURE - ILT3/IL9R/cGC-S				
source		1..595				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 84						
QAGPLPKPTL	WAEPGSVISW	GNSVTIWCQG	TLEAREYRLD	KEESPAPWDR	QNPLEPKNKA	60
RFSIPSMTE	YAGRYRCYR	SPVGWSQPSD	PLELVMTGAY	SKPTLSALPS	PLVTSGKSVT	120
LLCQSRSPMD	TFLLIKERAA	HPLLHLRSEH	GAQQHQAEFP	MSPVTSVHGG	TYRCFSSHGF	180
SHYLLSHPSD	PLELIVSGSL	EDPRPSPTRS	VSTAAGPEDQ	PLMPTGSVPH	SGLRRHWELI	240
PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ	300
TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP	360

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GNLSSSEDLVP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGRSSSSS	SSSSNNNNNYC	420
ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	QGVAVVLAGH	CQRPGLHEDL	480
QGMLLPVLS	KARSWTFQPQ	PQPQPQPQPE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	540
KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT	LKPET	595
SEQ ID NO: 85	moltype = AA length = 800					
FEATURE	Location/Qualifiers					
REGION	1..800					
	note = MISC_FEATURE - ILT4 IL9R/cGC-F					
source	1..800					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 85						
QTGTIPKPTL	WAEPDSVITQ	GSPVTLSCQG	SLEAQEYRLY	REKKSASWIT	RIRPELVKNG	60
QFHIPSITWE	HTGRYGCQYY	SRARWSELSD	PLVLVMTGAY	PKPTLSAQPS	PVVTSGGRVT	120
LQCESQVAFG	GFILCKEGEE	EHPQCLNSQP	HARGSSRAIF	SVGPVSPNRR	WSHRCYGYDL	180
NSPYVWSSPS	DLLELLVPGV	SKKPSLSVQP	GPVVAPGESL	TLQCVSDVG	DRFVLYKEGE	240
RDLRQLPGRQ	PQAGLSQANF	TLGPVRSYSG	GQYRCYGAHN	LSSECSAPSD	PLDILITGQI	300
RGTPPFISVQP	GPTVASGENV	TLLCQSWRQF	HTFLLTKAGA	ADAPLRLRSI	HEYPKYQAEF	360
PMSPV TSAHA	GTYRCYGS LN	SDPYLLSHPS	EPL ELVVSGP	SMGSSPPPTG	PISTPAGPED	420
QPLTPTGSDP	QSG LGRHLGV	LIPPWGWP GN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	480
QNVPS PAMFF	QPLYSVHNGN	FQ TWMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	540
PARPWKSVAL	EEEQEGPGTR	LPGNLSS EDV	LPAGCTEWRV	QTLAYLPQED	WAP TSLTRPA	600
PPDSEGRSSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	660
TQQGVAVVLA	GHCQRPGLHE	DLQGM LLPSV	LSKARSWTFG	GGSGGGGGSG	GGGSERTMPR	720
IP TLKNLEDL	VTEYHG NFSA	WSGVSKGLAE	SLQPDY SERL	CLVSEIP PKG	GALGEGPGAS	780
PCNQHSPYWA	PPCYTLKPET					800
SEQ ID NO: 86	moltype = AA length = 797					
FEATURE	Location/Qualifiers					
REGION	1..797					
	note = MISC_FEATURE - ILT4 IL9R/cGC-S					
source	1..797					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 86						
QTGTIPKPTL	WAEPDSVITQ	GSPVTLSCQG	SLEAQEYRLY	REKKSASWIT	RIRPELVKNG	60
QFHIPSITWE	HTGRYGCQYY	SRARWSELSD	PLVLVMTGAY	PKPTLSAQPS	PVVTSGGRVT	120
LQCESQVAFG	GFILCKEGEE	EHPQCLNSQP	HARGSSRAIF	SVGPVSPNRR	WSHRCYGYDL	180
NSPYVWSSPS	DLLELLVPGV	SKKPSLSVQP	GPVVAPGESL	TLQCVSDVG	DRFVLYKEGE	240
RDLRQLPGRQ	PQAGLSQANF	TLGPVRSYSG	GQYRCYGAHN	LSSECSAPSD	PLDILITGQI	300
RGTPPFISVQP	GPTVASGENV	TLLCQSWRQF	HTFLLTKAGA	ADAPLRLRSI	HEYPKYQAEF	360
PMSPV TSAHA	GTYRCYGS LN	SDPYLLSHPS	EPL ELVVSGP	SMGSSPPPTG	PISTPAGPED	420
QPLTPTGSDP	QSG LGRHLGV	LIPPWGWP GN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	480
QNVPS PAMFF	QPLYSVHNGN	FQ TWMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	540
PARPWKSVAL	EEEQEGPGTR	LPGNLSS EDV	LPAGCTEWRV	QTLAYLPQED	WAP TSLTRPA	600
PPDSEGRSSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	660
TQQGVAVVLA	GHCQRPGLHE	DLQGM LLPSV	LSKARSWTFQ	PQPQPQPQPQ	PERTMPRIPT	720
LKNLEDLVTE	YHG NFSAWSG	VSKGLAESLQ	PDYSERLCLV	SEIPPKGGAL	GEGPGASPCN	780
QHSPYWAPPC	YTLKPET					797
SEQ ID NO: 87	moltype = AA length = 798					
FEATURE	Location/Qualifiers					
REGION	1..798					
	note = MISC_FEATURE - ILT2 IL9R/cGC-F					
source	1..798					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 87						
GHLPKPTLWA	EPGSVITQGS	PVTLRCQGGQ	ETQ EYRLYRE	KKTALWITRI	PQELVKKGQF	60
PIPSITWEHA	GRYRCYYGSD	TAGRSESSDP	LELVVTGAYI	KPTLSAQPS	VVNSGGNVIL	120
QCDSQVAFDG	FSLCKEGEDE	HPQCLNSQPH	ARGSSRAIFS	VGPVSPSRRW	WYRCYAYDSN	180
SPYEWSLPSD	LLELLVLGVS	KKPSLSVQPG	PIVAPEETLT	LQCGSDAGYN	RFVLYKDGER	240
DFLQLAGAQP	QAGLSQANFT	LGPVRSYSGG	QYRCYGAHNL	SSEWSAPSDP	LDILIAGQFY	300
DRVSLSVQPG	PTVASGENVT	LLCQSQGWMQ	TFLLTKEGAA	DDPWRLRSTY	QSQKYQAEFP	360
MGPV TSAHAG	TYRCYGSQSS	KPYLLTHPSD	PLELVVSGPS	GGPSSPTTGP	TSTSGPEDQP	420
LTPTGSDPQS	GLGRHLGVLI	PPWGWP GN TL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	480
VPS PAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	540
RPWKSVALEE	EQEGPGTRLP	GNLSSSEDLVP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	600
DSEGRSSSSS	SSSSNNNNNYC	ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	660
QGVAVVLAGH	CQRPGLHEDL	QGMLLPVLS	KARSWTFGGG	GSGGGGGSGG	GSERTMPRI	720
TLKNLEDLVT	EYHG NFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	780
NQHSPYWAPP	CYTLKPET					798
SEQ ID NO: 88	moltype = AA length = 795					
FEATURE	Location/Qualifiers					

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REGION	1..795					
	note = MISC_FEATURE - ILT2 IL9R/cGC-S					
source	1..795					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 88						
GHLPKPTLWA	EPGSVITQGS	PVTLRCQGGQ	ETQEYRLYRE	KKTALWITRI	PQELVKKGQF	60
PIPSITWEHA	GRYRCYYGSD	TAGRSESSDP	LELVVTGAYI	KPTLSAQPS	VVNSGGNVIL	120
QCDSQVAFDG	FSLCKEGEDE	HPQCLNSQPH	ARGSSRAIFS	VGPVSPSRRW	WYRCYAYDSN	180
SPYEWSLP	SD LLELLVLGVS	KKPSLSVQPG	PIVAPEETLT	LQCGSDAGYN	RFVLYKDGER	240
DFLQLAGAP	QAGLSQANFT	LGPVSRSYGG	QYRCYGAHNL	SSEWSAPSDP	LDILIAGQFY	300
DRVSLSVQPG	PTVASGENVT	LLCQSQGWMQ	TFLLTKEGAA	DDPWRLRSTY	QSQKYQAEFP	360
MGPVTSAHAG	TYRCYGSQSS	KPYLLTHPSD	PLELVVSGPS	GGPSSPTTGP	TSTSGPEDQP	420
LTPTGSDPQS	GLGRHLGVLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	480
VPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	540
RPWKSVALEE	EQEGPGTRLP	GNLSSDVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	600
DSEGSRSSSS	SSSSNNNNYC	ALGCGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	660
QGVAVVL	AGH CQRPGLHEDL	QGMLLPSVLS	KARSWTFQPQ	PQPQPQPQPE	RTMPRIPTLK	720
NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	780
SPYWAPPCYT	LKPET					795
SEQ ID NO: 89	moltype = AA length = 486					
FEATURE	Location/Qualifiers					
REGION	1..486					
	note = MISC_FEATURE - CTLA4 IL9R/cGC-F					
source	1..486					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 89						
KAMHVAQPAV	VCLASSRGIAS	FVCEYASPGK	ATEVRVTVLR	QADSQVTEVC	AATYMMGNEL	60
TFLDDSICTG	TSSGNQVNLT	IQGLRAMDTG	LYICKVELMY	PPPYLIGIGN	GTQIYVIDPE	120
PCPDSDLIPP	WGWPNTLVA	VSIFLLLTGP	TYLLFKLS	PRVKRIFYQN	SPAMFFQPLY	180
SVHNGNFQ	TW MGAHGAGVLL	SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEEQ	240
EGPGTRLPGN	LSSDVLPAG	CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	300
SSNNNNNYCAL	GCGGWHL	LPGNTQSSGP	IPALACGLSC	DHQGLETQQG	VAWVLAGHCQ	360
RPGLHEDLQ	G MLLPSVLSKA	RSWTFGGGGS	GGGSGGGGS	ERTMPRIPTL	KNLEDLVTEY	420
HGNFSAWSGV	SKGLAESLQPD	DYSERLCLVS	EIPPKGGALG	EGPGASPCNQ	HSPYWAPPCY	480
TLKPET						486
SEQ ID NO: 90	moltype = AA length = 483					
FEATURE	Location/Qualifiers					
REGION	1..483					
	note = MISC_FEATURE - CTLA4 IL9R/cGC-S					
source	1..483					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 90						
KAMHVAQPAV	VCLASSRGIAS	FVCEYASPGK	ATEVRVTVLR	QADSQVTEVC	AATYMMGNEL	60
TFLDDSICTG	TSSGNQVNLT	IQGLRAMDTG	LYICKVELMY	PPPYLIGIGN	GTQIYVIDPE	120
PCPDSDLIPP	WGWPNTLVA	VSIFLLLTGP	TYLLFKLS	PRVKRIFYQN	SPAMFFQPLY	180
SVHNGNFQ	TW MGAHGAGVLL	SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEEQ	240
EGPGTRLPGN	LSSDVLPAG	CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	300
SSNNNNNYCAL	GCGGWHL	LPGNTQSSGP	IPALACGLSC	DHQGLETQQG	VAWVLAGHCQ	360
RPGLHEDLQ	G MLLPSVLSKA	RSWTFQPQPQ	PQPQPQP	MPRIPTLKNL	EDLVTEYHGN	420
FSAWSGVSKG	LAESLQPDYS	ERLCLVSEIP	PKGGALGEGP	GASPCNQHSP	YWAPPCYTLK	480
PET						483
SEQ ID NO: 91	moltype = AA length = 541					
FEATURE	Location/Qualifiers					
REGION	1..541					
	note = MISC_FEATURE - TIM3/IL9R/cGC-F					
source	1..541					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 91						
SEVEYRAEVG	QNAYLPCFYT	PAAPGNLVPV	CWKGKACPVF	ECGNVVLRTD	ERDVNYWTSR	60
YWLNGDFRKG	DVSLTIENVT	LADSGIYCCR	IQIPGIMNDE	KFNLKLVIKP	AKVTPAPTRQ	120
RDFTAAFP	PRM LTTRGHGPAE	TQTLGSLPDI	NLTQISTLAN	ELRDSRLAND	LRDSGATIRI	180
GLIPPWGWPG	NTLVAVSIFL	LLTGPTYLLF	KLSPRVKRIF	YQNVPSPAMF	FQPLYSVHNG	240
NFQTMGAHG	AGVLLSQDCA	GTPQGALEPC	VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	300
RLPGNLSS	ED VLPAGCTEWR	VQTLAYLPQE	DWAPTSLTRP	APPDSEGSRS	SSSSSSNNN	360
NYCALG	CGYG WHLSALPGNT	QSSGPIPALA	CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	420
EDLQGM	LLPS VLSKARSWTF	GGGSGGGGS	GGGGSERTMP	RIPTLKNLED	LVTEYHGNFS	480
AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	540
T						541

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SEQ ID NO: 92	moltype = AA length = 538					
FEATURE	Location/Qualifiers					
REGION	1..538					
	note = MISC_FEATURE - TIM3/IL9R/cGC-S					
source	1..538					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 92						
SEVEYRAEVG	QNAYLPCFYT	PAAPGNLVPV	CWKGKACPVF	ECGNVVLRTD	ERDVNYWTSR 60	
YWLNGDFRKG	DVSLTIENVT	LADSGIYCCR	IQIPGIMNDE	KFNLKLVIKP	AKVTPAPTRQ 120	
RDFTAAAFPRM	LTTRGHGPAE	TQTLGSLPDI	NLTQISTLAN	ELRDSRLAND	LRDSGATIRI 180	
GLIPPWGWPG	NTLVAVSIFL	LLTGPTYLLF	KLSPRVKRIF	YQNVPSPAMF	FQPLYSVHNG 240	
NFQTWMGAHG	AGVLLSQDCA	GTPQGALEPC	VQEATALLTC	GPARPWKSVA	LEEEQEGPGT 300	
RLPGNLSSSED	VLPAGCTEWR	VQTLAYLPQE	DWAPTSLTRP	APPDSEGSRS	SSSSSSSNNN 360	
NYCALGCYGG	WHLALPGNT	QSSGPIPALA	CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH 420	
EDLQGMLLPS	VLSKARSWTF	QPQPQPQPQP	QPERTMPRIP	TLKNLEDLVT	EYHGNFSAWS 480	
GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP	CYTLKPET 538	
SEQ ID NO: 93	moltype = AA length = 785					
FEATURE	Location/Qualifiers					
REGION	1..785					
	note = MISC_FEATURE - LAG3/IL9R/cGC-S					
source	1..785					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 93						
LQPGAEPVV	WAQEGAPAQL	PCSPTIPLQD	LSLLRRAGVT	WQHQPDSGPP	AAAPGHPLAP 60	
GPHPAAPSSW	GPRPRRYTVL	SVGPGGLRSG	RLPLQPRVQL	DERGRQRGDF	SLWLRPARRA 120	
DAGEYRAAVH	LRDRALSCRL	RLRLGQASMT	ASPPGSLRAS	DWVILNCSFS	RPDRPASVHW 180	
FRNRGQGRVP	VRESPPHHLA	ESFLFLPQVS	PMDSGPWGCI	LTYRDGFNVS	IMYNLTVLGL 240	
EPPTPLTVYA	GAGSRVGLPC	RLPAGVGTRS	FLTAKWTPPG	GGPDLLVTGD	NGDFTLRLED 300	
VSQAQAGTYT	CHIHLEQQQL	NATVTLAIIT	VTPKSFSGSPG	SLGKLLCEVT	PVSGQERFVW 360	
SSLDTPSQRS	FSGPWLEAQE	AQLLSQPWQC	QLYQGERLLG	AAVYFTELSS	PGAQRSGRAP 420	
GALPAGHLLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP 480	
LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE 540	
EQEGPGTRLP	GNLSSSEDVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGSRSSSS 600	
SSSSNNNNNYC	ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	QGVAVVLAGH 660	
CQRPGLHEDL	QGMLLPVLS	KARSWTFQPQ	PQPQPQPQPE	RTMPRIPTLK	NLEDLVTEYH 720	
GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT 780	
LKPET					785	
SEQ ID NO: 94	moltype = AA length = 788					
FEATURE	Location/Qualifiers					
REGION	1..788					
	note = MISC_FEATURE - LAG3/IL9R/cGC-F					
source	1..788					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 94						
LQPGAEPVV	WAQEGAPAQL	PCSPTIPLQD	LSLLRRAGVT	WQHQPDSGPP	AAAPGHPLAP 60	
GPHPAAPSSW	GPRPRRYTVL	SVGPGGLRSG	RLPLQPRVQL	DERGRQRGDF	SLWLRPARRA 120	
DAGEYRAAVH	LRDRALSCRL	RLRLGQASMT	ASPPGSLRAS	DWVILNCSFS	RPDRPASVHW 180	
FRNRGQGRVP	VRESPPHHLA	ESFLFLPQVS	PMDSGPWGCI	LTYRDGFNVS	IMYNLTVLGL 240	
EPPTPLTVYA	GAGSRVGLPC	RLPAGVGTRS	FLTAKWTPPG	GGPDLLVTGD	NGDFTLRLED 300	
VSQAQAGTYT	CHIHLEQQQL	NATVTLAIIT	VTPKSFSGSPG	SLGKLLCEVT	PVSGQERFVW 360	
SSLDTPSQRS	FSGPWLEAQE	AQLLSQPWQC	QLYQGERLLG	AAVYFTELSS	PGAQRSGRAP 420	
GALPAGHLLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP 480	
LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE 540	
EQEGPGTRLP	GNLSSSEDVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGSRSSSS 600	
SSSSNNNNNYC	ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	QGVAVVLAGH 660	
CQRPGLHEDL	QGMLLPVLS	KARSWTFGGG	GSGGGGSGGG	GSERTMPRIP	TLKNLEDLVT 720	
EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP 780	
CYTLKPET					788	
SEQ ID NO: 95	moltype = AA length = 580					
FEATURE	Location/Qualifiers					
REGION	1..580					
	note = MISC_FEATURE - PD1/IL9R/cGC-F					
source	1..580					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 95						
FTVTVPKDLY	VVEYGSNMTI	ECKFPVEKQL	DLAALIVYWE	MEDKNIIQFV	HGEEDLKVQH 60	
SSSYRQARLL	KDQLSLGNAA	LQITDVKLQD	AGVYRCMISY	GGADYKRITV	KVNAPYNKIN 120	
QRILVVDVPT	SEHELTCQAE	GYPKAEVIWT	SSDHQVLSGK	TTTTNSKREE	KLFNVTSTLR 180	
INTTTNEIFY	CTFRRLDPEE	NHTAELVIPE	LPLAHPPNER	LIPPWGWPGN	TLVAVSIFLL 240	

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LTGPTYLLFK	LSPRVKRIFY	QNVPSAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	300
TPQGALEPCV	QEATALTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSDEV	LPAGCTEWRV	360
QTLAYLPQED	WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	420
SSGPIPALAC	GLSCDHQGLE	TQQGVAWVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFG	480
GGGSGGGGSG	GGGSERTMPR	IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE	SLQPDYSERL	540
CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET			580
SEQ ID NO: 96	moltype = AA length = 577					
FEATURE	Location/Qualifiers					
REGION	1..577					
	note = MISC_FEATURE - PD1/IL9R/cGC-S					
source	1..577					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 96						
FFTVTVPKDLY	VVEYGSNMTI	ECKFPVEKQL	DLAALIVYWE	MEDKNIIQFV	HGEEDLKVQH	60
SSSYRQARLL	KDQLSLGNAA	LQITDVKLQD	AGVYRCMISY	GGADYKRITV	KVNAPYNKIN	120
QRILVVDPVT	SEHELTCQAE	GYPKAEVIWT	SSDHQVLSGK	TTTTNSKREE	KLFNVTSTLR	180
INTTTNEIFY	CTFRRLDPEE	NHTAELVIPE	LPLAHPPNER	LIPPWGWPGN	TLVAVSIFLL	240
LTGPTYLLFK	LSPRVKRIFY	QNVPSAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	300
TPQGALEPCV	QEATALTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSDEV	LPAGCTEWRV	360
QTLAYLPQED	WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	420
SSGPIPALAC	GLSCDHQGLE	TQQGVAWVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFQ	480
PQPQPQPQPQ	PERTMPRIPT	LKNLEDLVTE	YHGNFSAWSG	VSKGLAESLQ	PDYSERLCLV	540
SEIPPKGAL	GEGPGASPCN	QHSPYWAPPC	YTLKPET			577
SEQ ID NO: 97	moltype = AA length = 740					
FEATURE	Location/Qualifiers					
REGION	1..740					
	note = MISC_FEATURE - OPG/IL9R/cGC-F					
source	1..740					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 97						
ETFPKYLHY	DEETSHQLLC	DKCPPGTYLK	QHCTAKWKTV	CAPCPDHYYT	DSWHTSDECL	60
YCSPVCKELQ	YVKQECNRTH	NRVCECKEGR	YLEIEFCLKH	RSCPPGFGVV	QAGTPERNTV	120
CKRCPDGFFS	NETSSKAPCR	KHTNCSVFGL	LLTQKGNATH	DNICSGNSES	TQKCGIDVTL	180
CEEAFRRFAV	PTKFTPNWLS	VLVDNLPGTK	VNAESVERIK	RQHSSQEQT	QLLKLWKHQ	240
KDQDIVKKII	QDIDLCENSV	QRHIGHANLT	FEQLRSLMES	LPGKKVGAED	IEKTIKACKP	300
SDQILKLLSL	WRIKNGDQDT	LKGLMHALKH	SKTYHFPKTV	TQSLKKTIRF	LHSFTMYKLY	360
QKLFLMIGN	QVQSVKISCL	LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	420
QNVPSAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALTCG	480
PARPWKSVAL	EEEQEGPGTR	LPGNLSSDEV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	540
PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	600
TQQGVAWVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFG	GGGSGGGGSG	GGGSERTMPR	660
IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	720
PCNQHSPYWA	PPCYTLKPET					740
SEQ ID NO: 98	moltype = AA length = 737					
FEATURE	Location/Qualifiers					
REGION	1..737					
	note = MISC_FEATURE - OPG/IL9R/cGC-S					
source	1..737					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 98						
ETFPKYLHY	DEETSHQLLC	DKCPPGTYLK	QHCTAKWKTV	CAPCPDHYYT	DSWHTSDECL	60
YCSPVCKELQ	YVKQECNRTH	NRVCECKEGR	YLEIEFCLKH	RSCPPGFGVV	QAGTPERNTV	120
CKRCPDGFFS	NETSSKAPCR	KHTNCSVFGL	LLTQKGNATH	DNICSGNSES	TQKCGIDVTL	180
CEEAFRRFAV	PTKFTPNWLS	VLVDNLPGTK	VNAESVERIK	RQHSSQEQT	QLLKLWKHQ	240
KDQDIVKKII	QDIDLCENSV	QRHIGHANLT	FEQLRSLMES	LPGKKVGAED	IEKTIKACKP	300
SDQILKLLSL	WRIKNGDQDT	LKGLMHALKH	SKTYHFPKTV	TQSLKKTIRF	LHSFTMYKLY	360
QKLFLMIGN	QVQSVKISCL	LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	420
QNVPSAMFF	QPLYSVHNGN	FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALTCG	480
PARPWKSVAL	EEEQEGPGTR	LPGNLSSDEV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	540
PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	600
TQQGVAWVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFQ	PQPQPQPQPQ	PERTMPRIPT	660
LKNLEDLVTE	YHGNFSAWSG	VSKGLAESLQ	PDYSERLCLV	SEIPPKGAL	GEGPGASPCN	720
QHSPYWAPPC	YTLKPET					737
SEQ ID NO: 99	moltype = AA length = 525					
FEATURE	Location/Qualifiers					
REGION	1..525					
	note = MISC_FEATURE - TACI/IL9R/cGC-F					
source	1..525					
	mol_type = protein					

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		organism = synthetic construct			
SEQUENCE: 99					
MSGLGRSRRG	GRSRVDQEER	FPQGLWTGVA	MRSCPEEQYW	DPLLGTSCMSC	KTICNHQSQR 60
TCAAFCRSLS	CRKEQGKFYD	HLLRDCISCA	SICGQHPKQC	AYFCENKLRS	PVNLPPPELRR 120
QRSGEVENNS	DNSGRYQGLE	HRGSEASPAL	PGLKLSADQV	ALVYSLIPPW	GWPGNTLVAV 180
SIFLLLTGPT	YLLFKLSRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS 240
QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC 300
TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLASL 360
PGNTQSSGPI	PALACGLSCD	HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR 420
SWTFGGGGSG	GGSGGGGGSE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD 480
YSERLCLVSE	IPPKGGALGE	GPASPCNQH	SPYWAPPCYT	LKPET	525
SEQ ID NO: 100	moltype = AA length = 522				
FEATURE	Location/Qualifiers				
REGION	1..522				
	note = MISC_FEATURE - TACI/IL9R/cGC-S				
source	1..522				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 100					
MSGLGRSRRG	GRSRVDQEER	FPQGLWTGVA	MRSCPEEQYW	DPLLGTSCMSC	KTICNHQSQR 60
TCAAFCRSLS	CRKEQGKFYD	HLLRDCISCA	SICGQHPKQC	AYFCENKLRS	PVNLPPPELRR 120
QRSGEVENNS	DNSGRYQGLE	HRGSEASPAL	PGLKLSADQV	ALVYSLIPPW	GWPGNTLVAV 180
SIFLLLTGPT	YLLFKLSRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS 240
QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC 300
TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLASL 360
PGNTQSSGPI	PALACGLSCD	HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR 420
SWTFQPPQP	QPPQPPTM	PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	AESLQPDYSE 480
RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET	522
SEQ ID NO: 101	moltype = AA length = 414				
FEATURE	Location/Qualifiers				
REGION	1..414				
	note = MISC_FEATURE - BCMA/IL9R/cGC-F				
source	1..414				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 101					
MLQMAGQCSQ	NEYFDSLHA	CIPCQLRCSS	NTPLTCQRY	CNASVTNSVK	GTNALIPPWG 60
WPGNTLVAVS	IFLLLTGPTY	LLFKLSRVK	RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG 120
AHGAGVLLSQ	DCAGTPQAL	EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS 180
SEDVLPAGCT	EWVRVQTLAYL	PQEDWAPTS	LTRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC 240
YGGWHLASLP	GNTQSSGPIP	ALACGLSCDH	QGLETOQGVA	WVLAGHCQRP	GLHEDLQGML 300
LPSVLSKARS	WTFGGGGSGG	GGSGGGGGSER	TMPTRIPTLKN	LEDLVTEYHG	NFSAWSGVSK 360
GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	PGASPCNQHS	PYWAPPCYTL	KPET 414
SEQ ID NO: 102	moltype = AA length = 411				
FEATURE	Location/Qualifiers				
REGION	1..411				
	note = MISC_FEATURE - BCMA/IL9R/cGC-S				
source	1..411				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 102					
MLQMAGQCSQ	NEYFDSLHA	CIPCQLRCSS	NTPLTCQRY	CNASVTNSVK	GTNALIPPWG 60
WPGNTLVAVS	IFLLLTGPTY	LLFKLSRVK	RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG 120
AHGAGVLLSQ	DCAGTPQAL	EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS 180
SEDVLPAGCT	EWVRVQTLAYL	PQEDWAPTS	LTRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC 240
YGGWHLASLP	GNTQSSGPIP	ALACGLSCDH	QGLETOQGVA	WVLAGHCQRP	GLHEDLQGML 300
LPSVLSKARS	WTFQPPQPQ	PQPQPERTMP	RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA 360
ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	T 411
SEQ ID NO: 103	moltype = AA length = 582				
FEATURE	Location/Qualifiers				
REGION	1..582				
	note = MISC_FEATURE - NGFR/IL9R/cGC-F				
source	1..582				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 103					
KEACPTGLYT	HSGECKACN	LGEGVAQPCG	ANQTVCEPCL	DSVTFSDVVS	ATEPCKPCTE 60
CVGLQMSAP	CVEADDAVCR	CAYGYQDET	TGRCEACRVC	EAGSGLVFSC	QDKQNTVCEE 120
CPDGTYSDEA	NHVDPCLPCT	VCEDTERQLR	ECTRWADEAC	EEIPGRWITR	STPPEGSDST 180
APSTQEPEAP	PEQDLIASTV	AGVVTVMGS	SQPVVTRGTT	DNLIPPWGW	GNTLVAVSIF 240
LLLTGPTYLL	FKLSRVKRI	FYQNVPSAM	FFQPLYSVHN	GNFQTMGAH	GAGVLLSQDC 300
AGTPQGALEP	CVQEATALLT	CGPARPWKSV	ALEEEQEGPG	TRLPGNLSSE	DVLPAGCTEW 360

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RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGSR	SSSSSSSSNN	NNYCALGCGY	GWHLSALPGN	420
TQSSGPIPAL	ACGLSCDHQG	LETQQGVAVW	LAGHCQRPGL	HEDLQGMLLP	SVLSKARSWT	480
FGGGSGGGG	SGGGGSERTM	PRIPTLKNLE	DLVTEYHGNT	SAWSGVSKGL	AESLQPDYSE	540
RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET		582
SEQ ID NO: 104	moltype = AA length = 579					
FEATURE	Location/Qualifiers					
REGION	1..579					
	note = MISC_FEATURE - NGFR/IL9R/cGC-S					
source	1..579					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 104						
KEACPTGLYT	HSGECKACN	LGEGVAQPCG	ANQTVCEPCL	DSVTFSDVVS	ATEPCKPCTE	60
CVGLQSMSAP	CVEADDAVCR	CAYGYYQDET	TGRCEACRVC	EAGSGLVFSC	QDKQNTVCEE	120
CPDGTYSDEA	NHVDPCLPCT	VCEDTERQLR	ECTRWADAEC	EEIPGRWITR	STPPEGSDST	180
APSTQEPEAP	PEQDLIASTV	AGVVTVMGS	SQPVVTRGTT	DNLIPPWGW	GNTLVAVSIF	240
LLLLTGPTYLL	FKLSPRVKRI	FYQNVPSAM	FFQPLYSVHN	GNFQTMGAH	GAGVLLSQDC	300
AGTPQGALEP	CVQEATALLT	CGPARPWKSV	ALEEEQEGPG	TRLPGNLSSE	DVLPAGCTEW	360
RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGSR	SSSSSSSSNN	NNYCALGCGY	GWHLSALPGN	420
TQSSGPIPAL	ACGLSCDHQG	LETQQGVAVW	LAGHCQRPGL	HEDLQGMLLP	SVLSKARSWT	480
FQPPQPPQPP	QPPERTMPRI	PTLKNLEDLV	TEYHGNFSAW	SGVSKGLAES	LQPDYSERLC	540
LVSEIPPKGG	ALGEGPGASP	CNQHSPYWAP	PCYTLKPET			579
SEQ ID NO: 105	moltype = AA length = 521					
FEATURE	Location/Qualifiers					
REGION	1..521					
	note = MISC_FEATURE - EDAR/IL9R/cGC-F					
source	1..521					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 105						
EYNSCGENEY	YNQTTGLCQE	CPPCGPGEEP	YLSCGYGTKD	EDYGCVPCPA	EKFSKGGYQI	60
CRRHKDCGEF	FRATVLTTPGD	MENDAECGPC	LPGYYMLENR	PRNIYGMVCY	SCLLAPPNTK	120
ECVGATSGAS	ANFPGTSGSS	TLSPFQHAHK	ELSGQGHLAT	ALIPPWGWPG	NTLVAVSIFL	180
LLLTGPTYLLF	KLSPRVKRIF	YQNVPSAMF	FQPLYSVHNG	NFQTMGAHG	AGVLLSQDCA	240
GTPQGALEPC	VQEATALLTC	GPARPWKSV	LEEEQEGPGT	RLPGNLSSED	VLPAGCTEWR	300
VQTLAYLPQE	DWAPTSLTRP	APPDSEGSRS	SSSSSSSSNN	NYCALGCGY	WHLALPGNT	360
QSSGPIPALA	CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	VLSKARSWTF	420
GGGGSGGGGS	GGGGSERTMP	RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	480
LCLVSEIPPK	GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	T		521
SEQ ID NO: 106	moltype = AA length = 518					
FEATURE	Location/Qualifiers					
REGION	1..518					
	note = MISC_FEATURE - EDAR/IL9R/cGC-S					
source	1..518					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 106						
EYNSCGENEY	YNQTTGLCQE	CPPCGPGEEP	YLSCGYGTKD	EDYGCVPCPA	EKFSKGGYQI	60
CRRHKDCGEF	FRATVLTTPGD	MENDAECGPC	LPGYYMLENR	PRNIYGMVCY	SCLLAPPNTK	120
ECVGATSGAS	ANFPGTSGSS	TLSPFQHAHK	ELSGQGHLAT	ALIPPWGWPG	NTLVAVSIFL	180
LLLTGPTYLLF	KLSPRVKRIF	YQNVPSAMF	FQPLYSVHNG	NFQTMGAHG	AGVLLSQDCA	240
GTPQGALEPC	VQEATALLTC	GPARPWKSV	LEEEQEGPGT	RLPGNLSSED	VLPAGCTEWR	300
VQTLAYLPQE	DWAPTSLTRP	APPDSEGSRS	SSSSSSSSNN	NYCALGCGY	WHLALPGNT	360
QSSGPIPALA	CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	VLSKARSWTF	420
QPPQPPQPP	QPERTMPRI	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	480
VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP	CYTLKPET			518
SEQ ID NO: 107	moltype = AA length = 516					
FEATURE	Location/Qualifiers					
REGION	1..516					
	note = MISC_FEATURE - DCR2 (TNFRSF10D) /IL9R/cGC-F					
source	1..516					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 107						
ATIPRQDEVP	QQTVAQQQR	RSLKEEECPA	GSHRSEYTG	CNPCTEGVDY	TIASNNLPSC	60
LLCTVCKSGQ	TNKSSCTTTR	DTVCQCEKGS	FQDKNSPEMC	RTCRTGCPRG	MVKVSNCTPR	120
SDICKKNESA	ASSTGKTPAA	EETVTTILGM	LASPYHLIPP	WGWPGNTLVA	VSIFLLLTGP	180
TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQW	MGAGAGVLL	SQDCAGTPQG	240
ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN	LSSDVLPA	CTEWRVQTLA	300
YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNYCAL	GCGGWHLSA	LPGNTQSSGP	360
IPALACGLSC	DHQGLETTQQ	VAWVLGHQ	RPGLHEDLQ	MLLPSVLSKA	RSWTFGGGS	420
GGGGSGGGGS	ERTMPRIPTL	KNLEDLVTEY	HGNFSAWSGV	SKGLAESLQ	DYSERLCLVS	480

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EIPPKGGALG	EGPGASPCNQ	HSPYWAPPCY	TLKPET			516
SEQ ID NO: 108	moltype = AA length = 513					
FEATURE	Location/Qualifiers					
REGION	1..513					
	note = MISC_FEATURE - DCR2 (TNFRSF10D) /IL9R/cGC-S					
source	1..513					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 108						
ATIPRQDEVP	QQTVAPOQQQR	RSLKEEECPA	GSHRSEYTGA	CNPCTEGVDY	TIASNNLPSC	60
LLCTVCKSGQ	TNKSSCTTTR	DTVCQCEKGS	FQDKNSPEMC	RTCRTGCPRG	MVKVSNCTPR	120
SDIKCKNESA	ASSTGKTPAA	EETVTTILGM	LASPYHLIPP	WGWPGNTLVA	VSIFLLLTGP	180
TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW	MGAHGAGVLL	SQDCAGTPQG	240
ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN	LSSADVLPAG	CTEWRVQTLA	300
YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNYCAL	GCGGWHLSA	LPGNTQSSGP	360
IPALACGLSC	DHQGLETQQG	VAWVLAGHCQ	RPGLHEDLQG	MLLPSVLSKA	RSWTFQPQPQ	420
PQPQPQPPT	MPRIPTLKNL	EDLVTEYHGN	FAWSGVSKG	LAESLQPDYS	ERLCLVSEIP	480
PKGGALGEGP	GASPCNQHSP	YWAPPCYTLK	PET			513
SEQ ID NO: 109	moltype = AA length = 571					
FEATURE	Location/Qualifiers					
REGION	1..571					
	note = MISC_FEATURE - DCR1 (TNFRSF10C) /IL9R/cGC-F					
source	1..571					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 109						
ATTARQEEVP	QQTVAPOQQQR	HSPKGEPCPA	GSHRSEHTGA	CNPCTEGVDY	TNASNNEPSC	60
FFPCTVCKSDQ	KHKSSCTMTR	DTVCQCKEGT	FRNENSPEMC	RKCSRCPSGE	VQVSNCTSWD	120
DIQCVVEEFGA	NATVETPAAE	ETMNTSPGTP	APAAEETMNT	SPGTPAPAAE	ETMTTSPGTP	180
APAAEETMTT	SPGTPAPAAE	ETMITSPGTP	ALIPPWGWPG	NTLVAVSIFL	LLTGPTYLLF	240
KLSPRVKRIF	YQNVPSPAMF	FQPLYSVHNG	NFQTMWGAHG	AGVLLSQDCA	GTPQGALEPC	300
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSSD	VLPAGCTEWR	VQTLAYLPQE	360
DWAPTSLTRP	APPDSEGSRS	SSSSSSNNN	NYCALGCGYGG	WHLSALPGNT	QSSGPIPALA	420
CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	VLSKARSWTF	GGGGSGGGGS	480
GGGGSSERTMP	RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	540
GGALGEGPGA	SPCNQHSPY	APPCYTLKPE	T			571
SEQ ID NO: 110	moltype = AA length = 568					
FEATURE	Location/Qualifiers					
REGION	1..568					
	note = MISC_FEATURE - DCR1 (TNFRSF10C) /IL9R/cGC-S					
source	1..568					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 110						
ATTARQEEVP	QQTVAPOQQQR	HSPKGEPCPA	GSHRSEHTGA	CNPCTEGVDY	TNASNNEPSC	60
FFPCTVCKSDQ	KHKSSCTMTR	DTVCQCKEGT	FRNENSPEMC	RKCSRCPSGE	VQVSNCTSWD	120
DIQCVVEEFGA	NATVETPAAE	ETMNTSPGTP	APAAEETMNT	SPGTPAPAAE	ETMTTSPGTP	180
APAAEETMTT	SPGTPAPAAE	ETMITSPGTP	ALIPPWGWPG	NTLVAVSIFL	LLTGPTYLLF	240
KLSPRVKRIF	YQNVPSPAMF	FQPLYSVHNG	NFQTMWGAHG	AGVLLSQDCA	GTPQGALEPC	300
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSSD	VLPAGCTEWR	VQTLAYLPQE	360
DWAPTSLTRP	APPDSEGSRS	SSSSSSNNN	NYCALGCGYGG	WHLSALPGNT	QSSGPIPALA	420
CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	VLSKARSWTF	QPQPQPQPQP	480
QPERTMPRI	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	540
LGEGPGASPC	NQHSPYWAPP	CYTLKPET				568
SEQ ID NO: 111	moltype = AA length = 533					
FEATURE	Location/Qualifiers					
REGION	1..533					
	note = MISC_FEATURE - CD40/IL9R/cGC-F					
source	1..533					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 111						
EPPTACREKQ	YLINSQCCSL	CQPGQKLVS	CTEFTETECL	PCGESEFLDT	WNRETHCHQH	60
KYCDPNLGLR	VQQKGTSETD	TICTCEEGWH	CTSEACESCV	LHRSCSPGFG	VKQIATGVSD	120
TICEPCPVGF	FSNVSSAFEK	CHPWTSCETK	DLVVQAGTN	KTDVVCQPQD	RLRLIPPWGW	180
PGNTLVAVSI	FLLLTGPITYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	240
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	300
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSN	NNNYCALGCV	360
GGWHLSALPG	NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLGHQCRPG	LHEDLQGMLL	420
PSVLSKARSW	TGGGGSGGG	GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FAWSGVSKG	480
LAESLQPDYS	ERLCLVSEIP	PKGGALGEGP	GASPCNQHSP	YWAPPCYTLK	PET	533

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SEQ ID NO: 112	moltype = AA	length = 530
FEATURE	Location/Qualifiers	
REGION	1..530	
	note = MISC_FEATURE - CD40/IL9R/cGC-S	
source	1..530	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 112		
EPPTACREKQ	YLINSQCCSL	CQPGQKLVS
KYCDPNLGLR	VQQKGTSETD	TICTCEEGWH
TICEPCPVGF	FSNVSSAFEK	CHPWTSCETK
PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT
GGWHLSPALPG	NTQSSGPIPA	LACGLSCDHQ
PSVLSKARSW	TFQPQPQPQP	QPQPERTMPR
SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS
		PCNQHSPYWA
		PPCYTLKPET
		60
		120
		180
		240
		300
		360
		420
		480
		530
SEQ ID NO: 113	moltype = AA	length = 508
FEATURE	Location/Qualifiers	
REGION	1..508	
	note = MISC_FEATURE - FAS/IL9R/cGC-F	
source	1..508	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 113		
QVTDINSKGL	ELRKTVTTVE	TQNLEGLHHD
QEGKEYTDKA	HFSSKCRRCR	LCDEGHGLEV
CTKCEHGIK	ECTLTSNTKC	KEEGSRSNLI
PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ
ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP
PTSLTRPAPP	DSEGRSSSSS	SSSSNNNNYC
SCDHQGLETO	QGVAVLAGH	CQRPGLHEDL
GSERTMPRIIP	TLKNLEDLVT	EYHGNFSAWS
LGEFGASPC	NQHSPYWAPP	CYTLKPET
		60
		120
		180
		240
		300
		360
		420
		480
		508
SEQ ID NO: 114	moltype = AA	length = 505
FEATURE	Location/Qualifiers	
REGION	1..505	
	note = MISC_FEATURE - FAS/IL9R/cGC-S	
source	1..505	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 114		
QVTDINSKGL	ELRKTVTTVE	TQNLEGLHHD
QEGKEYTDKA	HFSSKCRRCR	LCDEGHGLEV
CTKCEHGIK	ECTLTSNTKC	KEEGSRSNLI
PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ
ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP
PTSLTRPAPP	DSEGRSSSSS	SSSSNNNNYC
SCDHQGLETO	QGVAVLAGH	CQRPGLHEDL
RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS
GPASPCNQH	SPYWAPPCYT	LKPET
		60
		120
		180
		240
		300
		360
		420
		480
		505
SEQ ID NO: 115	moltype = AA	length = 576
FEATURE	Location/Qualifiers	
REGION	1..576	
	note = MISC_FEATURE - DR4/IL9R/cGC-F	
source	1..576	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 115		
ASGTEAAAAT	PSKVGSSAG	RIEPRGGGRG
PRLRVHKTFK	FVVVGVLQV	VPSSAATIKL
ACNRCTEGVG	YTNASNNLFA	CLPCTACKSD
CRKCSRGCPR	GMVKVKDCTP	WSDIECVHKE
TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY
ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ
YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS
IPALACGLSC	DHQGLETOQG	VAWVLAGHCQ
GGGSGGGGS	ERTMPRIPTL	KNLEDLVTEY
EIPPKGGALG	EGPGASPCNQ	HSPYWAPPCY
		TLKPET
		60
		120
		180
		240
		300
		360
		420
		480
		540
		576
SEQ ID NO: 116	moltype = AA	length = 573
FEATURE	Location/Qualifiers	
REGION	1..573	

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		note = MISC_FEATURE - DR4/IL9R/cGC-S				
source		1..573				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 116						
ASGTEAAAAAT	PSKVGWSSAG	RIEPRGGGRG	ALPTSMGQHG	PSARARAGRA	PGPRPAREAS	60
PRLRVHKTFK	FVVVGVLQV	VPSSAATIKL	HDQSIGTQQW	EHSPLGELCP	PGSHRSEHPG	120
ACNRCTEGVG	YTNASNNLFA	CLPCTACKSD	EEERSPCTTT	RNTACQCKPG	TFRNDNSAEM	180
CRKCSRGCPR	GMVKVKDCTP	WSDIECVHKE	SGNGHNLIPP	WGWPGNTLVA	VSIFLLLTGP	240
TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW	MGAHGAGVLL	SQDCAGTPQG	300
ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN	LSSDEVLPAG	CTEWRVQTLA	360
YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNYCAL	GCVGGWHLSA	LPGNTQSSGP	420
IPALACGLSC	DHQGLETQQG	VAWVLAGHCQ	RPGLHEDLQG	MLLPSVLSKA	RSWTFQPQPQ	480
PQPQPQPPT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG	LAESLQPDYS	ERLCLVSEIP	540
PKGKALGEGP	GASPCNQHSP	YWAPPCYTLK	PET			573
SEQ ID NO: 117						
moltype = AA length = 668						
Location/Qualifiers						
1..668						
note = MISC_FEATURE - DR6/IL9R/cGC-F						
source						
1..668						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 117						
QPEQKASNLI	GTYRHVDRA	GQVLTCDKCP	AGTYVSEHCT	NTSLRVCSSC	PVGTFTRHEN	60
GIEKCHDCSQ	PCPWPMIEKL	PCAAALTDREC	TCPGFMFQSN	ATCAPHTVCP	VGWGVRRKGT	120
ETEDVRCKQC	ARGTFSDVPS	SVMKCKAYTD	CLSQNLVVIK	PGTKETDNVC	GTLPSFSSST	180
SPSPGTAIFP	RPEHMETHEV	PSSTYVPKGM	NSTESNSSAS	VRPKVLSSIQ	EGTVPDNTSS	240
ARGKEDVNKT	LPNLQVVNHQ	QGPHHRHILK	LLPSMEATGG	EKSSTPIKGP	KRGHPRQNLH	300
KHFDINEHLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP	360
LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE	420
EQEGPGTRLP	GNLSSDEVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGRSSSSS	480
SSSSNNNNNYC	ALGCVGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	QGVAVVLAGH	540
CQRPGLHEDL	QGMLLPSVLS	KARSWTFGGG	GSGGGGSGGG	GSERTMPRIP	TLKNLEDLVT	600
EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP	660
CYTLKPET						668
SEQ ID NO: 118						
moltype = AA length = 665						
Location/Qualifiers						
1..665						
note = MISC_FEATURE - DR6/IL9R/cGC-S						
source						
1..665						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 118						
QPEQKASNLI	GTYRHVDRA	GQVLTCDKCP	AGTYVSEHCT	NTSLRVCSSC	PVGTFTRHEN	60
GIEKCHDCSQ	PCPWPMIEKL	PCAAALTDREC	TCPGFMFQSN	ATCAPHTVCP	VGWGVRRKGT	120
ETEDVRCKQC	ARGTFSDVPS	SVMKCKAYTD	CLSQNLVVIK	PGTKETDNVC	GTLPSFSSST	180
SPSPGTAIFP	RPEHMETHEV	PSSTYVPKGM	NSTESNSSAS	VRPKVLSSIQ	EGTVPDNTSS	240
ARGKEDVNKT	LPNLQVVNHQ	QGPHHRHILK	LLPSMEATGG	EKSSTPIKGP	KRGHPRQNLH	300
KHFDINEHLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP	360
LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE	420
EQEGPGTRLP	GNLSSDEVLP	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGRSSSSS	480
SSSSNNNNNYC	ALGCVGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	QGVAVVLAGH	540
CQRPGLHEDL	QGMLLPSVLS	KARSWTFQPP	PQPQPQPQPE	RTMPRIPTLK	NLEDLVTEYH	600
GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT	660
LKPET						665
SEQ ID NO: 119						
moltype = AA length = 515						
Location/Qualifiers						
1..515						
note = MISC_FEATURE - DR5/IL9R/cGC-F						
source						
1..515						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 119						
ITQQDLAPQQ	RAAPQQKRSS	PSEGLCPPGH	HISEDGRDCI	SCKYGQDYST	HWNDLLFCLR	60
CTRCDSGEVE	LSPCTTTRNT	VCQCEEGTFR	EEDSPEMCRK	CRTGCPRGMV	KVGDCTPWSD	120
IECVHKESGT	KHSGEVPAVE	ETVTSSPGTP	ASPCSLIPPW	GWPGNTLVAV	SIFLLLTGPT	180
YLLFKLSPRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTMW	GAHGAGVLLS	QDCAGTPQGA	240
LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL	SSDEVLPAGC	TEWRVQTLAY	300
LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLSAL	PGNTQSSGPI	360
PALACGLSCD	HQGLETQQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR	SWTFGGGGSG	420
GGGSGGGGSE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	480
IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT	LKPET			515

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SEQ ID NO: 120	moltype = AA length = 512				
FEATURE	Location/Qualifiers				
REGION	1..512				
	note = MISC_FEATURE - DR5/IL9R/cGC-S				
source	1..512				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 120					
ITQQDLAPQQ	RAAPQQKRSS	PSEGLCPPGH	HISEDGRDCI	SCKYGQDYST	HWNDLLFCLR 60
CTRCDSGEVE	LSPCTTTRNT	VCQCEEGTFR	EEDSPEMCRK	CRTGCPRGMV	KVGDCTPWS 120
IECVHKESGT	KHSGEVP	ETVTSSPGTP	ASPCSLIPPW	GWPGNTLVAV	SIFLLLTGPT 180
YLLFKLS	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA 240
LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY 300
LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLSAL	PGNTQSSGPI 360
PALACGLSCD	HQGLE	AWVL	PGLHEDLQGM	LLPSVLSKAR	SWTFQPQPQP 420
QPQPQPERTM	PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP 480
KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET		512
SEQ ID NO: 121	moltype = AA length = 535				
FEATURE	Location/Qualifiers				
REGION	1..535				
	note = MISC_FEATURE - DR3/IL9R/cGC-F				
source	1..535				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 121					
QGGTRSPRCD	CAGDFHKKIG	LFCCRGCPAG	HYLKAPCTEP	CGNSTCLVCP	QDTFLAWENH 60
HNSECARCQA	CDEQASQVAL	ENCSAVADTR	CGCKPGWFVE	CQVSQCVSSS	PFYCQPCLD 120
GALHRHTRLL	CSRRDTCGT	CLPGFYEHGD	GCVSCTSTL	GSCPERCAAV	CGWRQLIPPW 180
GWPGNTLVAV	SIFLLLTGPT	YLLFKLS	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM 240
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL 300
SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG 360
CYGGWHLSAL	PGNTQSSGPI	PALACGLSCD	HQGLE	AWVL	PGLHEDLQGM 420
LLPSVLSKAR	SWTFGGGGSG	GGSGGGGGSE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGV 480
KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT	LKPET 535
SEQ ID NO: 122	moltype = AA length = 532				
FEATURE	Location/Qualifiers				
REGION	1..532				
	note = MISC_FEATURE - DR3/IL9R/cGC-S				
source	1..532				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 122					
QGGTRSPRCD	CAGDFHKKIG	LFCCRGCPAG	HYLKAPCTEP	CGNSTCLVCP	QDTFLAWENH 60
HNSECARCQA	CDEQASQVAL	ENCSAVADTR	CGCKPGWFVE	CQVSQCVSSS	PFYCQPCLD 120
GALHRHTRLL	CSRRDTCGT	CLPGFYEHGD	GCVSCTSTL	GSCPERCAAV	CGWRQLIPPW 180
GWPGNTLVAV	SIFLLLTGPT	YLLFKLS	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM 240
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL 300
SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG 360
CYGGWHLSAL	PGNTQSSGPI	PALACGLSCD	HQGLE	AWVL	PGLHEDLQGM 420
LLPSVLSKAR	SWTFQPQPQP	QPQPQPERTM	PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL 480
AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET 532
SEQ ID NO: 123	moltype = AA length = 595				
FEATURE	Location/Qualifiers				
REGION	1..595				
	note = MISC_FEATURE - TNFRSF1B/IL9R/cGC-F				
source	1..595				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 123					
LPAQVAFTPY	APEPGSTCRL	REYYDQTAQM	CCSKCSPGQH	AKVFCTKTS	TVCDSCEDST 60
YTQLWNWVPE	CLSCGSRCSS	DQVETQACTR	EQNRICTCRP	GWYCALSKQE	GCRLCAPLRK 120
CRPGFGVARP	GTETSDVCK	PCAPGTFSNT	TSSTDICRPH	QICNVVAIPG	NASMDAVCTS 180
TSPTSRMAPG	AVHLPQPVST	RSQHTQPTPE	PSTAPSTSFL	LPMGPSPPAE	GSTGDLIPPW 240
GWPGNTLVAV	SIFLLLTGPT	YLLFKLS	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM 300
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL 360
SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG 420
CYGGWHLSAL	PGNTQSSGPI	PALACGLSCD	HQGLE	AWVL	PGLHEDLQGM 480
LLPSVLSKAR	SWTFGGGGSG	GGSGGGGGSE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGV 540
KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT	LKPET 595
SEQ ID NO: 124	moltype = AA length = 592				
FEATURE	Location/Qualifiers				
REGION	1..592				

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	note = MISC_FEATURE - TNFRSF1B/IL9R/cGC-S				
source	1..592				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 124					
LPAQVAFTPY	APEPGSTCRL	REYYDQTAQM	CCSKCSPGQH	AKVFCTKTS	TVCDSCEDST 60
YTQLWNWVPE	CLSCGSRCSS	DQVETQACTR	EQNRICTCRP	GWYCALSKQE	GCRLCAPLRK 120
CRPGFGVARP	GTETSDVVCK	PCAPGTFSNT	TSSTDICRPH	QICNVVAIPG	NASMDAVCTS 180
TSPTRSMAPG	AVHLPQPVST	RSQHTQPTPE	PSTAPSTSFL	LPMGPSPPAE	GSTGDLIPPW 240
GWPGNTLVAV	SIFLLLTGPT	YLLFKLSPRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTMW 300
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL 360
SSSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNNYCALG 420
CYGGWHLALS	PGNTQSSGPI	PALACGLSCD	HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM 480
LLPSVLSKAR	SWTFQPQPQP	QPQPQPPTM	PRIPTLKNLE	DLVTEYHGNT	SAWSGVSKGL 540
AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET 592
SEQ ID NO: 125	moltype = AA length = 542				
FEATURE	Location/Qualifiers				
REGION	1..542				
	note = MISC_FEATURE - TNFRSF1/IL9R/cGC-F				
source	1..542				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 125					
LVPHLGDREK	RDSVCPQGKY	IHPQNNSICC	TKCHKGTYLY	NDCPGPGQDT	DCRECESGSF 60
TASENHLRHC	LSCSKCRKEM	GQVEISSCTV	DRDTVCGCRK	NQYRHYWSEN	LFQCFNCSLC 120
LNQTVHLSCQ	EKQNTVCTCH	AGFFLRENEC	VSCSNCKKSL	ECTKLCLPQI	ENVKGTEDSG 180
TTLIPPWGW	GNTLVAVSIF	LLLTGPTYLL	FKLSPRVKRI	FYQNVPSAM	FFQPLYSVHN 240
GNFQTMGAH	GAGVLLSQDC	AGTPQGALEP	CVQEATALLT	CGPARPWKSV	ALEEEQEGPG 300
TRLPGNLSSE	DVLPAGCTEW	RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGS	SSSSSSSSNN 360
NNYCALGCY	GWHLALPGN	TQSSGPIPAL	ACGLSCDHQ	LETQQGVAV	LAGHCQRPGL 420
HEDLQGMMLP	SVLSKARSW	FGGGSGGGG	SGGGGSERTM	PRIPTLKNLE	DLVTEYHGNT 480
SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP 540
ET					542
SEQ ID NO: 126	moltype = AA length = 539				
FEATURE	Location/Qualifiers				
REGION	1..539				
	note = MISC_FEATURE - TNFRSF1/IL9R/cGC-S				
source	1..539				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 126					
LVPHLGDREK	RDSVCPQGKY	IHPQNNSICC	TKCHKGTYLY	NDCPGPGQDT	DCRECESGSF 60
TASENHLRHC	LSCSKCRKEM	GQVEISSCTV	DRDTVCGCRK	NQYRHYWSEN	LFQCFNCSLC 120
LNQTVHLSCQ	EKQNTVCTCH	AGFFLRENEC	VSCSNCKKSL	ECTKLCLPQI	ENVKGTEDSG 180
TTLIPPWGW	GNTLVAVSIF	LLLTGPTYLL	FKLSPRVKRI	FYQNVPSAM	FFQPLYSVHN 240
GNFQTMGAH	GAGVLLSQDC	AGTPQGALEP	CVQEATALLT	CGPARPWKSV	ALEEEQEGPG 300
TRLPGNLSSE	DVLPAGCTEW	RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGS	SSSSSSSSNN 360
NNYCALGCY	GWHLALPGN	TQSSGPIPAL	ACGLSCDHQ	LETQQGVAV	LAGHCQRPGL 420
HEDLQGMMLP	SVLSKARSW	FQPPQPQPQ	PQPPTMPRI	PTLKNLEDLV	TEYHGNTSAW 480
SGVSKGLAES	LQPDYSERLC	LVSEIPPKGG	ALGEGPGASP	CNQHSPYWAP	PCYTLKPET 539
SEQ ID NO: 127	moltype = AA length = 473				
FEATURE	Location/Qualifiers				
REGION	1..473				
	note = MISC_FEATURE - BMPR1B/IL9R/cGC-F				
source	1..473				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 127					
KKKEDGESTAP	TPRPKVLRC	CHHHCPEDSV	NNICSTDGYC	FTMIEEDDSG	LPVVTSGCLG 60
LEGSDFQCRD	TIPIHQRRSI	ECCTERNECN	KDLHPTLPPL	KNRDFVDGPI	HHRLIPPWGW 120
PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSA	MFFQPLYSVH	NGNFQTMGA 180
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS 240
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY 300
GGWHLALPG	NTQSSGPIPA	LACGLSCDHQ	GLETOQGVAV	VLAGHCQRP	LHEDLQGMML 360
PSVLSKARSW	TFGGGSGGGG	SGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FAWSGVSKG 420
LAESLQPDYS	ERLCLVSEIP	PKGALGEGP	GASPCNQHSP	YWAPPCYTLK	PET 473
SEQ ID NO: 128	moltype = AA length = 470				
FEATURE	Location/Qualifiers				
REGION	1..470				
	note = MISC_FEATURE - BMPR1B/IL9R/cGC-S				
source	1..470				
	mol_type = protein				

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		organism = synthetic construct			
SEQUENCE: 128					
KKEDGESTAP	TPRPKVLRCK	CHHHCPEDSV	NNICSTDGYC	FTMIEEDDSG	LPVVTSGCLG 60
LEGSDFQCRD	TPIPHQRRSI	ECCTERNECN	KDLHPTLPPL	KNRDFVDGPI	HHRLIPPWGW 120
PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMWGA 180
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS 240
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCV 300
GGWHLALPG	NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGMML 360
PSVLSKARSW	TFQPQPQPQP	QPQPERTMPR	IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE 420
SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET	470
SEQ ID NO: 129		moltype = AA length = 489			
FEATURE		Location/Qualifiers			
REGION		1..489			
		note = MISC_FEATURE - BMPR1A/IL9R/cGC-F			
source		1..489			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 129					
QNLDSMLHGT	GMKSDSDQKK	SENGVTLAPE	DTLPFLKCYC	SGHCPDDAIN	NTCITNGHCF 60
AIIEEDDQGE	TTLASGCMKY	EGSDFQCKDS	PKAQLRRTIE	CCRTNLCNQY	LQPTLPPVVI 120
GPFFDGSIRL	IPPWGWPGNT	LVAVSIFLLL	TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ 180
PLYSVHNGNF	QTWMGAHGAG	VLLSQDCAGT	PQGALEPCVQ	EATALLTCGP	ARPWKSVALE 240
EEQEGPGTRL	PGNLSSDVL	PAGCTEWRVQ	TLAYLPQEDW	APTSLTRPAP	PDSEGSRSSS 300
SSSSSNNNNY	CALGCYGGWH	LSALPGNTQS	SGPIPALACG	LSCDHQGLET	QQGVAVVLAG 360
HCQRPGLHED	LQGMMLPSVL	SKARSWTFGG	GGSGGGSGG	GGSERTMPRI	PTLKNLEDLV 420
TEYHGNFSAW	SGVSKGLAES	LQPDYSERLC	LVSEIPPKG	ALGEGPGASP	CNQHSPYWAP 480
PCYTLKPET					489
SEQ ID NO: 130		moltype = AA length = 486			
FEATURE		Location/Qualifiers			
REGION		1..486			
		note = MISC_FEATURE - BMPR1A/IL9R/cGC-S			
source		1..486			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 130					
QNLDSMLHGT	GMKSDSDQKK	SENGVTLAPE	DTLPFLKCYC	SGHCPDDAIN	NTCITNGHCF 60
AIIEEDDQGE	TTLASGCMKY	EGSDFQCKDS	PKAQLRRTIE	CCRTNLCNQY	LQPTLPPVVI 120
GPFFDGSIRL	IPPWGWPGNT	LVAVSIFLLL	TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ 180
PLYSVHNGNF	QTWMGAHGAG	VLLSQDCAGT	PQGALEPCVQ	EATALLTCGP	ARPWKSVALE 240
EEQEGPGTRL	PGNLSSDVL	PAGCTEWRVQ	TLAYLPQEDW	APTSLTRPAP	PDSEGSRSSS 300
SSSSSNNNNY	CALGCYGGWH	LSALPGNTQS	SGPIPALACG	LSCDHQGLET	QQGVAVVLAG 360
HCQRPGLHED	LQGMMLPSVL	SKARSWTFQP	QPQPQPQPQP	ERTMPRIPTL	KNLEDLVTEY 420
HGNFSAWSGV	SKGLAESLQP	DYSERLCLVS	EIPPKGALG	EGPGASPCNQ	HSPYWAPPCY 480
TLKPET					486
SEQ ID NO: 131		moltype = AA length = 484			
FEATURE		Location/Qualifiers			
REGION		1..484			
		note = MISC_FEATURE - BMPR2/IL9R/cGC-F			
source		1..484			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 131					
SONQERLCAF	KDPYQQDLGI	GESRISHENG	TILCSKGSTC	YGLWEKSKGD	INLVKQGCWS 60
HIGDPQECHY	EECVVTTTPP	SIQNGTYRFC	CCSTDLCNVN	FTENFPPPD	TPLSPPHSFN 120
RDETLIPPWG	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	RIFYQNVPSP	AMFFQPLYSV 180
HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	LTCGPARPWK	SVALEEEQEG 240
PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTS	TRPAPPDSEG	SRSSSSSSSS 300
NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	ALACGLSCDH	QGLETTQQGVA	VVLAGHCQRP 360
GLHEDLQGM	LPSVLSKARS	WTFGGGGSGG	GGSGGGGSG	TMPIPTLKN	LEDLVTEYHG 420
NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	PPKGALGEG	PGASPCNQHS	PYWAPPCYTL 480
KPET					484
SEQ ID NO: 132		moltype = AA length = 481			
FEATURE		Location/Qualifiers			
REGION		1..481			
		note = MISC_FEATURE - BMPR2/IL9R/cGC-S			
source		1..481			
		mol_type = protein			
		organism = synthetic construct			
SEQUENCE: 132					
SONQERLCAF	KDPYQQDLGI	GESRISHENG	TILCSKGSTC	YGLWEKSKGD	INLVKQGCWS 60
HIGDPQECHY	EECVVTTTPP	SIQNGTYRFC	CCSTDLCNVN	FTENFPPPD	TPLSPPHSFN 120
RDETLIPPWG	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	RIFYQNVPSP	AMFFQPLYSV 180

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HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	240
PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTSL	TRPAPPDSEG	SRSSSSSSSS	300
NNNNNYCALGC	YGGWHLSPALP	GNTQSSGPIP	ALACGLSCDH	QGLETTQQGVA	WVLAGHCQRP	360
GLHEDLQGML	LPSVLSKARS	WTFQPQPQPQ	PQPQPERTMP	RIPTLKNLED	LVTEYHGNFS	420
AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	480
T						481
SEQ ID NO: 133	moltype = AA length = 963					
FEATURE	Location/Qualifiers					
REGION	1..963					
	note = MISC_FEATURE - CSF3R/IL9R/cGC-F					
source	1..963					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 133						
ECGHISVSAP	IVHLGDPITA	SCIHKQNCSE	LDPEPQILWR	LGAEELQPGGR	QQRLSDGTQE	60
SIITLPHLNH	TQAFLLSCCLN	WGNSLQILDQ	VELRAGYPPA	IPHNLSCLMN	LTTSSLICQW	120
EPGPETHLPT	SFTLKSFKSR	GNCQTQGDSE	LDCVPKDGQS	HCCIPRKHLL	LYQNMGIWVQ	180
AENALGTSMS	PQLCLDPM DV	VKLEPPMLRT	MDPSPEAAPP	QAGCLQLCWE	PWQPGHLINQ	240
KCELRHKPQR	GEASWALVGP	LPLEALQYEL	CGLLPATAYT	LQIRCIRWPL	PGHWSWSPS	300
LELRTTERAP	TVRLDTWWRQ	RQLDPRTVQL	FWKVPVLEED	SGRIQGYVVS	WRPSGQAGAI	360
LPLCNTTELS	CTFHLPSEAQ	EVALVAYNSA	GTSRPTPVVF	SESRGPALTR	LHAMARDPHS	420
LWVGWEPPNP	WPQGYVIEWG	LGPPSASNSN	KTWRMEQNGR	ATGFLLENKI	RPFQLEYEII	480
TPLYQDTMGP	SQHVYAYSQE	MAPSHAPELH	LKHIGKTWAQ	LEWVPEPPEL	GKSPLTHYTI	540
FWTNAQNQSF	SAILNASSRG	FVLHGLEPAS	LYHIHMAAS	QAGATNSTVL	TLMTLTPEGS	600
ELHLIPPWGW	PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	660
NGNFQTMWGA	HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	720
GTRLPGNLSS	EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	780
NNNNNYCALGCY	GGWHLSPALP	NTQSSGPIPA	LACGLSCDHQ	GLETTQQGVAW	VLAGHCQRP	840
LHEDLQGMML	PSVLSKARSW	TFGGGGSGGG	GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	900
FSAWSGVSKG	LAESLQPDYS	ERLCLVSEIP	PKGGALGEGP	GASPCNQHSP	YWAPPCYTLK	960
PET						963
SEQ ID NO: 134	moltype = AA length = 960					
FEATURE	Location/Qualifiers					
REGION	1..960					
	note = MISC_FEATURE - CSF3R/IL9R/cGC-S					
source	1..960					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 134						
ECGHISVSAP	IVHLGDPITA	SCIHKQNCSE	LDPEPQILWR	LGAEELQPGGR	QQRLSDGTQE	60
SIITLPHLNH	TQAFLLSCCLN	WGNSLQILDQ	VELRAGYPPA	IPHNLSCLMN	LTTSSLICQW	120
EPGPETHLPT	SFTLKSFKSR	GNCQTQGDSE	LDCVPKDGQS	HCCIPRKHLL	LYQNMGIWVQ	180
AENALGTSMS	PQLCLDPM DV	VKLEPPMLRT	MDPSPEAAPP	QAGCLQLCWE	PWQPGHLINQ	240
KCELRHKPQR	GEASWALVGP	LPLEALQYEL	CGLLPATAYT	LQIRCIRWPL	PGHWSWSPS	300
LELRTTERAP	TVRLDTWWRQ	RQLDPRTVQL	FWKVPVLEED	SGRIQGYVVS	WRPSGQAGAI	360
LPLCNTTELS	CTFHLPSEAQ	EVALVAYNSA	GTSRPTPVVF	SESRGPALTR	LHAMARDPHS	420
LWVGWEPPNP	WPQGYVIEWG	LGPPSASNSN	KTWRMEQNGR	ATGFLLENKI	RPFQLEYEII	480
TPLYQDTMGP	SQHVYAYSQE	MAPSHAPELH	LKHIGKTWAQ	LEWVPEPPEL	GKSPLTHYTI	540
FWTNAQNQSF	SAILNASSRG	FVLHGLEPAS	LYHIHMAAS	QAGATNSTVL	TLMTLTPEGS	600
ELHLIPPWGW	PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	660
NGNFQTMWGA	HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	720
GTRLPGNLSS	EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	780
NNNNNYCALGCY	GGWHLSPALP	NTQSSGPIPA	LACGLSCDHQ	GLETTQQGVAW	VLAGHCQRP	840
LHEDLQGMML	PSVLSKARSW	TFQPQPQPQP	QPQPERTMPR	IPTLKNLEDL	VTEYHGNFSA	900
WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET	960
SEQ ID NO: 135	moltype = AA length = 858					
FEATURE	Location/Qualifiers					
REGION	1..858					
	note = MISC_FEATURE - CSF1R/IL9R/cGC-F					
source	1..858					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 135						
IPVIEPSVPE	LVVKPGATVT	LRCVGNNGSVE	WDGPPSPHWT	LYSDGSSSIL	STNNATFQNT	60
GTYRCTEPGD	PLGGSAAIHL	YVKDPARPWN	VLAQEVVVFE	DQDALLPCLL	TDPVLEAGVS	120
LVRVRGRPLM	RHTNYSFSPW	HGFTIHRAKF	IQSQDYQCSA	LMGGRKVMSI	SIRLKVQKVI	180
PGPPALTLPV	AELVRIRGEA	AQIVCSASSV	DVNFDFVLQH	NNTKLAIPQQ	SDFHNNRYQK	240
VLTLNLDQVD	FQHAGNYSYV	ASNVQGHST	SMFFRVVESA	YLNLSSEQNL	IQEVTVEGEL	300
NNLKVMVEAYP	GLQGFNWTYL	GPFSDHQPEP	KLANATTKDT	YRHTFTLSLP	RLKPSEAGRY	360
SFLARNPGGW	RALTFFELTLR	YPPEVSVIWT	FINGSGTLLC	AASGYQPNV	TWLQCSGHTD	420
RCDEAQVLQV	WDDPYPEVLS	QEPFHKVTVQ	SLLTVETLEH	NQTYECRAHN	SVGSGSWAFI	480
PISAGATHTP	PDEFLLFTPLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	540
VPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	600

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RPWKSVALEE	EQEGPGTRLP	GNLSSSEVL	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	660
DSEGSRSSSS	SSSSNNNNYC	ALGCGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	720
QGVAVVL	AGH CQRPGLHEDL	QGMLLP	SVLS KARSWTFGGG	GSGGGSGGG	GSERTMPRIP	780
TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	840
NQHSPYWAPP	CYTLKPET					858
SEQ ID NO: 136	moltype = AA length = 855					
FEATURE	Location/Qualifiers					
REGION	1..855					
	note = MISC_FEATURE - CSF1R/IL9R/cGC-S					
source	1..855					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 136						
IPVIEPSVPE	LVVKPGATVT	LRCVGN	GSVE	WDGPPSPHWT	LYSDGSSSIL	STNNATFQNT 60
GTYRCTEPGD	PLGGSAAIHL	YVKDPA	RPWN	VLAQEVVVE	DQDALLPCLL	TDPVLEAGVS 120
LVRVRGRPLM	RHTNYSFSPW	HGFTIHR	AKF	IQSQDYQCSA	LMGGRKVMSI	SIRLKVQKVI 180
PGPPALTLVP	AELVRIRGEA	AQIVCS	ASSV	DVNFDFLQ	H	NNTKLAIPQQ SDFHNNRYQK 240
VLTLNLDQVD	FQHAGNYSCV	ASNVQ	GKHST	SMFFRVVESA	YLNLSSEQNL	IQEVTVGEGL 300
NLKVMVEAYP	GLQGFNWTYL	GPFS	DHQP	EP KLANATTKDT	YRHTFTLSLP	RLKPSEAGRY 360
SFLARNPGGW	RALTFFELTLR	YPPEV	SVIWT	FINGSGTLLC	AASGYQPQNV	TWLQCSGHTD 420
RCDEAQVLQV	WDDPYPEVLS	QEPFH	KVTVQ	SLLTVETLEH	NQTYECRAHN	SVSGSGWAFI 480
PISAGATHHP	PDEFLEFTPLI	PPWGW	PGNTL	VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN 540
VPSPAMFFQP	LYSVHNGNFQ	TWMGA	HGAGV	LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA 600
RPWKSVALEE	EQEGPGTRLP	GNLSSSEVL	AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	660
DSEGSRSSSS	SSSSNNNNYC	ALGCGGWHL	SALPGNTQSS	GPIPALACGL	SCDHQGLETO	720
QGVAVVL	AGH CQRPGLHEDL	QGMLLP	SVLS KARSWTFQ	PQ	PQ	PQ
NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGALGE	GPGASPCNQH	840
SPYWAPPCYT	LKPET					855
SEQ ID NO: 137	moltype = AA length = 1092					
FEATURE	Location/Qualifiers					
REGION	1..1092					
	note = MISC_FEATURE - VEGF Receptor 1/IL9R/cGC-F					
source	1..1092					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 137						
SKLKDPELSL	KGTQHIMQAG	QTLHLQ	CRGE	AAHKWSLP	EM VSKESERLSI	TKSACGRNGK 60
QFCSTLTLNT	AQANHTGFYS	CKYLAV	PTSK	KKETESAIYI	FISDTGRPFV	EMYSEIPEII 120
HMTEGRELVI	PCRVTSPNIT	VTLKKF	PLDT	LIPDGKRIIW	DSRKGFIISN	ATYKEIGLLT 180
CEATVNGHLY	KTNYLTHRQT	NTIIDV	QIST	PRPVKLLRGH	TLVLNCTATT	PLNTRVQMTW 240
SYPDEKNKRA	SVRRRIDQSN	SHANIF	YSVL	TIDKMQNKDK	GLYTCRVRSG	PSFKSVNTSV 300
HIYDKAFITV	KHRKQVLET	VAGKRS	YRLS	MKVKAFFSPE	VVWLKDGLPA	TEKSARYLTR 360
GYSLIIDKVT	EEDAGNYTIL	LSIKQS	NVFK	NLTATLIVNV	KPQIYEKAVS	SFPDPALYPL 420
GSRQILTCTA	YGIPQPTIKW	FWHPC	NHNHS	EARCDFCSNN	EESFILDADS	NMGNRIESIT 480
QRMAIIEGKN	KMASTLVVAD	SRISGI	YICI	ASNKVGTVGR	NISFYITDVP	NGFHVNLEKM 540
PTEGEDLKLS	CTVNKFLYRD	VTWILL	RTVN	NRTMHYSISK	QKMAITKEHS	ITLNLTIMNV 600
SLQDSGTYAC	RARNVYTGEE	ILQKKE	ITIR	DQEAPYLLRN	LSDHTVAISS	STTLDCHANG 660
VPEPQITWFK	NNHKIQQEPG	IILGPG	SSTL	FIERVTEEDE	GVYHCKATNQ	KGSVESSAYL 720
TVQGTSDKSN	LELIPPWGW	GNTLV	AVSIF	LLLTGPTYLL	FKLSPRVKRI	FYQNVPSAM 780
FFQPLYSVHN	GNFQTMGAH	GAGVLL	SQDC	AGTPQGALEP	CVQEATAALLT	CGPARPWKSV 840
ALEEEQEGPG	TRLPGNLSSE	DVLPAG	CTEW	RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGSR 900
SSSSSSSSNN	NNYCALGCY	GWHL	SALPGN	TQSSGPIPAL	ACGLSCDHQ	LETQQGVAVV 960
LAGHCQRPGL	HEDLQGMLLP	SVLS	KARSWT	FGGGSGGGG	SGGGGSERTM	PRIPTLKNLE 1020
DLVTEYHGNF	SAWSGVSKGL	AESLQPD	YSE	RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY 1080
WAPPCYTCLKP	ET					1092
SEQ ID NO: 138	moltype = AA length = 1089					
FEATURE	Location/Qualifiers					
REGION	1..1089					
	note = MISC_FEATURE - VEGF Receptor 1/IL9R/cGC-S					
source	1..1089					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 138						
SKLKDPELSL	KGTQHIMQAG	QTLHLQ	CRGE	AAHKWSLP	EM VSKESERLSI	TKSACGRNGK 60
QFCSTLTLNT	AQANHTGFYS	CKYLAV	PTSK	KKETESAIYI	FISDTGRPFV	EMYSEIPEII 120
HMTEGRELVI	PCRVTSPNIT	VTLKKF	PLDT	LIPDGKRIIW	DSRKGFIISN	ATYKEIGLLT 180
CEATVNGHLY	KTNYLTHRQT	NTIIDV	QIST	PRPVKLLRGH	TLVLNCTATT	PLNTRVQMTW 240
SYPDEKNKRA	SVRRRIDQSN	SHANIF	YSVL	TIDKMQNKDK	GLYTCRVRSG	PSFKSVNTSV 300
HIYDKAFITV	KHRKQVLET	VAGKRS	YRLS	MKVKAFFSPE	VVWLKDGLPA	TEKSARYLTR 360
GYSLIIDKVT	EEDAGNYTIL	LSIKQS	NVFK	NLTATLIVNV	KPQIYEKAVS	SFPDPALYPL 420
GSRQILTCTA	YGIPQPTIKW	FWHPC	NHNHS	EARCDFCSNN	EESFILDADS	NMGNRIESIT 480
QRMAIIEGKN	KMASTLVVAD	SRISGI	YICI	ASNKVGTVGR	NISFYITDVP	NGFHVNLEKM 540
PTEGEDLKLS	CTVNKFLYRD	VTWILL	RTVN	NRTMHYSISK	QKMAITKEHS	ITLNLTIMNV 600

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SLQDSGTYAC	RARNVYTGEE	ILQKKEITIR	DQEAPYLLRN	LSDHTVAISS	STTLDCHANG	660
VPEPQITWFK	NNHKIQQEPG	IILGPGSSTL	FIERVTEEDE	GVYHCKATNQ	KGSVESSAYL	720
TVQGTSDKSN	LELIPPWGWP	GNTLVAVSIF	LLLTGPTYLL	FKLSPRVKRI	FYQNVPSAM	780
FFQPLYSVHN	GNFQTMGAH	GAGVLLSQDC	AGTPQGALEP	CVQEATALLT	CGPARPWKSV	840
ALEEEQEGPG	TRLPGNLSSE	DVLPAGCTEW	RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGSR	900
SSSSSSSSNN	NNYCALGCGY	GWHLASALPGN	TQSSGPIPAL	ACGLSCDHQG	LETQQGVAVV	960
LAGHCQRPGL	HEDLQGMLLP	SVLSKARSWT	FQPQPQPQPQ	PQPERTMPRI	PTLKNLEDLV	1020
TEYHGNFSAW	SGVSKGLAES	LQPDYSERLC	LVSEIPPKGG	ALGEGPGASP	CNQHSPLYWAP	1080
PCYTLKPET						1089
SEQ ID NO: 139	moltype = AA length = 1105					
FEATURE	Location/Qualifiers					
REGION	1..1105					
	note = MISC_FEATURE - VEGF Receptor 2/IL9R/cGC-F					
source	1..1105					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 139						
ASVGLPSVSL	DLPRLSIQKD	ILTIKANTTL	QITCRGQRDL	DWLWPNNQSG	SEQRVEVTEC	60
SSDGLFCKTLT	IPKVIGNDTG	AYKCFYRETD	LASVIYVYVQ	DYRSPFIASV	SDQHGVVYIT	120
ENKNKTVVIP	CLGSISNLNV	SLCARYPEKR	FVPDGNRISW	DSKKGFTIPS	YMISYAGMVF	180
CEAKINDESY	QSIMYIVVVV	GYRIYDVVLS	PSHGIELSVG	EKLVLNCTAR	TELVNGIDFN	240
WEYPSSKHQH	KKLVNRDLKT	QSGSEMKKFL	STLTIDGVTR	SDQGLYTCAA	SSGLMTKKNS	300
TFVRVHEKPF	VAFGSGMESL	VEATVGERVR	IPAKYLGYP	PEIKWYKNGI	PLESNHTIKA	360
GHVLTIMEVS	ERDTGNYTVI	LTNPISKEKQ	SHVSVLVVYV	PPQIGEKSLI	SPVDSYQYGT	420
TQTLTCTVYA	IPPPHHIHWY	WQLEEEECANE	PSQAVSVTNP	YPCEEWRSVE	DFQGGNKIEV	480
NKNKQFALIEG	KNKTVSTLVI	QAANVSALYK	CEAVNKVGRG	ERVISFHVTR	GPEITLQPD	540
QPTQESVSL	WCTADRSTFE	NLTWYKLG	PLPIHVGELP	TPVCKNLDTL	WKLNATMFSN	600
STNDILIMEL	KNASLQDQGD	YVCLAQDRKT	KKRHCVVRQL	TVLERVAPTI	TGNLENQTTS	660
IGESIEVSCT	ASGNPPQIM	WFKDNETLVE	DSGIVLKDGN	RNLTIRVRK	EDEGLYTCQA	720
CSVLGCAKVE	AFFIIEGAQE	KTNLELIPPW	GWPGNTLVAV	SIFLLLTGPT	YLLFKLSRV	780
KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	840
LLTCGPARPW	KSVALEEEQE	GPGRTPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	900
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLAS	PGNTQSSGPI	PALACGLSCD	960
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLKAR	SWTFGGGSG	GGGSGGGGSE	1020
RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	1080
GPGASPCNQH	SPYWAPPCYT	LKPET				1105
SEQ ID NO: 140	moltype = AA length = 1102					
FEATURE	Location/Qualifiers					
REGION	1..1102					
	note = MISC_FEATURE - VEGF Receptor 2/IL9R/cGC-S					
source	1..1102					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 140						
ASVGLPSVSL	DLPRLSIQKD	ILTIKANTTL	QITCRGQRDL	DWLWPNNQSG	SEQRVEVTEC	60
SSDGLFCKTLT	IPKVIGNDTG	AYKCFYRETD	LASVIYVYVQ	DYRSPFIASV	SDQHGVVYIT	120
ENKNKTVVIP	CLGSISNLNV	SLCARYPEKR	FVPDGNRISW	DSKKGFTIPS	YMISYAGMVF	180
CEAKINDESY	QSIMYIVVVV	GYRIYDVVLS	PSHGIELSVG	EKLVLNCTAR	TELVNGIDFN	240
WEYPSSKHQH	KKLVNRDLKT	QSGSEMKKFL	STLTIDGVTR	SDQGLYTCAA	SSGLMTKKNS	300
TFVRVHEKPF	VAFGSGMESL	VEATVGERVR	IPAKYLGYP	PEIKWYKNGI	PLESNHTIKA	360
GHVLTIMEVS	ERDTGNYTVI	LTNPISKEKQ	SHVSVLVVYV	PPQIGEKSLI	SPVDSYQYGT	420
TQTLTCTVYA	IPPPHHIHWY	WQLEEEECANE	PSQAVSVTNP	YPCEEWRSVE	DFQGGNKIEV	480
NKNKQFALIEG	KNKTVSTLVI	QAANVSALYK	CEAVNKVGRG	ERVISFHVTR	GPEITLQPD	540
QPTQESVSL	WCTADRSTFE	NLTWYKLG	PLPIHVGELP	TPVCKNLDTL	WKLNATMFSN	600
STNDILIMEL	KNASLQDQGD	YVCLAQDRKT	KKRHCVVRQL	TVLERVAPTI	TGNLENQTTS	660
IGESIEVSCT	ASGNPPQIM	WFKDNETLVE	DSGIVLKDGN	RNLTIRVRK	EDEGLYTCQA	720
CSVLGCAKVE	AFFIIEGAQE	KTNLELIPPW	GWPGNTLVAV	SIFLLLTGPT	YLLFKLSRV	780
KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	840
LLTCGPARPW	KSVALEEEQE	GPGRTPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	900
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLAS	PGNTQSSGPI	PALACGLSCD	960
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLKAR	SWTFQPPQP	QPPQPPTM	1020
PRIPPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	1080
ASPCNQHSPLY	WAPPCYTLKP	ET				1102
SEQ ID NO: 141	moltype = AA length = 1108					
FEATURE	Location/Qualifiers					
REGION	1..1108					
	note = MISC_FEATURE - VEGF Receptor 3/IL9R/cGC-S					
source	1..1108					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 141						
YSMTPTTLNI	TEESHVIDTG	DSLISISCRGQ	HPLEWAWPGA	QEAPATGDKD	SEDGTVVRDC	60
EGTDARPYCK	VLLLHEVHAN	DTGSYVCYK	YIKARIEGTT	AASSYVFVRD	FEQPFINKPD	120

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TLLVNRKDAM	WVPCLVSIPG	LNVTILRSQSS	VLWPDGQEVV	WDDRRGMLVS	TPLLHDALYL	180
QCETTWGDQD	FLSNPFLVHI	TGNELYDIQL	LPRKSLELLV	GEKLVLNCTV	WAEFNsgvTF	240
DWDYPGKQAE	RGKWVPERRS	QQTHTELSSI	LTIHNVSQHD	LGSYVCKANN	GIQRFRESTE	300
VIVHENPFIS	VEWLKGPIL	ATAGDELVKL	PVKLAAYPPP	EFQWYKDGA	LSGRHSPHAL	360
VLKEVTEAST	GTYTALWNS	AAGLRRNISL	ELVVNVPPQI	HEKEASSPSI	YSRHSRQALT	420
CTAYGVPLPL	SIQWHWRPWT	PCKMFAQRSL	RRRQQQDLMP	QCRDWRAVTT	QDAVNPIESL	480
DTWTEFVEGK	NKTVSKLVIQ	NANVSAMYKC	VVSNNKVGQDE	RLIYFYVTTI	PDGFTIESKP	540
SEELLEGQPV	LLSCQADS	YEHLRWYRLN	LSTLHDAHGN	PLLLDCKNVH	LFATPLAASL	600
EEVAPGARHA	TLSLSIPRVA	PEHEGHYVCE	VQDRRSHDKH	CHKKYLsvQA	LEAPRLTQNL	660
TDLLVNVSDS	LEMQCLVAGA	HAPSIVWYKD	ERLLEEKSGV	DLADSNQKLS	IQRVREEDAG	720
RYLCSVCNAK	GCVNSSASVA	VEGSEDKGS	ELIPPGWPG	NTLVAVSIFL	LLTGPTYLLF	780
KLSPRVKRIF	YQNVSPAMF	FQPLYSVHNG	NFQTWGAHG	AGVLLSQDCA	GTPQGALEPC	840
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSS	VLPAAGCTEWR	VQTLAYLPQE	900
DWAPTSLTRP	APPDSEGSRS	SSSSSSNNN	NYCALGCYGG	WHLsalpgNT	QSSGPIPALA	960
CGLSCDHQGL	ETQQGVAVL	AGHCQRPLGH	EDLQGMLLPS	VLSKARSWTF	QPPQPPQPPQ	1020
QPERTMPRIP	TLKNLEDLVT	EYHGNFSAWS	GVSGLAESL	QPDYSERLCL	VSEIPPKGGA	1080
LGEFGASPC	NQHSPYWAPP	CYTLPKET				1108
SEQ ID NO: 142	moltype = AA length = 1111					
FEATURE	Location/Qualifiers					
REGION	1..1111					
	note = MISC_FEATURE - VEGF Receptor 3/IL9R/cGC-F					
source	1..1111					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 142						
YSMTPTLNI	TEESHVIDTG	DSLSISCRGQ	HLEWAWPGA	QEAPATGDKD	SEDtGVVRDC	60
EGTDARPYCK	VLLLHEVHAN	DTGSYVCYYK	YIKARIEGTT	AASSYVFVRD	FEQPFINKPD	120
TLLVNRKDAM	WVPCLVSIPG	LNVTILRSQSS	VLWPDGQEVV	WDDRRGMLVS	TPLLHDALYL	180
QCETTWGDQD	FLSNPFLVHI	TGNELYDIQL	LPRKSLELLV	GEKLVLNCTV	WAEFNsgvTF	240
DWDYPGKQAE	RGKWVPERRS	QQTHTELSSI	LTIHNVSQHD	LGSYVCKANN	GIQRFRESTE	300
VIVHENPFIS	VEWLKGPIL	ATAGDELVKL	PVKLAAYPPP	EFQWYKDGA	LSGRHSPHAL	360
VLKEVTEAST	GTYTALWNS	AAGLRRNISL	ELVVNVPPQI	HEKEASSPSI	YSRHSRQALT	420
CTAYGVPLPL	SIQWHWRPWT	PCKMFAQRSL	RRRQQQDLMP	QCRDWRAVTT	QDAVNPIESL	480
DTWTEFVEGK	NKTVSKLVIQ	NANVSAMYKC	VVSNNKVGQDE	RLIYFYVTTI	PDGFTIESKP	540
SEELLEGQPV	LLSCQADS	YEHLRWYRLN	LSTLHDAHGN	PLLLDCKNVH	LFATPLAASL	600
EEVAPGARHA	TLSLSIPRVA	PEHEGHYVCE	VQDRRSHDKH	CHKKYLsvQA	LEAPRLTQNL	660
TDLLVNVSDS	LEMQCLVAGA	HAPSIVWYKD	ERLLEEKSGV	DLADSNQKLS	IQRVREEDAG	720
RYLCSVCNAK	GCVNSSASVA	VEGSEDKGS	ELIPPGWPG	NTLVAVSIFL	LLTGPTYLLF	780
KLSPRVKRIF	YQNVSPAMF	FQPLYSVHNG	NFQTWGAHG	AGVLLSQDCA	GTPQGALEPC	840
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSS	VLPAAGCTEWR	VQTLAYLPQE	900
DWAPTSLTRP	APPDSEGSRS	SSSSSSNNN	NYCALGCYGG	WHLsalpgNT	QSSGPIPALA	960
CGLSCDHQGL	ETQQGVAVL	AGHCQRPLGH	EDLQGMLLPS	VLSKARSWTF	GGGSGGGGS	1020
GGGGSERTMP	RIPTLKNLE	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	1080
GGALGEGPGA	SPCNQHSPYW	APPCYTLPKE	T			1111
SEQ ID NO: 143	moltype = AA length = 463					
FEATURE	Location/Qualifiers					
REGION	1..463					
	note = MISC_FEATURE - Activin R1A ectodomain/IL9R/cGC-F					
source	1..463					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 143						
MEDEKPKVNP	KLYMCVCEGL	SCGNEDHCEG	QQCFSSLSIN	DGFHVYQKGC	FQVYEQGKMT	60
CKTPPSPGQA	VECCQGDWCN	RNITAQLPTK	GKSFPGTQNF	HLELIPPWGW	PGNTLVAVSI	120
FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	HGAGVLLSQD	180
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	240
WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHLsalPG	300
NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRPG	LHEDLQGMLL	PSVLSKARSW	360
TFGGGSGGGG	GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG	LAESLQPDYS	420
ERLCLVSEIP	PKGGALGEGP	GASPCNQHSP	YWAPPCYTLP	PET		463
SEQ ID NO: 144	moltype = AA length = 460					
FEATURE	Location/Qualifiers					
REGION	1..460					
	note = MISC_FEATURE - Activin R1A ectodomain/IL9R/cGC-S					
source	1..460					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 144						
MEDEKPKVNP	KLYMCVCEGL	SCGNEDHCEG	QQCFSSLSIN	DGFHVYQKGC	FQVYEQGKMT	60
CKTPPSPGQA	VECCQGDWCN	RNITAQLPTK	GKSFPGTQNF	HLELIPPWGW	PGNTLVAVSI	120
FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	HGAGVLLSQD	180
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	240
WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHLsalPG	300

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NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGM	PSVLSKARS	360
TFQPQPQP	QPQPERTMPR	IPTLKNLE	DLVTEYHGNF	WSGVSKGLAE	SLQPDYSERL	420
CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET			460
SEQ ID NO: 145	moltype = AA length = 463					
FEATURE	Location/Qualifiers					
REGION	1..463					
	note = MISC_FEATURE - Activin R1B ectodomain/IL9R/cGC-F					
source	1..463					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 145						
SSGPRGVQALL	CACTSCLQAN	YTCETDGACM	VSIFNLDGME	HHVRTCIPKV	ELVPAGKPFY	60
CLSSDLRNT	HCCYTDYCN	IDLRVPSGHL	KEPEHPSMWG	PVELIPPWGW	PGNTLVAVSI	120
FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	HGAGVLLSQD	180
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	240
WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSN	NNNYCALGCY	GGWHL	300
NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGM	PSVLSKARS	360
TFGGGSGGG	GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG	LAESLQPDYS	420
ERLCLVSEIP	PKGALGEGP	GASPCNQHSP	YWAPPCYTLK	PET		463
SEQ ID NO: 146	moltype = AA length = 460					
FEATURE	Location/Qualifiers					
REGION	1..460					
	note = MISC_FEATURE - Activin R1B ectodomain/IL9R/cGC-S					
source	1..460					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 146						
SSGPRGVQALL	CACTSCLQAN	YTCETDGACM	VSIFNLDGME	HHVRTCIPKV	ELVPAGKPFY	60
CLSSDLRNT	HCCYTDYCN	IDLRVPSGHL	KEPEHPSMWG	PVELIPPWGW	PGNTLVAVSI	120
FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	HGAGVLLSQD	180
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	240
WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSN	NNNYCALGCY	GGWHL	300
NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGM	PSVLSKARS	360
TFQPQPQP	QPQPERTMPR	IPTLKNLE	DLVTEYHGNF	WSGVSKGLAE	SLQPDYSERL	420
CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET			460
SEQ ID NO: 147	moltype = AA length = 452					
FEATURE	Location/Qualifiers					
REGION	1..452					
	note = MISC_FEATURE - Activin R1C ectodomain/IL9R/cGC-F					
source	1..452					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 147						
LSPGLKCVCL	LCDSSNFTCQ	TEGACWASVM	LTNGKEQVIK	SCVSLPELNA	QVFCHSSNNV	60
TKTECCFTDF	CNNITLHLPT	ASPNAPKLGP	MELIPPWGW	GNTLVAVSIF	LLLTGPTYLL	120
FKLSPRVKRI	FYQNVPSAM	FFQPLYSVHN	GNFQTMGAH	GAGVLLSQDC	AGTPQGALEP	180
CVQEATALLT	CGPARPWKSV	ALEEEQEGPG	TRLPGNLSSE	DVLPAGCTEW	RVQTLAYLPQ	240
EDWAPTSLTR	PAPPDSEGS	SSSSSSSN	NNYCALGCY	GWHL	300	
ACGLSCDHQ	LETQQGVAV	LAGHCQRPGL	HEDLQGM	SVLSKARS	FGGGSGGGG	360
SGGGGSERTM	PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP	420
KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET			452
SEQ ID NO: 148	moltype = AA length = 449					
FEATURE	Location/Qualifiers					
REGION	1..449					
	note = MISC_FEATURE - Activin R1C ectodomain/IL9R/cGC-S					
source	1..449					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 148						
LSPGLKCVCL	LCDSSNFTCQ	TEGACWASVM	LTNGKEQVIK	SCVSLPELNA	QVFCHSSNNV	60
TKTECCFTDF	CNNITLHLPT	ASPNAPKLGP	MELIPPWGW	GNTLVAVSIF	LLLTGPTYLL	120
FKLSPRVKRI	FYQNVPSAM	FFQPLYSVHN	GNFQTMGAH	GAGVLLSQDC	AGTPQGALEP	180
CVQEATALLT	CGPARPWKSV	ALEEEQEGPG	TRLPGNLSSE	DVLPAGCTEW	RVQTLAYLPQ	240
EDWAPTSLTR	PAPPDSEGS	SSSSSSSN	NNYCALGCY	GWHL	300	
ACGLSCDHQ	LETQQGVAV	LAGHCQRPGL	HEDLQGM	SVLSKARS	FQPQPQPQP	360
PQPERTMPRI	PTLKNLE	TEYHGNFSAW	SGVSKGLAES	LQPDYSERLC	LVSEIPPKGG	420
ALGEGPGASP	CNQHSPYWAP	PCYTLKPET				449
SEQ ID NO: 149	moltype = AA length = 479					
FEATURE	Location/Qualifiers					
REGION	1..479					
	note = MISC_FEATURE - Activin R2B ectodomain/IL9R/cGC-F					

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source	1..479				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 149					
SGRGEAETRE	CIYYNANWEL	ERTNQSGLER	CEGEQDKRLH	CYASWRNSSG	TIELVKKGCW 60
LDDDFNCYDRQ	ECVATEENPQ	VYFCCCEGNF	CNERFTHLPE	AGGPEVTYEP	PPTAPTLLTL 120
IPPWGWPGNT	LVAVSIFLLL	TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ	PLYSVHNGNF 180
QTWMGAHGAG	VLLSQDCAGT	PQGALEPCVQ	EATALLTCGP	ARPWKSVALE	EEQEGPGTRL 240
PGNLSSSEDL	PAGCTEWRVQ	TLAYLPQEDW	APTSLTRPAP	PDSEGSRSSS	SSSSSNNNNY 300
CALGCYGGWH	LSALPGNTQS	SGPIPALACG	LSCDHQGLT	QQGVAVVLAG	HCQRPGLHED 360
LQGMLLPSVL	SKARSWTFGG	GGSGGGGSGG	GGSERTMPRI	PTLKNLEDLV	TEYHGNFSAW 420
SGVSKGLAES	LQPDYSERLC	LVSEIPPKGG	ALGEGPGASP	CNQHSPYWAP	PCYTLPKET 479
SEQ ID NO: 150	moltype = AA length = 476				
FEATURE	Location/Qualifiers				
REGION	1..476				
	note = MISC_FEATURE - Activin R2B ectodomain/IL9R/cGC-S				
source	1..476				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 150					
SGRGEAETRE	CIYYNANWEL	ERTNQSGLER	CEGEQDKRLH	CYASWRNSSG	TIELVKKGCW 60
LDDDFNCYDRQ	ECVATEENPQ	VYFCCCEGNF	CNERFTHLPE	AGGPEVTYEP	PPTAPTLLTL 120
IPPWGWPGNT	LVAVSIFLLL	TGPTYLLFKL	SPRVKRIFYQ	NVPSPAMFFQ	PLYSVHNGNF 180
QTWMGAHGAG	VLLSQDCAGT	PQGALEPCVQ	EATALLTCGP	ARPWKSVALE	EEQEGPGTRL 240
PGNLSSSEDL	PAGCTEWRVQ	TLAYLPQEDW	APTSLTRPAP	PDSEGSRSSS	SSSSSNNNNY 300
CALGCYGGWH	LSALPGNTQS	SGPIPALACG	LSCDHQGLT	QQGVAVVLAG	HCQRPGLHED 360
LQGMLLPSVL	SKARSWTFQP	QPQPQPQPQP	ERTMPRIPTL	KNLEDLVTEY	HGNFSAWSGV 420
SKGLAESLQP	DYSERLCLVS	EIPPKGGALG	EGPGASPCNQ	HSPYWAPPCY	TLKPET 476
SEQ ID NO: 151	moltype = AA length = 476				
FEATURE	Location/Qualifiers				
REGION	1..476				
	note = MISC_FEATURE - Activin R2A ectodomain/IL9R/cGC-F				
source	1..476				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 151					
AILGRSETQE	CLFFNANWEK	DRTNQTGVEP	CYGDKDKRRH	CFATWKNISG	SIEIVKQGCW 60
LDDINCYDRT	DCVEKKDSPE	VYFCCCEGNM	CNEKFSYFPE	MEVTQPTSNP	VTPKPPLIPP 120
WGWPGNTLVA	VSIFLLLTGP	TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW 180
MGAHGAGVLL	SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN 240
LSSEDLVPAG	CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNNYCAL 300
GCYGGWHLSA	LPGNTQSSGP	IPALACGLSC	DHQGLETTQQG	VAWVLAGHCQ	RPGLHEDLQG 360
MLLPSVLSKA	RSWTFGGGGS	GGGGSGGGGS	ERTMPRIPTL	KNLEDLVTEY	HGNFSAWSGV 420
SKGLAESLQP	DYSERLCLVS	EIPPKGGALG	EGPGASPCNQ	HSPYWAPPCY	TLKPET 476
SEQ ID NO: 152	moltype = AA length = 473				
FEATURE	Location/Qualifiers				
REGION	1..473				
	note = MISC_FEATURE - Activin R2A ectodomain/IL9R/cGC-S				
source	1..473				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 152					
AILGRSETQE	CLFFNANWEK	DRTNQTGVEP	CYGDKDKRRH	CFATWKNISG	SIEIVKQGCW 60
LDDINCYDRT	DCVEKKDSPE	VYFCCCEGNM	CNEKFSYFPE	MEVTQPTSNP	VTPKPPLIPP 120
WGWPGNTLVA	VSIFLLLTGP	TYLLFKLSPR	VKRIFYQNVP	SPAMFFQPLY	SVHNGNFQTW 180
MGAHGAGVLL	SQDCAGTPQG	ALEPCVQEAT	ALLTCGPARP	WKSVALEEEQ	EGPGTRLPGN 240
LSSEDLVPAG	CTEWRVQTLA	YLPQEDWAPT	SLTRPAPPDS	EGSRSSSSSS	SSNNNNNYCAL 300
GCYGGWHLSA	LPGNTQSSGP	IPALACGLSC	DHQGLETTQQG	VAWVLAGHCQ	RPGLHEDLQG 360
MLLPSVLSKA	RSWTFQPQPQ	PQPQPQPPT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG 420
LAESLQPDYS	ERLCLVSEIP	PKGGLGEGP	GASPCNQHSP	YWAPPCYTLK	PET 473
SEQ ID NO: 153	moltype = AA length = 574				
FEATURE	Location/Qualifiers				
REGION	1..574				
	note = MISC_FEATURE - IL10R-alpha/IL9R/cGC-F				
source	1..574				
	mol_type = protein				
	organism = synthetic construct				
SEQUENCE: 153					
HGTELPSPPS	VWFEEFFHH	ILHWTPIPNO	SESTCYEVAL	LRYGIESWNS	ISNCSQTLSY 60
DLTAVTLDLY	HSNGYRARVR	AVDGSRHSNW	TVTNTRFSVD	EVTLTVGSVN	LEIHNGFILG 120
KIQLPRPKMA	PANDTYESIF	SHFREYEIAI	RKVPGNFTFT	HKKVKHENFS	LLTSGEVGEF 180
CVQVKPSVAS	RSNKGWWSKE	ECISLTRQYF	TVTNLIPPWG	WPGNTLVAVS	IFLLLTGPTY 240

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LLFKLSPRVK	RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	300
EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	360
PQEDWAPTS	TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	420
ALACGLSCDH	QGLETOQGV	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTFGGGSGG	480
GGSGGGGSR	TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	540
PPKGGALGEG	PGASPCNQHS	PYWAPPCYTL	KPET			574
SEQ ID NO: 154	moltype = AA length = 571					
FEATURE	Location/Qualifiers					
REGION	1..571					
	note = MISC_FEATURE - IL10R-alpha/IL9R/cGC-S					
source	1..571					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 154						
HGTELPSPPS	VWFEEFFHH	ILHWTPIPNQ	SESTCYEVAL	LRYGIESWNS	ISNCSQTL	60
DLTAVTLDLY	HSNGYRVR	AVDGSRHSNW	TVTNTFRSVD	EVTLTVGSVN	LEIHNGFILG	120
KIQLPRPKMA	PANDTYESIF	SHFREYEIAI	RKVPGNFTFT	HKKVKHENFS	LLTSGEVGEF	180
CVQVKPSVAS	RSNKGMSKE	ECISLTRQYF	TVTNLIPPWG	WPGNTLVAVS	IFLLLTGPTY	240
LLFKLSPRVK	RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	300
EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	360
PQEDWAPTS	TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	420
ALACGLSCDH	QGLETOQGV	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTFQPPQPQ	480
PQPQPERTMP	RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	540
GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	T			571
SEQ ID NO: 155	moltype = AA length = 504					
FEATURE	Location/Qualifiers					
REGION	1..504					
	note = MISC_FEATURE - TGFBR2 ectodomain/IL9R/cGC-F					
source	1..504					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 155						
TIPPHVQKSV	NNDMIVTDNN	GAVKFPQLCK	FCDVRFSTCD	NQKSCMSNCS	ITSICEKPQE	60
VVCVAVWRKND	ENITLETVCH	DPKLPYHDFI	LEDAASPKCI	MKEKKKPGET	FFMCSCSSDE	120
CNDNIIFSEE	YNTSNPDLLL	VIFQLIPPWG	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	180
RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	240
LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTS	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	ALACGLSCDH	360
QGLETOQGV	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTFGGGSGG	GGSGGGGSR	420
TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	480
PGASPCNQHS	PYWAPPCYTL	KPET				504
SEQ ID NO: 156	moltype = AA length = 501					
FEATURE	Location/Qualifiers					
REGION	1..501					
	note = MISC_FEATURE - TGFBR2 ectodomain/IL9R/cGC-S					
source	1..501					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 156						
TIPPHVQKSV	NNDMIVTDNN	GAVKFPQLCK	FCDVRFSTCD	NQKSCMSNCS	ITSICEKPQE	60
VVCVAVWRKND	ENITLETVCH	DPKLPYHDFI	LEDAASPKCI	MKEKKKPGET	FFMCSCSSDE	120
CNDNIIFSEE	YNTSNPDLLL	VIFQLIPPWG	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	180
RIFYQNVPS	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	240
LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	PQEDWAPTS	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	ALACGLSCDH	360
QGLETOQGV	WVLAGHCQRP	GLHEDLQGM	LPSVLSKARS	WTFQPPQPQ	PQPQPERTMP	420
RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	480
SPCNQHSPYW	APPCYTLKPE	T				501
SEQ ID NO: 157	moltype = AA length = 453					
FEATURE	Location/Qualifiers					
REGION	1..453					
	note = MISC_FEATURE - TGFBR1 ectodomain/IL9R/cGC-F					
source	1..453					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 157						
LQCFCHLCTK	DNFTCVTDGL	CFVSVTETTD	KVIHNSMCIA	EIDLIPRDRP	FVCAPSSKTG	60
SVTTTYCCNQ	DHCNKIELPT	TVKSSPGLGP	VELLIPPWGW	PGNTLVAVSI	FLLLTGPTYL	120
LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMWGA	HGAGVLLSQD	CAGTPQGALE	180
PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	WRVQTLAYLP	240
QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHLALPG	NTQSSGPIPA	300
LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP	LHEDLQGM	PSVLSKARSW	TFGGGGSGGG	360

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GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG	LAESLQPDYS	ERLCLVSEIP	420
PKGALGEGP	GASPCNQHSP	YWAPPCYTLK	PET			453
SEQ ID NO: 158	moltype = AA length = 450					
FEATURE	Location/Qualifiers					
REGION	1..450					
	note = MISC_FEATURE - TGFBR1 ectodomain/IL9R/cGC-S					
source	1..450					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 158						
LQCFCHLCTK	DNFTCVTDGL	CFVSVTETTD	KVIHNSMCIA	EIDLIPRDRP	FVCAPSSKTG	60
SVTTTYCCNQ	DHCNKIELPT	TVKSSPGLGP	VELLIPPWGW	PGNTLVAVSI	FLLLTGPTYL	120
LFKLSPRVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQTMGA	HGAGVLLSQD	CAGTPQGALE	180
PCVQEATALL	TCGPAPPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	WRVQTLAYLP	240
QEDWAPTSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCV	GGWHLASALPG	NTQSSGPIPA	300
LACGLSCDHQ	GLETQQGVAV	VLAGHCQRPQ	LHEDLQGMLL	PSVLSKARSW	TFQPQPQPQP	360
QPQPERTMPR	IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	420
GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET				450
SEQ ID NO: 159	moltype = AA length = 480					
FEATURE	Location/Qualifiers					
REGION	1..480					
	note = MISC_FEATURE - TIGIT/IL9R/cGC-F					
source	1..480					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 159						
MMTGTIETT	G	ILQCHLSSTT	AQVTQVNWEQ	QDQLLAICNA	DLGWHISPSF	60
KDRVAPGPGL	GLTLQSLTVN	DTGEYFCIYH	TYPDGYTGR	IFLEVLESSV	AEHGARFQIP	120
LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	QNVPSAMFF	QPLYSVHNGN	180
FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	240
LPGNLSSDV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	PPDSEGRSS	SSSSSSNNNN	300
YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	360
DLQGMLLPSV	LSKARSWTFG	GGGSGGGSG	GGGSERTMPR	IPTLKNLEDL	VTEYHGNFSA	420
WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET	480
SEQ ID NO: 160	moltype = AA length = 477					
FEATURE	Location/Qualifiers					
REGION	1..477					
	note = MISC_FEATURE - TIGIT/IL9R/cGC-S					
source	1..477					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 160						
MMTGTIETT	G	ILQCHLSSTT	AQVTQVNWEQ	QDQLLAICNA	DLGWHISPSF	60
KDRVAPGPGL	GLTLQSLTVN	DTGEYFCIYH	TYPDGYTGR	IFLEVLESSV	AEHGARFQIP	120
LIPPWGWPGN	TLVAVSIFLL	LTGPTYLLFK	LSPRVKRIFY	QNVPSAMFF	QPLYSVHNGN	180
FQTMGAHGA	GVLLSQDCAG	TPQGALEPCV	QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	240
LPGNLSSDV	LPAGCTEWRV	QTLAYLPQED	WAPTSLTRPA	PPDSEGRSS	SSSSSSNNNN	300
YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	360
DLQGMLLPSV	LSKARSWTFQ	PQPQPQPQPQ	PERTMPRIPT	LKNLEDLVTE	YHGNFSAWSG	420
VSKGLAESLQ	PDYSERLCLV	SEIPPKGAL	GEGPGASPCN	QHSPYWAPPC	YTLKPET	477
SEQ ID NO: 161	moltype = AA length = 535					
FEATURE	Location/Qualifiers					
REGION	1..535					
	note = MISC_FEATURE - FCGR2B/IL9R/cGC-F					
source	1..535					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 161						
TPAAPPKAVL	KLEPQWINVL	QEDSVTLTCR	GTHSPESDSI	QWFHNGNLIP	THTQPSYRFK	60
ANNDSGEYT	CQTGQTSLS	PVHLTVLSEW	LVLQTPHLEF	QEGETIVLRC	HSWKDKPLVK	120
VTFFQNGKSK	KFSRSDPNFS	IPQANHSHSG	DYHCTGNIGY	TLYSSKPVTI	TVQAPLIPPW	180
GWPGNTLVAV	SIFLLLTGPT	YLLFKLSPRV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTMW	240
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPAPPW	KSVALEEEQE	GPGTRLPGNL	300
SSDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	360
CYGGWHLAS	PGNTQSSGPI	PALACGLSCD	HQGLETQQGV	AWVLAGHCQR	PGLHEDLQGM	420
LLPSVLKAR	SWTFGGGGSG	GGGSGGGGSE	RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	480
KGLAESLQPD	YSERLCLVSE	IPPKGALGE	GPGASPCNQH	SPYWAPPCYT	LKPET	535
SEQ ID NO: 162	moltype = AA length = 532					
FEATURE	Location/Qualifiers					
REGION	1..532					
	note = MISC_FEATURE - FCGR2B/IL9R/cGC-S					

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source	1..532					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 162						
TPAAPPKAVL	KLEPQWINVL	QEDSVTLTCR	GTHSPESDSI	QWFHNGNLIP	THTQPSYRFK	60
ANNNDSGEYT	CQTGQTSLS	PVHLTVLSEW	LVLQTPHLEF	QEGETIVLRC	HSWKDKPLVK	120
VTFFQNGKSK	KFSRSDPNFS	IPQANHSHSG	DYHCTGNIGY	TLYSSKPVTI	TVQAPLIPPW	180
GWPGNTLVAV	SIFLLLTGPT	YLLFKLSRPV	KRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	240
GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	LLTCGPARPW	KSVALEEEQE	GPGTRLPGNL	300
SSSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	LTRPAPPDSE	GSRSSSSSSS	SNNNNNYCALG	360
CYGGWHLALS	PGNTQSSGPI	PALACGLSCD	HQGLETQQGV	AWVLAGHCQR	PGLHEDLQGM	420
LLPSVLSKAR	SWTFQPQPQP	QPQPQPERTM	PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	480
AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP	ET	532
SEQ ID NO: 163	moltype = AA length = 637					
FEATURE	Location/Qualifiers					
REGION	1..637					
	note = MISC_FEATURE - FCGR1/IL9R/cGC-F					
source	1..637					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 163						
QVDTTKAVIT	LQPPWVSVFQ	EETVTLHCEV	LHLPGSSSTQ	WFLNGTATQT	STPSYRITSA	60
SVNDSGEYRC	QRGLSGRSDP	IQLEIHRGWL	LLQVSSRVFT	EGEPLALRCH	AWKDKLVYNV	120
LYYRNGKAFK	FFHWNSNLTI	LKTNISHNGT	YHCSGMGKHR	YTSAGISVTV	KELFPAPVLN	180
ASVTSPLLEG	NLVTLSCE	LLLQRPGLQL	YFSFYMGSKT	LRGRNTSSEY	QILTARREDS	240
GLYWCEAATE	DGNVLKRSPE	LELQVLGLQL	PTPVWFHLIP	PWGWP	AVSIFLLLTG	300
PTYLLFKLSP	RVKRIFYQNV	PSPAMFFQPL	YSVHNGNFQT	WMGAHGAGVL	LSQDCAGTPQ	360
GALEPCVQEA	TALLTCGPAR	PWKSVALEEE	QEGPGTRLPG	NLSSSEDVLP	GCTEWRVQTL	420
AYLPQEDWAP	TSLTRPAPPD	SEGSRSSSSS	SSSNNNNNYCA	LG	ALPGNTQSSG	480
PIPALACGLS	CDHQGLETQQ	GVAWVL	QRPGLHEDLQ	GMLLPSVLSK	ARSWTFGGGG	540
SGGGGSGGGG	SERTMPRIPT	LKNLEDLVTE	YHGNFSAWSG	VSKGLAESLQ	PDYSERLCLV	600
SEIPPKGGAL	GEGPGASPCN	QHSPYWAPPC	YTLKPET			637
SEQ ID NO: 164	moltype = AA length = 634					
FEATURE	Location/Qualifiers					
REGION	1..634					
	note = MISC_FEATURE - FCGR1/IL9R/cGC-S					
source	1..634					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 164						
QVDTTKAVIT	LQPPWVSVFQ	EETVTLHCEV	LHLPGSSSTQ	WFLNGTATQT	STPSYRITSA	60
SVNDSGEYRC	QRGLSGRSDP	IQLEIHRGWL	LLQVSSRVFT	EGEPLALRCH	AWKDKLVYNV	120
LYYRNGKAFK	FFHWNSNLTI	LKTNISHNGT	YHCSGMGKHR	YTSAGISVTV	KELFPAPVLN	180
ASVTSPLLEG	NLVTLSCE	LLLQRPGLQL	YFSFYMGSKT	LRGRNTSSEY	QILTARREDS	240
GLYWCEAATE	DGNVLKRSPE	LELQVLGLQL	PTPVWFHLIP	PWGWP	AVSIFLLLTG	300
PTYLLFKLSP	RVKRIFYQNV	PSPAMFFQPL	YSVHNGNFQT	WMGAHGAGVL	LSQDCAGTPQ	360
GALEPCVQEA	TALLTCGPAR	PWKSVALEEE	QEGPGTRLPG	NLSSSEDVLP	GCTEWRVQTL	420
AYLPQEDWAP	TSLTRPAPPD	SEGSRSSSSS	SSSNNNNNYCA	LG	ALPGNTQSSG	480
PIPALACGLS	CDHQGLETQQ	GVAWVL	QRPGLHEDLQ	GMLLPSVLSK	ARSWTFQPQP	540
QPQPQPQPER	TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	600
PPKGGALGEG	PGASPCNQHS	PYWAPPCYTL	KPET			634
SEQ ID NO: 165	moltype = AA length = 568					
FEATURE	Location/Qualifiers					
REGION	1..568					
	note = MISC_FEATURE - 2B4/IL9R/cCG-F					
source	1..568					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 165						
CQGSADHVVS	ISGVPLQLQP	NSIQTKVDSI	AWKKLLPSQN	GFHHILKWEN	GSLPSNTSND	60
RFSFIVKNLS	LLIKAAQQQD	SGLYCLEVTS	ISGKVQTATF	QVFVFESLLP	DKVEKPRLQG	120
QGKILDRGRC	QVALSCLVSR	DGNVSYAWYR	GSKLIQTAGN	LTYLDEEVDI	NGTHTYTCNV	180
SNPVSWESHT	LNLTDQCQNA	HQEFRFWPLI	PPWGWP	VAVSIFLLLT	GPTYLLFKLS	240
PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLS	QGALEPCVQE	300
ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP	GNLSS	AGCTEWRVQT	LAYLPQEDWA	360
PTSLTRPAPP	DSEGSRSSSS	SSSSNNNNNYC	ALG	GI	PIPALACGL	420
SCDHQGLTQ	QGVAVVLAGH	CQRPGLHEDL	QGM	KAR	SGGGGSGGGG	480
GSERTMPRIIP	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	540
LGEGPGASPC	NQHSPYWAPP	CYTLKPET				568
SEQ ID NO: 166	moltype = AA length = 565					
FEATURE	Location/Qualifiers					
REGION	1..565					

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source		note = MISC_FEATURE - 2B4/IL9R/cCG-S				
		1..565				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 166						
CQGSADHVVS	ISGVPLQLQP	NSIQTKVDSI	AWKKLLPSQN	GFHHILKWEN	GSLPSNTSND	60
RFRSFIVKNLS	LLIKAAQQQD	SGLYCLEVTS	ISGKVQTATF	QVVFVFESLLP	DKVEKPRLQG	120
QKGILDRGRC	QVALSCLVSR	DGNVSYAWYR	GSKLIQTAGN	LTYLDEEVDI	NGTHTYTCNV	180
SNPVSWESHT	LNLTDQCQNA	HQEFRFWPLI	PPWGWPGNTL	VAVSIFLLLT	GPTYLLFKLS	240
PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	LLSQDCAGTP	QGALEPCVQE	300
ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP	GNLSSDEVLP	AGCTEWRVQT	LAYLPQEDWA	360
PTSLTRPAPP	DSEGRSSSSS	SSSSNNNNYC	ALGCYGGWHL	SALPGNTQSS	GPIPALACGL	420
SCDHQGLETQ	QGVAVVLAGH	CQRPGLHEDL	QGMLLPSVLS	KARSWTFQPQ	PQPQPQPQPE	480
RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	540
GPGASPCNQH	SPYWAPPCYT	LKPET				565
SEQ ID NO: 167		moltype = AA length = 504				
FEATURE		Location/Qualifiers				
REGION		1..504				
		note = MISC_FEATURE - LAIR1/IL9R/cGC-F				
source		1..504				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 167						
QEEDLPRPSI	SAEPGTVIPL	GSHVTFVCRG	PVGVTQFRLE	RESRSTYNDT	EDVSQASPSE	60
SEARFRIDSV	SEGNAGPYRC	IYYKPPKWSE	QSDYLELLVK	ETSGGPDSPD	TEPGSSAGPT	120
QRPSDNSHNE	HAPASQGLKA	EHLYLIPWP	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	180
RIFYQNVPS	AMFFQPLYS	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	240
LTCGPAPRWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	EWRVQTLAYL	PQEDWAPTS	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	ALACGLSCDH	360
QGLETOQGVA	WVLAGHCQRP	GLHEDLQGML	LPSVLSKARS	WTFGGGGSGG	GGSGGGGSGR	420
TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	480
PGASPCNQHS	PYWAPPCYTL	KPET				504
SEQ ID NO: 168		moltype = AA length = 501				
FEATURE		Location/Qualifiers				
REGION		1..501				
		note = MISC_FEATURE - LAIR1/IL9R/cGC-S				
source		1..501				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 168						
QEEDLPRPSI	SAEPGTVIPL	GSHVTFVCRG	PVGVTQFRLE	RESRSTYNDT	EDVSQASPSE	60
SEARFRIDSV	SEGNAGPYRC	IYYKPPKWSE	QSDYLELLVK	ETSGGPDSPD	TEPGSSAGPT	120
QRPSDNSHNE	HAPASQGLKA	EHLYLIPWP	WPGNTLVAVS	IFLLLTGPTY	LLFKLSPRVK	180
RIFYQNVPS	AMFFQPLYS	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	EPCVQEATAL	240
LTCGPAPRWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	EWRVQTLAYL	PQEDWAPTS	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHLALP	GNTQSSGPIP	ALACGLSCDH	360
QGLETOQGVA	WVLAGHCQRP	GLHEDLQGML	LPSVLSKARS	WTFQPPQPQ	PQPQPPTMP	420
RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	480
SPCNQHSPYW	APPCYTLKPE	T				501
SEQ ID NO: 169		moltype = AA length = 708				
FEATURE		Location/Qualifiers				
REGION		1..708				
		note = MISC_FEATURE - CD5/IL-9R/cGC-F				
source		1..708				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 169						
RLSWYDPDFQ	ARLTRSNSKC	QGQLEVYLKD	GWHMVCSQSW	GRSSKQWEDP	SQASKVCQRL	60
NCGVPLSLGP	FLVYTPQSS	IICYGQLGSF	SNCSSHRNDM	CHSLGLTCL	PQKTTPTTTR	120
PPPTTTTPEPT	APPRLQLVAQ	SGGQHCAGVV	EFYSGSLGGT	ISYEAQDKTQ	DLENFLCNNL	180
QCGSFLKHL	ETEAGRAQDP	GEPREHQPLP	IQWKIQNSSC	TSLEHCFRKI	KPQKSGRVLA	240
LLCSGFQPKV	QSRLVGGSSI	CEGTVEVRQG	AQWAALCDSS	SARSSLRWEE	VCREQQCGSV	300
NSYRVLDAGD	PTSRGLFCPH	QKLSQCHELW	ERNSYCKKVF	VTCQDPNPLI	PPWGWPGNTL	360
VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP	LYSVHNGNFQ	TWMGAHGAGV	420
LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE	EQEGPGTRLP	GNLSSDEVLP	480
AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGRSSSSS	SSSSNNNNYC	ALGCYGGWHL	540
SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	QGVAVVLAGH	CQRPGLHEDL	QGMLLPSVLS	600
KARSWTFGGG	GSGGGGSGGG	GSERTMPRIP	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	660
QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP	CYTLKPET		708
SEQ ID NO: 170		moltype = AA length = 705				
FEATURE		Location/Qualifiers				
REGION		1..705				

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		note = MISC_FEATURE - CD5/IL-9R/cGC-S	
source		1..705	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 170			
RLSWYDPDFQ	ARLTRSNSKC	QGQLEVYLKD	GWHMVCSQSW
GRSSKQWEDP	SQASKVCQRL	60	
NCGVPLSLGP	FLVITYTPQSS	IICYGQLGSF	SNCSHSRNDM
CHSLGLTCLE	PQKTTPTTTR	120	
PPPTTTTPEPT	APPRLQLVAQ	SGGQHCAGVV	EFYSGSLGGT
ISYEAQDKTQ	DLENFLCNNL	180	
QCGSFLKHLF	ETEAGRAQDP	GEPREHQPLP	IQWKIQNSSC
TSLEHCFRKI	KPQKSGRVLA	240	
LLCSGFQPKV	QSRLVGGSSI	CEGTVEVRQG	AQWAALCDSS
SARSSLRWEE	VCREQQCGSV	300	
NSYRVLDAGD	PTSRGLFCPH	QKLSQCHELW	ERNSYCKKVF
VTCQDPNPLI	PPWGWPGNTL	360	
VAVSIFLLLT	GPTYLLFKLS	PRVKRIFYQN	VPSPAMFFQP
LYSVHNGNFQ	TWMGAHGAGV	420	
LLSQDCAGTP	QGALEPCVQE	ATALLTCGPA	RPWKSVALEE
EQEGPGTRLP	GNLSSDEVLP	480	
AGCTEWRVQT	LAYLPQEDWA	PTSLTRPAPP	DSEGSRSSSS
SSSSNNNNYC	ALGCYGGWHL	540	
SALPGNTQSS	GPIPALACGL	SCDHQGLETQ	QGVAVVLAGH
CQRPGLHEDL	QGMLLPSVLS	600	
KARSWTFQPQ	PQPQPQPQPE	RTMPRIPTLK	NLEDLVTEYH
GNFSAWSGVS	KGLAESLQPD	660	
YSERLCLVSE	IPPKGGALGE	GPGASPCNQH	SPYWAPPCYT
LKPET		705	
SEQ ID NO: 171			
FEATURE		moltype = AA length = 413	
REGION		Location/Qualifiers	
		1..413	
		note = MISC_FEATURE - TWEAKR/IL9R/cGC-F	
source		1..413	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 171			
EQAPGTAPCS	RGSSWSADLD	KCMDCASCRA	RPHSDFCLGC
AAAPPAPFRL	LWPLIPPWGW	60	
PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA
MFFQPLYSVH	NGNFQTMGA	120	
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPAPWKS
VALEEEQEGP	GTRLPGNLSS	180	
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS
RSSSSSSSN	NNNYCALGCY	240	
GGWHLALPG	NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV
VLAGHCQRP	LHEDLQGM	300	
PSVLSKARSW	TFGGGSGGG	GSGGGGSERT	MPRIPTLKNL
EDLVTEYHGN	PSAWSGVSKG	360	
LAESLQPDYS	ERLCLVSEIP	PKGALGEGP	GASPCNQHSP
YWAPPCYTLK	PET	413	
SEQ ID NO: 172			
FEATURE		moltype = AA length = 410	
REGION		Location/Qualifiers	
		1..410	
		note = MISC_FEATURE - TWEAKR/IL9R/cGC-S	
source		1..410	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 172			
EQAPGTAPCS	RGSSWSADLD	KCMDCASCRA	RPHSDFCLGC
AAAPPAPFRL	LWPLIPPWGW	60	
PGNTLVAVSI	FLLLTGPTYL	LFKLSPRVKR	IFYQNVPSPA
MFFQPLYSVH	NGNFQTMGA	120	
HGAGVLLSQD	CAGTPQGALE	PCVQEATALL	TCGPAPWKS
VALEEEQEGP	GTRLPGNLSS	180	
EDVLPAGCTE	WRVQTLAYLP	QEDWAPTSLT	RPAPPDSEGS
RSSSSSSSN	NNNYCALGCY	240	
GGWHLALPG	NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV
VLAGHCQRP	LHEDLQGM	300	
PSVLSKARSW	TFQPPQPQP	QPQPERTMPR	IPTLKNLEDL
VTEYHGNFSA	WSGVSKGLAE	360	
SLQPDYSERL	CLVSEIPPKG	GALGEGPGAS	PCNQHSPYWA
PPCYTLKPET		410	
SEQ ID NO: 173			
FEATURE		moltype = AA length = 402	
REGION		Location/Qualifiers	
		1..402	
		note = MISC_FEATURE - TWEAKR/IL9R/cGC-F/TNFR1-TM	
source		1..402	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 173			
EQAPGTAPCS	RGSSWSADLD	KCMDCASCRA	RPHSDFCLGC
LWPVLLPLVI	60		
FFGLCLLSLL	FIGLMYVKRI	FYQNVPSAM	FFQPLYSVHN
GNFQTMGAH	GAGVLLSQDC	120	
AGTPQGALEP	CVQEATALLT	CGPARPWKSV	ALEEEQEGPG
TRLPGNLSSE	DVLPAGCTEW	180	
RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGS	SSSSSSSN
NNYCALGCY	GWHLALPGN	240	
TQSSGPIPAL	ACGLSCDHQ	LETQQGVAV	LAGHCQRPGL
HEDLQGM	SVLSKARSW	300	
FGGGSGGGG	SGGGGSERTM	PRIPTLKNLE	DLVTEYHGNF
SAWSGVSKGL	AESLQPDYSE	360	
RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY	WAPPCYTLKP
ET		402	
SEQ ID NO: 174			
FEATURE		moltype = AA length = 399	
REGION		Location/Qualifiers	
		1..399	
		note = MISC_FEATURE - TWEAKR/IL9R/cGC-S/TNFR1-TM	
source		1..399	
		mol_type = protein	
		organism = synthetic construct	
SEQUENCE: 174			
EQAPGTAPCS	RGSSWSADLD	KCMDCASCRA	RPHSDFCLGC
LWPVLLPLVI	60		
FFGLCLLSLL	FIGLMYVKRI	FYQNVPSAM	FFQPLYSVHN
GNFQTMGAH	GAGVLLSQDC	120	

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AGTPQGALEP CVQEATALLT CGPARPWKSV ALEEEQEGPG TRLPGNLSSE DVLPACTEW 180
RVQTLAYLPQ EDWAPTSLTR PAPPDSEGRS SSSSSSSSNN NNYCALGCYG GWHLSALPGN 240
TQSSGPIPAL AGLSCDHQG LETQQGVAVW LAGHCQRPGL HEDLQGMLLP SVLSKARSWT 300
FQPQPQPQPQ PQPERTMPRI PTLKNLEDLV TEYHGNFSAW SGVSKGLAES LQPDYSERLC 360
LVSEIPPKGG ALGEGPGASP CNQHSPYWAP PCYTLKPET 399

SEQ ID NO: 175      moltype = AA  length = 729
FEATURE            Location/Qualifiers
REGION            1..729
                  note = MISC_FEATURE - OPG/IL9R/cGC-F/TNFR1-TM
source            1..729
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 175
ETFPKYLHY DEETSHQLLC DKCPPGYTLK QHCTAKWKTV CAPCPDHYYT DSWHTSDECL 60
YCSPVCKELQ YVKQECNRTH NRVCECKEGR YLEIEFCLKH RSCPPGFGVV QAGTPERNVT 120
CKRCPDGFES NETSSKAPCR KHTNCSVFGL LLTQKGNATH DNICSGNSES TQKCGIDVTL 180
CEEAFRRFAV PTKFTPNWLS VLVDNLPGTK VNAESVERIK RQHSSQEQTQ QLLKLWKHQN 240
KDQDIVKKII QDIDLCEVSV QRHIGHANLT FEQLRSLMES LPGKKVGAED IEKTIKACKP 300
SDQILKLLSL WRIKNGDQDT LKGLMHALKH SKTYHFPKTV TQSLKKTIRF LHSFTMYKLY 360
QKLFLFLEMIGN QVQSVKISCL VLLPLVIFFG LCLLSLLFIG LMYVKRIFYQ NVPSPAMFFQ 420
PLYSVHNGNF QTWMGAHGAG VLLSQDCAGT PQGALEPCVQ EATALLTCGP ARPWKSVALE 480
EEQEGPGTRL PGNLSSSEVL PAGCTEWRVQ TLAYLPQEDW APTSLTRPAP PDSEGRSSSS 540
SSSSSSNNNY CALGCYGGWH LSALPGNTQS SGPIPALACG LSCDHQGLET QQGVAVVLAG 600
HCQRPGLHED LQGMLLPSVL SKARSWTFGG GSGGGGSGG GGSERTMPRI PTLKNLEDLV 660
TEYHGNFSAW SGVSKGLAES LQPDYSERLC LVSEIPPKGG ALGEGPGASP CNQHSPYWAP 720
PCYTLKPET 729

SEQ ID NO: 176      moltype = AA  length = 726
FEATURE            Location/Qualifiers
REGION            1..726
                  note = MISC_FEATURE - OPG/IL9R/cGC-S/TNFR1-TM
source            1..726
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 176
ETFPKYLHY DEETSHQLLC DKCPPGYTLK QHCTAKWKTV CAPCPDHYYT DSWHTSDECL 60
YCSPVCKELQ YVKQECNRTH NRVCECKEGR YLEIEFCLKH RSCPPGFGVV QAGTPERNVT 120
CKRCPDGFES NETSSKAPCR KHTNCSVFGL LLTQKGNATH DNICSGNSES TQKCGIDVTL 180
CEEAFRRFAV PTKFTPNWLS VLVDNLPGTK VNAESVERIK RQHSSQEQTQ QLLKLWKHQN 240
KDQDIVKKII QDIDLCEVSV QRHIGHANLT FEQLRSLMES LPGKKVGAED IEKTIKACKP 300
SDQILKLLSL WRIKNGDQDT LKGLMHALKH SKTYHFPKTV TQSLKKTIRF LHSFTMYKLY 360
QKLFLFLEMIGN QVQSVKISCL VLLPLVIFFG LCLLSLLFIG LMYVKRIFYQ NVPSPAMFFQ 420
PLYSVHNGNF QTWMGAHGAG VLLSQDCAGT PQGALEPCVQ EATALLTCGP ARPWKSVALE 480
EEQEGPGTRL PGNLSSSEVL PAGCTEWRVQ TLAYLPQEDW APTSLTRPAP PDSEGRSSSS 540
SSSSSSNNNY CALGCYGGWH LSALPGNTQS SGPIPALACG LSCDHQGLET QQGVAVVLAG 600
HCQRPGLHED LQGMLLPSVL SKARSWTFQ PQQPQPQPQ ERTMPRIPTL KNLEDLVTEY 660
HGNFSAWSGV SKGLAESLQP DYSERLCLVS EIPPKGGALG EGPASPCNQ HSPYWAPPCY 720
TLKPET 726

SEQ ID NO: 177      moltype = AA  length = 514
FEATURE            Location/Qualifiers
REGION            1..514
                  note = MISC_FEATURE - TACI/IL9R/cGC-F/TNFR1-TM
source            1..514
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 177
MSGGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCTMSC KTICNHQSQR 60
TCAAFCRSL S CRKEQGKFYD HLLRDCISCA SICGQHPKQC AYFCENKLRS PVNLPPELRR 120
QRSGEVENNS DNSGRYQGLE HRGSEASPAL PGLKLSADQV ALVYSVLLPL VIFFGLCLLS 180
LLFIGLMYVK RIFYQNPVSP AMFFQPLYSV HNGNFQTWMG AHGAGVLLSQ DCAGTPQAGAL 240
EPCVQEATAL LTCGPAPRWK SVALEEEQEG PGTSLPGLNS SEDVLPAGCT EWRVQTLAYL 300
PQEDWAPTS TRPAPPDSEG SRSSSSSSSS NNNNYCALGC YGGWHLALP GNTQSSGPIP 360
ALACGLSCDH QGLETQQGVA WVLAGHCQRP GLHEDLQGM LPSVLSKARS WTFGGGSGG 420
GSGGGGSGSER TMPRIPTLKN LEDLVTEYHG NFSAWSGVSK GLAESLQPDY SERLCLVSEI 480
PPKGGALGEG PGASPCNQHS PYWAPPCYTL KPET 514

SEQ ID NO: 178      moltype = AA  length = 511
FEATURE            Location/Qualifiers
REGION            1..511
                  note = MISC_FEATURE - TACI/IL9R/cGC-S/TNFR1-TM
source            1..511
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 178

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MSGLGSRRRG	GRSRVDQEER	FPQGLWTGVA	MRS CP EEQYW	DPLLGT C MSC	KTICNHQSQR	60
TCAAFCRSL S	CRKEQ GK FYD	HLLRDCISCA	SICGQHPKQC	AYFCENKLRS	PVNLPP ELRR	120
QRSGEVENNS	DNSGRYQGLE	HRGSEASPAL	PGLKLSADQV	ALVYSVLLPL	VIFFGLCLLS	180
LLFIGLMYVK	RIFYQNVPS P	AMFFQPLYSV	HNGNFQ TWMG	AHGAGVLLSQ	DCAGTPQGAL	240
EPCVQEATAL	LTCGPARPWK	SVALEEEQEG	PGTRLPGNLS	SEDVLPAGCT	EWRVQTLAYL	300
PQEDWAP TSL	TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHL S ALP	GNTQSSGPIP	360
ALACGLSCDH	QGLE TQQGVA	WVLAGHCQRP	GLHEDLQ GML	LPSVLSKARS	WTFQPQPQPQ	420
PQPQPERTMP	RIPTLKNLED	LVTEYHG NFS	AWSGVSKGLA	ESLQPDY SER	LCLVSEIPPK	480
GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	T			511
SEQ ID NO: 179						
FEATURE						
REGION						
source						
SEQUENCE: 179						
MLQ MAGQCSQ	NEYFDSL LHA	CIPCQLRCSS	NTPPLTCQRY	CNASVTNSVK	GTNAVLLPLV	60
IFFGLCLLSL	LFIGLMYVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQ TWMGA	HGAGVLLSQD	120
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	180
WRVQTLAYLP	QEDWAP TSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHL S ALPG	240
NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP G	LHEDLQ GMLL	PSVLSKARSW	300
TFGGGSGGGG	GSGGGGSERT	MPRIPTLKNL	EDLVTEYHGN	FSAWSGVSKG	LAESLQPDYS	360
ERLCLVSEIP	PKG GALGEGP	GASPCNQHSP	YWAPPCYTLK	PET		403
SEQ ID NO: 180						
FEATURE						
REGION						
source						
SEQUENCE: 180						
MLQ MAGQCSQ	NEYFDSL LHA	CIPCQLRCSS	NTPPLTCQRY	CNASVTNSVK	GTNAVLLPLV	60
IFFGLCLLSL	LFIGLMYVKR	IFYQNVPSPA	MFFQPLYSVH	NGNFQ TWMGA	HGAGVLLSQD	120
CAGTPQGALE	PCVQEATALL	TCGPARPWKS	VALEEEQEGP	GTRLPGNLSS	EDVLPAGCTE	180
WRVQTLAYLP	QEDWAP TSLT	RPAPPDSEGS	RSSSSSSSSN	NNNYCALGCY	GGWHL S ALPG	240
NTQSSGPIPA	LACGLSCDHQ	GLETQQGVAV	VLAGHCQRP G	LHEDLQ GMLL	PSVLSKARSW	300
TFQPQPQPQP	QPQPERTMPR	IPTLKNLEDL	VTEYHG NFSA	WSGVSKGLAE	SLQPDYSERL	360
CLVSEIP PKG	GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET			400
SEQ ID NO: 181						
FEATURE						
REGION						
source						
SEQUENCE: 181						
KEACPTGLYT	HSGECKKACN	LGEGVAQPCG	ANQTVCEPCL	DSVTFSDVVS	ATEPCKPCTE	60
CVGLQSMSAP	CVEADDAVCR	CAYGYYQDET	TGRCEACRVC	EAGSGLVFSC	QDKQNTVCEE	120
CPDGTYSDEA	NHVDPCLPCT	VCEDTERQLR	ECTRWA DAEC	EEIPGRWITR	STPPEGSDST	180
APSTQEPEAP	PEQDLIASTV	AGVVTTVMGS	SQPVVTRGTT	DNVLLPLVIF	FGLCLLSLLF	240
IGLMYVKRIF	YQNVSPAMF	FQPLYSVHNG	NFQ TWMGAHG	AGVLLSQDCA	GTPQGALEPC	300
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSS ED	VLPAGCTEWR	VQTLAYLPQE	360
DWAP TSLTRP	APPDSEGSRS	SSSSSSSSNN	NYCALGCYGG	WHL S ALPGNT	QSSGPIPALA	420
CGLSCDHQGL	ETQQGVAVL	AGHCQRPGLH	EDLQ GMLLPS	VLSKARSWTF	GGGGSGGGGS	480
GGGGSER TMP	RIPTLKNLED	LVTEYHG NFS	AWSGVSKGLA	ESLQPDY SER	LCLVSEIPPK	540
GGALGEGPGA	SPCNQHSPYW	APPCYTLKPE	T			571
SEQ ID NO: 182						
FEATURE						
REGION						
source						
SEQUENCE: 182						
KEACPTGLYT	HSGECKKACN	LGEGVAQPCG	ANQTVCEPCL	DSVTFSDVVS	ATEPCKPCTE	60
CVGLQSMSAP	CVEADDAVCR	CAYGYYQDET	TGRCEACRVC	EAGSGLVFSC	QDKQNTVCEE	120
CPDGTYSDEA	NHVDPCLPCT	VCEDTERQLR	ECTRWA DAEC	EEIPGRWITR	STPPEGSDST	180
APSTQEPEAP	PEQDLIASTV	AGVVTTVMGS	SQPVVTRGTT	DNVLLPLVIF	FGLCLLSLLF	240
IGLMYVKRIF	YQNVSPAMF	FQPLYSVHNG	NFQ TWMGAHG	AGVLLSQDCA	GTPQGALEPC	300
VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSS ED	VLPAGCTEWR	VQTLAYLPQE	360
DWAP TSLTRP	APPDSEGSRS	SSSSSSSSNN	NYCALGCYGG	WHL S ALPGNT	QSSGPIPALA	420

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CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	VLSKARSWTF	QPQPQPQPQP	480
QPERTMPRIP	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	QPDYSERLCL	VSEIPPKGGA	540
LGEGPGASPC	NQHSPYWAPP	CYTLKPET				568
SEQ ID NO: 183	moltype = AA length = 510					
FEATURE	Location/Qualifiers					
REGION	1..510					
	note = MISC_FEATURE - EDAR/IL9R/cGC-F/TNFR1-TM					
source	1..510					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 183						
EYSNCGENEY	YNQTTGLCQE	CPPCGPGEED	YLSCGYGTKD	EDYGCVPCPA	EKFSKGGYQI	60
CRRHKDCGEF	FRATVLTGPD	MENDAECGPC	LPGYYMLENR	PRNIYGMVCY	SCLLAPPNTK	120
ECVGATSGAS	ANFPGTSGSS	TLSPFQHAHK	ELSGQGHLAT	AVLLPLVIFF	GLCLLSLLFI	180
GLMYVKRIFY	QNVPSAMFF	QPLYSVHNGN	FQTMWGAHGA	GVLLSQDCAG	TPQGALEPCV	240
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSADV	LPAGCTEWRV	QTLAYLPQED	300
WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	360
GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFG	GGSGGGGGSG	420
GGGSERTMPR	IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE	SLQPDYSERL	CLVSEIPPKG	480
GALGEGPGAS	PCNQHSPYWA	PPCYTLKPET				510
SEQ ID NO: 184	moltype = AA length = 507					
FEATURE	Location/Qualifiers					
REGION	1..507					
	note = MISC_FEATURE - EDAR/IL9R/cGC-S/TNFR1-TM					
source	1..507					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 184						
EYSNCGENEY	YNQTTGLCQE	CPPCGPGEED	YLSCGYGTKD	EDYGCVPCPA	EKFSKGGYQI	60
CRRHKDCGEF	FRATVLTGPD	MENDAECGPC	LPGYYMLENR	PRNIYGMVCY	SCLLAPPNTK	120
ECVGATSGAS	ANFPGTSGSS	TLSPFQHAHK	ELSGQGHLAT	AVLLPLVIFF	GLCLLSLLFI	180
GLMYVKRIFY	QNVPSAMFF	QPLYSVHNGN	FQTMWGAHGA	GVLLSQDCAG	TPQGALEPCV	240
QEATALLTCG	PARPWKSVAL	EEEQEGPGTR	LPGNLSSADV	LPAGCTEWRV	QTLAYLPQED	300
WAPTSLTRPA	PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW	HLSALPGNTQ	SSGPIPALAC	360
GLSCDHQGLE	TQQGVAVVLA	GHCQRPGLHE	DLQGMLLPSV	LSKARSWTFQ	PQPQPQPQPQ	420
PERTMPRIPT	LKNLEDLVTE	YHGNFSAWSG	VSKGLAESLQ	PDYSERLCLV	SEIPPKGGAL	480
GEGPGASPCN	QHSPYWAPPC	YTLKPET				507
SEQ ID NO: 185	moltype = AA length = 505					
FEATURE	Location/Qualifiers					
REGION	1..505					
	note = MISC_FEATURE - DCR2 (TNFRSF10D) /IL9R/cGC-F/TNFR1-TM					
source	1..505					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 185						
ATIPRQDEVP	QQTVAQQQR	RSLKEEECPA	GSHRSEYTG	CNPCTEGVDY	TIASNNLPSC	60
LLCTVCKSGQ	TNKSSCTTTR	DTVCQCEKGS	FQDKNSPEMC	RTCRTGCPRG	MVKVSNCTPR	120
SSDIKCKNESA	ASSTGKTPAA	EETVTILGM	LAPYHVLLP	LVIFFGLCLL	SLLFIGLMYV	180
KKRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	240
LLTCGPAPRW	KVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	300
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLSAL	PGNTQSSGPI	PALACGLSCD	360
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR	SWTFGGGGSG	GGSGGGGGSE	420
RTMPRIPTLK	NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	480
GPGASPCNQH	SPYWAPPCYT	LKPET				505
SEQ ID NO: 186	moltype = AA length = 502					
FEATURE	Location/Qualifiers					
REGION	1..502					
	note = MISC_FEATURE - DCR2 (TNFRSF10D) /IL9R/cGC-S/TNFR1-TM					
source	1..502					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 186						
ATIPRQDEVP	QQTVAQQQR	RSLKEEECPA	GSHRSEYTG	CNPCTEGVDY	TIASNNLPSC	60
LLCTVCKSGQ	TNKSSCTTTR	DTVCQCEKGS	FQDKNSPEMC	RTCRTGCPRG	MVKVSNCTPR	120
SSDIKCKNESA	ASSTGKTPAA	EETVTILGM	LAPYHVLLP	LVIFFGLCLL	SLLFIGLMYV	180
KKRIFYQNVPS	PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	240
LLTCGPAPRW	KVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	300
LTRPAPPDSE	GSRSSSSSSS	SNNNNYCALG	CYGGWHLSAL	PGNTQSSGPI	PALACGLSCD	360
HQGLETOQGV	AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR	SWTFQPQPQP	QPQPQPPTMT	420
PRIPTLKNLE	DLVTEYHGNF	SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	480
ASPCNQHSPY	WAPPCYTLKP	ET				502

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SEQ ID NO: 187	moltype = AA	length = 560
FEATURE	Location/Qualifiers	
REGION	1..560	
	note = MISC_FEATURE - DCR1 (TNFRSF10C) /IL9R/cGC-F/TNFR1-TM	
source	1..560	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 187		
ATTARQEEVP	QQTVAPQQQR	HSFKGEECPA GSHRSEHTGA CNPCTEGVDY TNASNNEPSC 60
FPCTVCKSDQ	KHKSSCTMTR	DTVCQCKEGT FRNENSP EMC RKCSRCPSGE VQVSNCTSWD 120
DIQCVEEFGA	NATVETPAAE	ETMNTSPGTP APAAEETMNT SPGTPAPAAE ETMTTSPGTP 180
APAAEETMTT	SPGTPAPAAE	ETMITSPGTP AVLLPLVIFF GLCLLSLLFI GLMYVKRIFY 240
QNVPSPAMFF	QPLYSVHNGN	FQTWMGAHGA GVLLSQDCAG TPQGALEPCV QEATALLTCTG 300
PARPWKSVAL	EEEQEGPGTR	LPGNLSSSEDV LPAGCTEWRV QTLAYLPQED WAPTSLTRPA 360
PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW HLSALPGNTQ SSGPIPALAC GLSCDHQGLE 420
TQQGVAVVLA	GHCQRPGLHE	DLQGMLLPSV LSKARSWTFG GGGSGGGSG GGGsertmpr 480
IPTLKNLEDL	VTEYHGNFSA	WSGVSKGLAE SLQPDYSERL CLVSEIPPKG GALGEGPGAS 540
PCNQHSPYWA	PPCYTLKPET	
		560
SEQ ID NO: 188	moltype = AA	length = 557
FEATURE	Location/Qualifiers	
REGION	1..557	
	note = MISC_FEATURE - DCR1 (TNFRSF10C) /IL9R/cGC-S/TNFR1-TM	
source	1..557	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 188		
ATTARQEEVP	QQTVAPQQQR	HSFKGEECPA GSHRSEHTGA CNPCTEGVDY TNASNNEPSC 60
FPCTVCKSDQ	KHKSSCTMTR	DTVCQCKEGT FRNENSP EMC RKCSRCPSGE VQVSNCTSWD 120
DIQCVEEFGA	NATVETPAAE	ETMNTSPGTP APAAEETMNT SPGTPAPAAE ETMTTSPGTP 180
APAAEETMTT	SPGTPAPAAE	ETMITSPGTP AVLLPLVIFF GLCLLSLLFI GLMYVKRIFY 240
QNVPSPAMFF	QPLYSVHNGN	FQTWMGAHGA GVLLSQDCAG TPQGALEPCV QEATALLTCTG 300
PARPWKSVAL	EEEQEGPGTR	LPGNLSSSEDV LPAGCTEWRV QTLAYLPQED WAPTSLTRPA 360
PPDSEGSRSS	SSSSSSNNNN	YCALGCYGGW HLSALPGNTQ SSGPIPALAC GLSCDHQGLE 420
TQQGVAVVLA	GHCQRPGLHE	DLQGMLLPSV LSKARSWTFQ PQPQPQPQPQ PERTMPRIPT 480
LKNLEDLVTE	YHGNFSAWSG	VSKGLAESLQ PDYSERLCLV SEIPPKGGAL GEGPGASPCN 540
QHSPYWAPPC	YTLKPET	
		557
SEQ ID NO: 189	moltype = AA	length = 522
FEATURE	Location/Qualifiers	
REGION	1..522	
	note = MISC_FEATURE - CD40/IL9R/cGC-F/TNFR1-TM	
source	1..522	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 189		
EPPTACREKQ	YLINSQCCSL	CQPGQKLVS D CTEFTETECL PCGESEFLDT WNRETHCHQH 60
KYCDPNLGLR	VQQKGTSETD	TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD 120
TICEPCPVGF	FSNVSSAFEK	CHPWTSCETK DLVVQQAGTN KTDVVCGPQD RLRVLLPLVI 180
FFGLCLLSLL	FIGLMYVKRI	FYQNVPSPAM FFQPLYSVHN GNFQTMGAH GAGVLLSQDC 240
AGTPQGALEP	CVQEATALLT	CGPARPWKSV ALEEEQEGPG TRLPGNLSSE DVLPAGCTEW 300
RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGS R SSSSSSSNN NNYCALGCY GWHLSALPGN 360
TQSSGPIPAL	ACGLSCDHQG	LETQQGVAVW LAGHCQRPG L HEDLQGM LLP SVLSKARSWT 420
FGGGSGGGG	SGGGGSERTM	PRIPTLKNLE DLVTEYHGNF SAWSGVSKGL AESLQPDYSE 480
RLCLVSEIPP	KGGALGEGPG	ASPCNQHSPY WAPPCYTLKP ET 522
SEQ ID NO: 190	moltype = AA	length = 519
FEATURE	Location/Qualifiers	
REGION	1..519	
	note = MISC_FEATURE - CD40/IL9R/cGC-S/TNFR1-TM	
source	1..519	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 190		
EPPTACREKQ	YLINSQCCSL	CQPGQKLVS D CTEFTETECL PCGESEFLDT WNRETHCHQH 60
KYCDPNLGLR	VQQKGTSETD	TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD 120
TICEPCPVGF	FSNVSSAFEK	CHPWTSCETK DLVVQQAGTN KTDVVCGPQD RLRVLLPLVI 180
FFGLCLLSLL	FIGLMYVKRI	FYQNVPSPAM FFQPLYSVHN GNFQTMGAH GAGVLLSQDC 240
AGTPQGALEP	CVQEATALLT	CGPARPWKSV ALEEEQEGPG TRLPGNLSSE DVLPAGCTEW 300
RVQTLAYLPQ	EDWAPTSLTR	PAPPDSEGS R SSSSSSSNN NNYCALGCY GWHLSALPGN 360
TQSSGPIPAL	ACGLSCDHQG	LETQQGVAVW LAGHCQRPG L HEDLQGM LLP SVLSKARSWT 420
FQPQPQPQPQ	PQPERTMPRI	PTLKNLEDLV TEYHGNFSAW SGVSKGLAES LQPDYSERLC 480
LVSEIPPKGG	ALGEGPGASP	CNQHSPYWAP PCYTLKPET 519
SEQ ID NO: 191	moltype = AA	length = 497
FEATURE	Location/Qualifiers	

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REGION	1..497					
	note = MISC_FEATURE - FAS/IL9R/cGC-F/TNFR1-TM					
source	1..497					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 191						
QVTDINSKGL ELRKTVTTVE	TQNLEGLHHD	GQFCHKPCPP	GERKARDCTV	NGDEPDCVPC	60	
QEGKEYTDKA HFSSKCRRCR	LCDEGHGLEV	EINCTRTQNT	KCRCKPNFFC	NSTVCEHCDP	120	
CTKCEHGIK ECTLTSNTKC	KEEGSRSNVL	LPLVIFFGLC	LLSLLFIGLM	YVKRIFYQNV	180	
PSPAMFFQPL YSVHNGNFQT	WMGAHGAGVL	LSQDCAGTPQ	GALEPCVQEA	TALLTCGPAR	240	
PWKSVALEEEE QEGPGTRLPG	NLSSEDVLP	GCTEWRVQTL	AYLPQEDWAP	TSLTRPAPPD	300	
SEGSRSSSSS SSSNNNNYCA	LGCYGGWHL	ALPGNTQSSG	PIPALACGLS	CDHQGLETQQ	360	
GVAWVLAGHC QRPGLHEDLQ	GMLLPSVLSK	ARSWTFGGGG	SGGGGSGGGG	SERTMPRIPT	420	
LKNLEDLVTE YHGNFSAWSG	VSKGLAESLQ	PDYSERLCLV	SEIPPKGGAL	GEGPGASPCN	480	
QHSPYWAPPC YTLKPET					497	
SEQ ID NO: 192	moltype = AA	length = 494				
FEATURE	Location/Qualifiers					
REGION	1..494					
	note = MISC_FEATURE - FAS/IL9R/cGC-S/TNFR1-TM					
source	1..494					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 192						
QVTDINSKGL ELRKTVTTVE	TQNLEGLHHD	GQFCHKPCPP	GERKARDCTV	NGDEPDCVPC	60	
QEGKEYTDKA HFSSKCRRCR	LCDEGHGLEV	EINCTRTQNT	KCRCKPNFFC	NSTVCEHCDP	120	
CTKCEHGIK ECTLTSNTKC	KEEGSRSNVL	LPLVIFFGLC	LLSLLFIGLM	YVKRIFYQNV	180	
PSPAMFFQPL YSVHNGNFQT	WMGAHGAGVL	LSQDCAGTPQ	GALEPCVQEA	TALLTCGPAR	240	
PWKSVALEEEE QEGPGTRLPG	NLSSEDVLP	GCTEWRVQTL	AYLPQEDWAP	TSLTRPAPPD	300	
SEGSRSSSSS SSSNNNNYCA	LGCYGGWHL	ALPGNTQSSG	PIPALACGLS	CDHQGLETQQ	360	
GVAWVLAGHC QRPGLHEDLQ	GMLLPSVLSK	ARSWTFQPPQ	QPQPQPQPER	TMPRIPTLKN	420	
LEDLVTEYHG NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	PGASPCNQHS	480	
PYWAPPCYTL KPET					494	
SEQ ID NO: 193	moltype = AA	length = 565				
FEATURE	Location/Qualifiers					
REGION	1..565					
	note = MISC_FEATURE - DR4/IL9R/cGC-F/TNFR1-TM					
source	1..565					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 193						
ASGTEAAAAAT PSKVGSSAG	RIEPRGGGRG	ALPTSMGQHG	PSARARAGRA	PGPRPAREAS	60	
PRLRVHKTFK FVVVGVLQV	VPSSAATIKL	HDQSIGTQQW	EHSPLGELCP	PGSHRSEHPG	120	
ACNRCTEGVG YTNASNNLFA	CLPCTACKSD	EEERSPCTTT	RNTACQCKPG	TFRNDNSAEM	180	
CRKCSRGCPR GMVKVKDCTP	WSDIECVHKE	SGNGHNVLLP	LVIFFGLCLL	SLLFIGLMYV	240	
KRIFYQNVPS PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	300	
LLTCGPARPW KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	360	
LTRPAPPDSE GSRSSSSSSS	SNNNNYCALG	CYGGWHL	PGNTQSSGPI	PALACGLSCD	420	
HQGLETQQGV AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR	SWTFGGGGSG	GGGSGGGGSE	480	
RTMPRIPTLK NLEDLVTEYH	GNFSAWSGVS	KGLAESLQPD	YSERLCLVSE	IPPKGGALGE	540	
GPGASPCNQH SPYWAPPCYT	LKPET				565	
SEQ ID NO: 194	moltype = AA	length = 562				
FEATURE	Location/Qualifiers					
REGION	1..562					
	note = MISC_FEATURE - DR4/IL9R/cGC-S/TNFR1-TM					
source	1..562					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 194						
ASGTEAAAAAT PSKVGSSAG	RIEPRGGGRG	ALPTSMGQHG	PSARARAGRA	PGPRPAREAS	60	
PRLRVHKTFK FVVVGVLQV	VPSSAATIKL	HDQSIGTQQW	EHSPLGELCP	PGSHRSEHPG	120	
ACNRCTEGVG YTNASNNLFA	CLPCTACKSD	EEERSPCTTT	RNTACQCKPG	TFRNDNSAEM	180	
CRKCSRGCPR GMVKVKDCTP	WSDIECVHKE	SGNGHNVLLP	LVIFFGLCLL	SLLFIGLMYV	240	
KRIFYQNVPS PAMFFQPLYS	VHNGNFQTM	GAHGAGVLLS	QDCAGTPQGA	LEPCVQEATA	300	
LLTCGPARPW KSVALEEEQE	GPGTRLPGNL	SSEDVLPAGC	TEWRVQTLAY	LPQEDWAPTS	360	
LTRPAPPDSE GSRSSSSSSS	SNNNNYCALG	CYGGWHL	PGNTQSSGPI	PALACGLSCD	420	
HQGLETQQGV AWVLAGHCQR	PGLHEDLQGM	LLPSVLSKAR	SWTFQPPQP	QPQPQPRTM	480	
PRIPTLKNLE DLVTEYHGNE	SAWSGVSKGL	AESLQPDYSE	RLCLVSEIPP	KGGALGEGPG	540	
ASPCNQHSPY WAPPCYTLKP	ET				562	
SEQ ID NO: 195	moltype = AA	length = 654				
FEATURE	Location/Qualifiers					
REGION	1..654					
	note = MISC_FEATURE - DR6/IL9R/cGC-S/TNFR1-TM					

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source	1..654					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 195						
QPEQKASNLI	GTYRHVDRAT	GQVLTCDKCP	AGTYVSEHCT	NTSLRVCSSC	PVGTFTRHEN	60
GIEKCHDCSQ	PCPWPMIEKL	PCAALTDREC	TCPPGMFQSN	ATCAPHTVCP	VGWGVRRKGT	120
ETEDVRCKQC	ARGTFSDVPS	SVMKCKAYTD	CLSQNLVVIK	PGTKETDNVC	GTLPSFSSST	180
SPSPGTAIFP	RPEHMETHEV	PSSTYVPKGM	NSTESNSSAS	VRPKVLSSIQ	EGTVPDNTSS	240
ARGKEDVNKT	LPNLQVVDHQ	QGPVHRHILK	LLPSMEATGG	EKSSTPIKGP	KRGHPRQNLH	300
KHFDINEHVL	LPLVIFFGLC	LLSLFFIGLM	YVKRIFYQNV	PSPAMFFQPL	YSVHNGNFQT	360
WMGAHGAGVL	LSQDCAGTPQ	GALEPCVQEA	TALLTCGPAP	PWKSVALEEE	QEGPGTRLPG	420
NLSSQEDVLP	A	AYLPQEDWAP	TSLTRPAPPD	SEGSRSSSSS	SSSNNNNYCA	480
LGICYGGWHL	S	PIPALACGLS	CDHQGLETTQ	GVAWVLGH	QRPGLHEDLQ	540
GMLLPSVL	SK	ARSWTFQPPQ	QPQPQPQPER	TMPRIPTLKN	LEDLVTEYHG	600
GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	PGASPCNQHS	PYWAPPCYTL	KPET	654
SEQ ID NO: 196	moltype = AA	length = 504				
FEATURE	Location/Qualifiers					
REGION	1..504					
	note = MISC_FEATURE - DR5/IL9R/cGC-F/TNFR1-TM					
source	1..504					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 196						
ITQQDLAPQQ	RAAPQQKRSS	PSEGLCPPGH	HISEDGRDCI	SCKYGQDYST	HWNDLLFCLR	60
CTRCDSGEVE	LSPCTTTRNT	VCQCEEGTFR	EEDSPEMCRK	CRTGCPRGMV	KVGDCPTWSD	120
IECVHKESGT	KHSGEVPAVE	ETVTSSPGTP	ASPCSVLLPL	VIFFGLCLLS	LLFIGLMYVK	180
RIFYQNVPS	P	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	240
LTCGPAPWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	EWVQTLAYL	PQEDWAPTSL	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHL	SALP	GNTQSSGPIP	360
QGLETTQGGVA	WVLAGHCQRP	GLHEDLQGM	LPSVL	SKARS	WTFGGGGSGG	420
TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	GLAESLQPDY	SERLCLVSEI	PPKGGALGEG	480
PGASPCNQHS	PYWAPPCYTL	KPET				504
SEQ ID NO: 197	moltype = AA	length = 501				
FEATURE	Location/Qualifiers					
REGION	1..501					
	note = MISC_FEATURE - DR5/IL9R/cGC-S/TNFR1-TM					
source	1..501					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 197						
ITQQDLAPQQ	RAAPQQKRSS	PSEGLCPPGH	HISEDGRDCI	SCKYGQDYST	HWNDLLFCLR	60
CTRCDSGEVE	LSPCTTTRNT	VCQCEEGTFR	EEDSPEMCRK	CRTGCPRGMV	KVGDCPTWSD	120
IECVHKESGT	KHSGEVPAVE	ETVTSSPGTP	ASPCSVLLPL	VIFFGLCLLS	LLFIGLMYVK	180
RIFYQNVPS	P	AMFFQPLYSV	HNGNFQTMWG	AHGAGVLLSQ	DCAGTPQGAL	240
LTCGPAPWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	EWVQTLAYL	PQEDWAPTSL	300
TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHL	SALP	GNTQSSGPIP	360
QGLETTQGGVA	WVLAGHCQRP	GLHEDLQGM	LPSVL	SKARS	WTFQPPQPQ	420
RIPTLKNLED	LVTEYHGNFS	AWSGVSKGLA	ESLQPDYSER	LCLVSEIPPK	GGALGEGPGA	480
SPCNQHSPYW	APPCYTLKPE	T				501
SEQ ID NO: 198	moltype = AA	length = 524				
FEATURE	Location/Qualifiers					
REGION	1..524					
	note = MISC_FEATURE - DR3/IL9R/cGC-F/TNFR1-TM					
source	1..524					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 198						
QGGTRSPRCD	CAGDFHKKIG	LFCCRGCPAG	HYLKAPCTEP	CGNSTCLVCP	QDTFLAWENH	60
HNSECARCQA	CDEQASQVAL	ENCSAVADTR	CGCKPGWFVE	CQVSQCVSSS	PFYCQPCLD	120
GALHRHTRL	L	CSRRTDCGT	CLPGFYEHD	GVCSCPTSTL	GSCPERCAAV	180
VIFFGLCLLS	LLFIGLMYVK	RIFYQNVPS	P	AMFFQPLYSV	HNGNFQTMWG	240
DCAGTPQGAL	EPCVQEATAL	LTCGPAPWK	SVALEEEQEG	PGTRLPGNLS	SEDLVPAGCT	300
EWVQTLAYL	PQEDWAPTSL	TRPAPPDSEG	SRSSSSSSSS	NNNNYCALGC	YGGWHL	360
GNTQSSGPIP	ALACGLSCDH	QGLETTQGGVA	WVLAGHCQRP	GLHEDLQGM	LPSVL	420
WTFGGGGSGG	GGSGGGG	SER	TMPRIPTLKN	LEDLVTEYHG	NFSAWSGVSK	480
SERLCLVSEI	PPKGGALGEG	PGASPCNQHS	PYWAPPCYTL	KPET		524
SEQ ID NO: 199	moltype = AA	length = 521				
FEATURE	Location/Qualifiers					
REGION	1..521					
	note = MISC_FEATURE - DR3/IL9R/cGC-S/TNFR1-TM					
source	1..521					
	mol_type = protein					

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organism = synthetic construct	
SEQUENCE: 199	
QGGTRSPRCD	CAGDFHKKIG LFCCRGCPAG HYLKAPCTEP CGNSTCLVCP QDTFLAWENH 60
HNSECARCQA	CDEQASQVAL ENCSAVADTR CGCKPGWFVE CQVSQCVSSS PFYCQPCLDC 120
GALHRHTRL	LLCSRRDTCGT CLPGFYEHDG GCVSCPTSTL GSCPERCAAV CGWRQVLLPL 180
VIFFGLCLLS	LLFIGLMYVK RIFYQNVPS AMFFQPLYSV HNGNFQTMWG AHGAGVLLSQ 240
DCAGTPQGAL	EPCVQEATAL LTCGPAPRWK SVALEEEQEG PGTRLPGNLS SEDVLPAGCT 300
EWVQTLAYL	PQEDWAPTS TRPAPPDSEG SRSSSSSSSS NNNNYCALGC YGGWHLALP 360
GNTQSSGPIP	ALACGLSCDH QGLETQQVA WVLAGHCORP GLHEDLQGM LPSVLSKARS 420
WTFQPPQPP	QPPQPERTMP RIPTLKNLED LVTEYHGNFS AWSGVSKGLA ESLQPDYSER 480
LCLVSEIPPK	GGALGEGPGA SPCNQHSPYW APPCYTLKPE T 521
SEQ ID NO: 200	
moltype = AA length = 584	
FEATURE	
Location/Qualifiers	
REGION	
1..584	
note = MISC_FEATURE - TNFRSF1B/IL9R/cGC-F/TNFR1-TM	
source	
1..584	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 200	
LPAQVAFTPY	APEPGSTCRL REYYDQTAQM CCSKCSPGQH AKVFCTKTS TVCDSCEDST 60
YTQLWNWVPE	CLSCGSRCS DQVETQACTR EQNRICTRP GWYCALSKQE GCRLCAPLRK 120
CRPGFGVARP	GTETSDVCK PCAPGTFSNT TSSTDICRPH QICNVVAIPG NASMDAVCTS 180
TSPTSRMAPG	AVHLPQPVST RSQHTQPTPE PSTAPSTSFL LPMGPSPPAE GSTGDVLLPL 240
VIFFGLCLLS	LLFIGLMYVK RIFYQNVPS AMFFQPLYSV HNGNFQTMWG AHGAGVLLSQ 300
DCAGTPQGAL	EPCVQEATAL LTCGPAPRWK SVALEEEQEG PGTRLPGNLS SEDVLPAGCT 360
EWVQTLAYL	PQEDWAPTS TRPAPPDSEG SRSSSSSSSS NNNNYCALGC YGGWHLALP 420
GNTQSSGPIP	ALACGLSCDH QGLETQQVA WVLAGHCORP GLHEDLQGM LPSVLSKARS 480
WTFGGGGSGG	GGSGGGGSR TMPRIPTLKN LEDLVTEYHG NFSAWSGVSK GLAESLQPDY 540
SERLCLVSEI	PPKGALGEG PGASPCNQHS PYWAPPCYTL KPET 584
SEQ ID NO: 201	
moltype = AA length = 581	
FEATURE	
Location/Qualifiers	
REGION	
1..581	
note = MISC_FEATURE - TNFRSF1B/IL9R/cGC-S/TNFR1-TM	
source	
1..581	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 201	
LPAQVAFTPY	APEPGSTCRL REYYDQTAQM CCSKCSPGQH AKVFCTKTS TVCDSCEDST 60
YTQLWNWVPE	CLSCGSRCS DQVETQACTR EQNRICTRP GWYCALSKQE GCRLCAPLRK 120
CRPGFGVARP	GTETSDVCK PCAPGTFSNT TSSTDICRPH QICNVVAIPG NASMDAVCTS 180
TSPTSRMAPG	AVHLPQPVST RSQHTQPTPE PSTAPSTSFL LPMGPSPPAE GSTGDVLLPL 240
VIFFGLCLLS	LLFIGLMYVK RIFYQNVPS AMFFQPLYSV HNGNFQTMWG AHGAGVLLSQ 300
DCAGTPQGAL	EPCVQEATAL LTCGPAPRWK SVALEEEQEG PGTRLPGNLS SEDVLPAGCT 360
EWVQTLAYL	PQEDWAPTS TRPAPPDSEG SRSSSSSSSS NNNNYCALGC YGGWHLALP 420
GNTQSSGPIP	ALACGLSCDH QGLETQQVA WVLAGHCORP GLHEDLQGM LPSVLSKARS 480
WTFQPPQPP	QPPQPERTMP RIPTLKNLED LVTEYHGNFS AWSGVSKGLA ESLQPDYSER 540
LCLVSEIPPK	GGALGEGPGA SPCNQHSPYW APPCYTLKPE T 581
SEQ ID NO: 202	
moltype = AA length = 531	
FEATURE	
Location/Qualifiers	
REGION	
1..531	
note = MISC_FEATURE - TNFRSF1/IL9R/cGC-F/TNFR1-TM	
source	
1..531	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 202	
LVPHLGDREK	RDSVCPQGY IHPQNSICC TKCHKGTLY NDCPGPGQDT DCRECESGSF 60
TASENHLRHC	LSCSKCRKEM GQVEISSCTV DRDTCVGRK NQYRHYWSEN LFQCFNCSLC 120
LNGTVHLSCQ	EKQNTVCTCH AGFFLRENEC VSCSNCKKSL ECTKLCLPQI ENVKGTEDSG 180
TTVLLPLVIF	FGLCLLSLLF IGLMYVKRIF YQNVPSAMF FQPLYSVHNG NFQTMGAHG 240
AGVLLSQDCA	GTPQGALEPC VQEATAL LTC GPAPRWK SVALEEEQEG RLPGNLSSD 300
VLPAGCTEWR	VQTLAYLPQE DWAPTSLTRP APPDSEGSR SSSSSSSNN NYCALGCYGG 360
WHLALPGNT	QSSGPIPALA CGLSCDHQGL ETQQGVAVL AGHCORPLH EDLQGMLLPS 420
VLSKARSWTF	GGGGSGGGG GGGGSERTMP RIPTLKNLED LVTEYHGNFS AWSGVSKGLA 480
ESLQPDYSER	LCLVSEIPPK GGALGEGPGA SPCNQHSPYW APPCYTLKPE T 531
SEQ ID NO: 203	
moltype = AA length = 528	
FEATURE	
Location/Qualifiers	
REGION	
1..528	
note = MISC_FEATURE - TNFRSF1/IL9R/cGC-S/TNFR1-TM	
source	
1..528	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 203	

- continued						
LVPHLGDREK	RDSVCPQGY	IHPQNNISIC	TKCHKGTLY	NDCPGPGQDT	DCRECESGSF	60
TASENHLRHC	LSCSKCRKEM	GQVEISSCTV	DRDTVCGCRK	NQYRHYWSEN	LFQCFNCSLC	120
LNQTVHLSCQ	EKQNTVCTCH	AGFFLRENEC	VSCSNCKKSL	ECTKLCLPQI	ENVKGTEDSG	180
TTVLLPLVIF	FGLCLLSLLF	IGLMYVKRIF	YQNVPSPAMF	FQPLYSVHNG	NFQTMGAHG	240
AGVLLSQDCA	GTPQGALEPC	VQEATALLTC	GPARPWKSVA	LEEEQEGPGT	RLPGNLSSSED	300
VLPAGCTEWR	VQTLAYLPQE	DWAPTSLTRP	APPDSEGSRS	SSSSSSSNNN	NYCALGCYGG	360
WHLALPGNT	QSSGPIPALA	CGLSCDHQGL	ETQQGVAVVL	AGHCQRPGLH	EDLQGMLLPS	420
VLSKARSWTF	QPQPQPQPQP	QPERTMPRIP	TLKNLEDLVT	EYHGNFSAWS	GVSKGLAESL	480
QPDYSERLCL	VSEIPPKGGA	LGEGPGASPC	NQHSPYWAPP	CYTLKPET		528
SEQ ID NO: 204						
FEATURE		moltype = AA length = 489				
REGION		Location/Qualifiers				
		1..489				
		note = MISC_FEATURE - anti-HER2 CAR (4D5)				
source		1..489				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 204						
MDFQVQIFSF	LLISASVIMS	RGDIQMTQSP	SSLSASVGDR	VTITCRASQD	VNTAVAWYQQ	60
KPGKAPKLLI	YSASFLYSGV	PSRFSGSRSG	TDFTLTISSL	QPEDFATYYC	QQHYTTPPTF	120
GQGTKVEIKR	TGSTSGSGKP	GSSEGSEVQL	VESGGGLVQP	GGSLRLSCAA	SGFNICKDTYI	180
HWVRQAPGKG	LEWVARIYPT	NGYTRYADSV	KGRFTISADT	SKNTAYLQMN	SLRAEDTAVY	240
YCSRWGGDGF	YAMDVWGQGT	LVTVSSTTTP	APRPPTPAPT	IASQPLSLRP	EACRPAAGGA	300
VHTRGLDFAC	DIYIWAPLAG	TCGVLLLSLV	ITLYCKRGRK	KLLYIFKQPF	MRPVQTTQEE	360
DGCSRFPPEE	EEGGCELRVK	FSRSADAPAY	KQQNQQLYNE	LNLGRREEYD	VLDKRRGRDP	420
EMGKPPRRKN	PQEGLYNELQ	KDKMAEAYSE	IGMKGERRRG	KGHDGLYQGL	STATKDTYDA	480
LHMQUALPPR						489
SEQ ID NO: 205						
FEATURE		moltype = AA length = 657				
REGION		Location/Qualifiers				
		1..657				
		note = MISC_FEATURE - DR6/IL9R/cGC-F/TNFR1-TM				
source		1..657				
		mol_type = protein				
		organism = synthetic construct				
SEQUENCE: 205						
QPEQKASNLI	GTYRHVDRAT	GQVLTCDKCP	AGTYVSEHCT	NTSLRVCSSC	PVGTFTRHEN	60
GIEKCHDCSQ	PCPWPMEIEKL	PCAALTDREC	TCPPGMFQSN	ATCAPHTVCP	VGWGVRRKGT	120
ETEDVRCKQC	ARGTFSDVPS	SVMKCKAYTD	CLSQNLVVIK	PGTKETDNVC	GTLPSFSSST	180
SPSPGTAIFP	RPEHMETHEV	PSSTYVPKGM	NSTESNSSAS	VRPKVLSSIQ	EGTVPDNTSS	240
ARGKEDVNKT	LPNLQVVNHQ	QGPVHHRHILK	LLPSMEATGG	EKSSTPIKGP	KRGHPRQNLH	300
KHFDINEHVL	LPLVIFFGLC	LLSLLFIGLM	YVKRIFYQNV	PSPAMFFQPL	YSVHNGNFQT	360
WMGAHGAGVL	LSQDCAGTPQ	GALEPCVQEA	TALLTCGPAR	PWKSVALEEE	QEGPGTRLPG	420
NLSSEDLVPA	GCTEWRVQTL	AYLPQEDWAP	TSLTRPAPPD	SEGSRSSSSS	SSSNNNNYCA	480
LGCGYGGWHL	ALPGNTQSSG	PIPALACGLS	CDHQGLETOQ	GVAWVLAGHC	QRPGLHEDLQ	540
GMLLPSVLSK	ARSWTFGGGG	SGGGGSGGGG	SERTMPRIPT	LKNLEDLVTE	YHGNFSAWSG	600
VSKGLAESLQ	PDYSERLCLV	SEIPPKGGAL	GEGPGASPCN	QHSPYWAPPC	YTLKPET	657

- What is claimed is:
1. A recombinant nucleic acid molecule encoding a chimeric receptor, said chimeric receptor comprising:

an extracellular portion comprising a binding domain of an endogenous cytokine receptor;

an intracellular portion comprising an endodomain of an IL-9 receptor; and

a transmembrane domain that joins the extracellular portion and the intracellular portion.

2. The recombinant nucleic acid molecule of claim 1 further comprising one or more linkers.

3. The recombinant nucleic acid molecule of claim 1, wherein the endogenous cytokine receptor is selected from IL-2rb, IL-2ra, IL-4r, IL-7ra, IL-15ra, and IL-21ra.

4. The recombinant nucleic acid molecule according to claim 1, wherein the endogenous cytokine receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 1-6.

5. The recombinant nucleic acid molecule according to claim 1, wherein the transmembrane domain is selected from the transmembrane domain of IL-9, IL-7ra, IL-2rb, and TNFR1.

6. The recombinant nucleic acid molecule according to claim 5, wherein the transmembrane domain comprises an amino acid sequence selected from SEQ ID Nos: 53-56.

7. The recombinant nucleic acid molecule according to claim 1, wherein the recombinant nucleic acid molecule is incorporated into a vector.

8. The recombinant nucleic acid molecule according to claim 1, wherein the chimeric receptor comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 63-80.

9. The recombinant nucleic acid molecule according to claim 1, wherein the chimeric receptor comprises the amino acid sequence selected from SEQ ID Nos. 63 and 72.

10. The recombinant nucleic acid molecule according to claim 1, further comprising a signal sequence.

11. The recombinant nucleic acid molecule according to claim 10, wherein the signal sequence comprises the amino acid sequence of MAAPALSWRLPLLILLPLATSWASA (SEQ ID NO: 62).

12. The recombinant nucleic acid molecule according to claim **1** further comprising a 2A linker.

13. The recombinant nucleic acid molecule according to claim **1** further comprising a nucleic acid sequence encoding a chimeric antigen receptor.

14. An expression vector comprising the recombinant nucleic acid molecule of claim **1**.

15. A recombinant cell comprising the recombinant nucleic acid construct according to claim **1**.

16. The recombinant cell of claim **15**, wherein the recombinant cell is a eukaryotic cell.

17. The recombinant cell of claim **16**, wherein the eukaryotic cell is an animal cell.

18. The recombinant cell of claim **17**, wherein the animal cell is a mammalian cell.

19. The recombinant cell of claim **18**, wherein the mammalian cell is an immune cell, a neuron, an epithelial cell, and endothelial cell, or a stem cell.

20. The recombinant cell of claim **19**, wherein the recombinant cell is an immune cell or a dendritic cell.

21. The recombinant cell of claim **20**, wherein the immune cell is a B cell, a monocyte, a natural killer (NK) cell, a basophil, an eosinophil, a neutrophil, a dendritic cell, a macrophage, a regulatory T cell, a helper T cell (T_H), a cytotoxic T cell (T_{CTL}), or other T cell.

22. A polypeptide encoded by the recombinant nucleic acid of claim **1**.

23. The polypeptide of claim **22**, wherein the polypeptide comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 1-6.

24. The polypeptide of claim **22**, wherein the polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 53-56.

25. The polypeptide of claim **22**, wherein the polypeptide comprises an amino acid sequence having at least 80% sequence identity to an amino acid sequence selected from SEQ ID Nos: 63-80.

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