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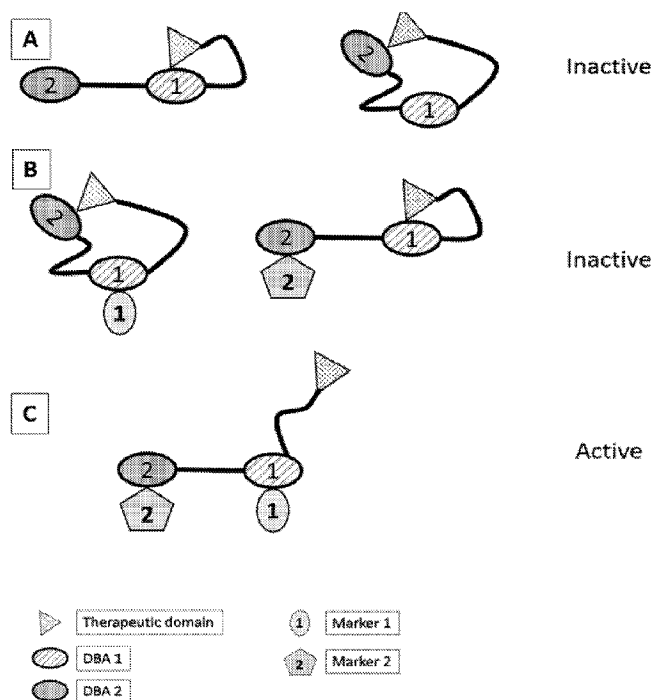


FIG. 13

(57) Abrégé/Abstract:

Provided herein are protein complexes comprising a sensor domain and a therapeutic domain linked by a linker, and methods of use thereof. In aspects of the present disclosure, activity of the therapeutic domain comprises a dependence on sensor domain binding to target markers.



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Abstract:

Provided herein are protein complexes comprising a sensor domain and a therapeutic domain linked by a linker, and methods of use thereof. In aspects of the present disclosure, activity of the therapeutic domain comprises a dependence on sensor domain binding to target markers.

COMPOSITIONS OF PROTEIN COMPLEXES AND METHODS OF USE THEREOF**CROSS-REFERENCE**

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/024,422, filed May 13, 2020, which is entirely incorporated herein by reference in its entirety.

BACKGROUND

[0002] Many promising therapeutics that are needed locally exhibit toxicity upon systemic administration. There is a need for drugs that can be delivered systemically but can be regulated to exhibit therapeutic activity locally or in the presence of markers for disease.

SUMMARY

[0003] In various aspects, the present disclosure provides a complex comprising: a) a therapeutic domain; b) a linker; and c) a sensor domain, wherein the therapeutic domain is linked to the sensor domain by the linker, and wherein the sensor domain is capable of binding the therapeutic domain and a marker.

[0004] In some aspects, the sensor domain is bound to the therapeutic domain in an absence of the marker. In some aspects, the therapeutic domain is blocked from binding the sensor domain upon binding of the sensor domain to the marker. In some aspects, the activity of the therapeutic domain is reduced upon binding of the therapeutic domain to the sensor domain. In some aspects, the therapeutic domain is capable of exhibiting therapeutic activity upon binding of the sensor domain to the marker. In some aspects, the therapeutic domain is therapeutically active upon binding of the sensor domain to the marker.

[0005] In some aspects, the sensor domain comprises an antibody. In some aspects, the antibody is an antibody fragment or antibody derivative. In some aspects, the complex comprises an Fc domain. In some aspects, the complex comprises a domain that improves kinetic properties. In some aspects, the complex includes two heavy chains and two light chains.

[0006] In some aspects, the complex comprises two therapeutic domains. In some aspects, the complex comprises two sensor domains. In some aspects, the complex is a regulated therapeutic protein. In some aspects, the therapeutic domain is a cytokine, a chemokine, an antibody, an antibody fragment, a peptide agonist, a peptide antagonist, an enzyme, a soluble receptor, a growth factor, a protein toxin, a soluble ligand, a small molecule, or any combination thereof. In some aspects, the antibody or the antibody fragment comprises an IgG, a single domain antibody fragment, a nanobody, or a single chain variable fragment (scFv).

[0007] In some aspects, the therapeutic domain is an IL-2 receptor agonist. In some aspects, the IL-2 receptor agonist is IL-2, IL-15, or variants or fusions thereof. In some aspects, the therapeutic domain is IFN α , IFN γ , IL-12, IL-4, IL-8, IL-10, IL-15, IL-18, IL-21, TGF beta, an anti-CD3 antibody, an anti-CD28 antibody or ligand, an antibody to or ligand of CD40, GITR, OX40, CD137, CD27, or Death Receptors, the extracellular domain of TGFBR2, VEGF-C, kynureninase, IL-7, TNF, MICA, MICB, CD47, an anti-CTLA4 antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody. In some aspects, the therapeutic domain binds to the sensor domain.

[0008] In some aspects, the linker is a polypeptide linker. In some aspects, the linker comprises from 2 to 200 amino acids in length. In some aspects, the linker is: attached to a heavy chain of the sensor domain, attached to a light chain of the sensor domain, is a fusion with an N-terminus of the sensor domain, or is a fusion with a C-terminus of the sensor domain. In some aspects, the linker is: attached to a heavy chain of the therapeutic domain, attached to a light chain of the therapeutic domain, is a fusion with an N-terminus of the therapeutic domain, or is a fusion with a C-terminus of the therapeutic domain.

[0009] In some aspects, the activity of the therapeutic domain is reduced when bound to the sensor domain. In some aspects, the therapeutic domain is inactive when bound to the sensor domain. In some aspects, the sensor domain blocks the activity of the therapeutic domain when bound to the therapeutic domain. In some aspects, the therapeutic domain is active when the sensor domain is bound to the marker. In some aspects, an affinity of the sensor domain for the marker is equal to or greater than an affinity of the sensor domain for the therapeutic domain.

[0010] In some aspects, an affinity of the sensor domain for the marker is at least 2 times, 5 times, 10 times, 100 times, 1000 times, 10000, or 100000 times greater than an affinity of the sensor domain for the therapeutic domain.

[0011] In some aspects, the sensor domain is an antibody or a fragment thereof. In some aspects, the sensor domain comprises one or both antigen binding domains of a bispecific antibody. In some aspects, the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and is capable of binding to the marker, and a second antigen binding domain that is capable of binding to the marker. In some aspects, the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and the marker and a second antigen binding domain that is capable of binding to a second marker. In some aspects, the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and the marker and a second antigen binding domain that is capable of binding to the therapeutic domain and a second marker. In some aspects, the bispecific antibody comprises a single therapeutic domain.

[0012] In some aspects, the therapeutic domain is IFN α , the first marker is ATP, and the second marker is CEA. In some aspects, the sensor domain binds to an IL-2 receptor agonist and to PD-1. In some aspects, the IL-2 receptor agonist is IL-2, IL-15, or variants or fusions thereof. In some aspects, the sensor domain binds to IFN α and PD-L1.

[0013] In some aspects, the marker is a surface protein, a cell surface marker, or soluble ATP. In some aspects, the marker is a secreted protein. In some aspects, the marker is expressed by a cancer cell. In some aspects, the marker is expressed by an immune cell. In some aspects, the marker is PD-1. In some aspects, the marker is PD-L1. In some aspects, the marker is CEACAM5. In some aspects, the marker is FAP. In some aspects, the marker is LRRC15. In some aspects, the marker is expressed by a stromal cell. In some aspects, the marker is expressed by an endothelial cell. In some aspects, the marker is a metabolite. In some aspects, the marker is adenosine, AMP, ADP, or ATP. In some aspects, the marker is kynurenine.

[0014] In some aspects, the sensor domain comprises a complementarity determining region selected from **TABLE 13** or **TABLE 18**. In some aspects, the sensor domain is selected from **TABLE 13**. In some aspects, the complex is selected from **TABLE 15**.

In some aspects, the sensor domain comprises a complementarity determining region having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20 or SEQ ID NO: 142 – SEQ ID NO: 173, or SEQ ID NO: 238-252. In some aspects, the sensor domain has at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 21 – SEQ ID NO: 27, SEQ ID NO: 31 – SEQ ID NO: 39, or SEQ ID NO: 127 – SEQ ID NO: 141. In some aspects, the protein complex has at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, SEQ ID NO: 289- 293, or a fragment thereof.

[0015] In various aspects, the present disclosure provides a method comprising administering any of the above complexes to a subject in need thereof. In various aspects, the present disclosure provides a method of treating a subject in need thereof comprising administering any of the above complexes to the subject in need thereof. In some aspects, the administering comprises intravenous, intramuscular, or subcutaneous administration. In some aspects, the subject in need thereof has cancer. In some aspects, the subject in need thereof has an autoimmune disease. In some aspects, the subject in need thereof has a viral disease. In some

aspects, the therapeutic domain treats the subject in need thereof. In some aspects, the subject in need thereof is a mammal. In some aspects, the subject in need thereof is a human.

INCORPORATION BY REFERENCE

[0016] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] The novel features of the disclosure are set forth with particularity in the appended claims. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee. A better understanding of the features and advantages of the present disclosure will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the disclosure are utilized, and the accompanying drawings of which:

[0018] **FIG. 1A and 1B** shows a schematic of the protein complexes of the present disclosure. **FIG. 1A** shows an exemplary dual binding protein complex in an inactive state. The protein complex has a sensor domain and a therapeutic domain. The sensor domain and therapeutic domain are linked by a linker. The sensor domain is shown bound to the therapeutic domain, rendering the therapeutic domain inactive. **FIG. 1B** shows an exemplary dual binding protein complex in an active state. The protein complex has a sensor domain and a therapeutic domain. The sensor domain and therapeutic domain are linked by a linker. The sensor domain is shown bound to a marker (e.g., a tumor marker or other disease marker), rendering the therapeutic domain active.

[0019] **FIG. 2** shows an example of a protein complex in an active state when bound to a tumor and examples of protein complex in an inactive state when not bound to a tumor.

[0020] **FIG. 3** shows an exemplary gBlock sequence used for cell-free expression of scFv antibodies.

[0021] **FIG. 4** shows candidate PD-L1/IFN α DBAs bind IFN α .

[0022] **FIG. 5** shows candidate PD-L1/IFN α DBAs bind PD-L1.

[0023] **FIG. 6** shows inhibition of IFN α binding to IFNAR by candidate PD-L1/IFN α DBAs.

[0024] **FIG. 7** shows IFN α can compete with PD-L1 for binding to candidate PD-L1/IFN α DBAs of SEQ ID NO: 24 and SEQ ID NO: 26.

[0025] **FIG. 8** shows a schematic of a protein complex comprising a cytokine therapeutic domain and a DBA (at left) and said protein complex's sequence (at right).

[0026] **FIG. 9A-F** shows schematics of other protein complexes of the present disclosure comprising one or more sensor domains and one or more therapeutic domain.

[0027] **FIG. 10** shows that interferon signaling by two exemplary PD-L1/IFN α DBA cytokine protein complexes (C08 IFN α and B09 IFN α , SEQ ID NO: 57 – SEQ ID NO: 58 and SEQ ID NO: 59 – SEQ ID NO: 60 respectively) is reduced as compared to two control IFN α -antibody protein complexes (Anti-HER2 IFN α and Anti-PD-L1 IFN α , SEQ ID NO: 63 – SEQ ID NO: 64 and SEQ ID NO: 61 – SEQ ID NO: 62 respectively).

[0028] **FIG. 11** shows that IL-2 signaling by five exemplary PD-1/IL-2 DBA-cytokine protein complexes (2_A08, 2_A11, 2_B05, 2_B07, and 7_A04, SEQ ID NO: 67 – SEQ ID NO: 68, SEQ ID NO: 69 – SEQ ID NO: 70, SEQ ID NO: 71 – SEQ ID NO: 72, SEQ ID NO: 73 – SEQ ID NO: 74 and SEQ ID NO: 75 – SEQ ID NO: 76 respectively) is reduced as compared to a control IL-2-Anti-HER2 protein complex (SEQ ID NO: 65 – SEQ ID NO: 66).

[0029] **FIG. 12** shows PD-L1 regulated IFN α activity of an exemplary PD-L1/IFN α DBA-cytokine protein complex.

[0030] **FIG. 13A-C** shows a schematic of a bispecific antibody comprising a therapeutic domain and two sensor domains such that both sensor domains must bind their target marker to allow activity of the therapeutic domain.

[0031] **FIG. 14A-C** illustrate immunoglobulin-containing protein complexes consistent with the present disclosure.

[0032] **FIG. 15A-D** provide IL-2 activity of IL-2-linked protein complexes comprising the structure depicted in **FIG. 14A** in wells coated with PD-1-Fc or an IgG1 control protein. Activity was measured as growth of a 630 nm signal from HEK-Blue™ IL-2 reporter cells (an engineered human kidney cell line which generates a detectable color change in upon activation of its IL-2 receptor). **FIG. 15A** provides the IL-2 activity of an PD-1/IL-2 DBA-IL-2 complex. **FIG. 15B** provides the IL-2 activity of an anti-Her2 antibody-IL-2 complex. **FIG. 15C** provides the activity of an anti-IL-2 antibody-IL-2 complex. **FIG. 15D** provides the activity of an anti-PD-1 antibody-IL-2 complex.

[0033] **FIG. 16A-F** provide IL-2 activity of protein complexes comprising the structure depicted in **FIG. 14B** in wells coated with PD-1-Fc or an IgG1 control protein. Activity was measured as growth of a 630 nm signal from HEK-Blue™ IL-2 reporter cells. **FIG. 16A-C** provide the IL-2 activities of three different PD-1/IL-2 DBA-IL-2 complexes. **FIG. 16D** provides the activity of an anti-PD-1 antibody-IL-2 complex. **FIG. 16E** provides the activity of

an anti-Her-2 antibody-IL-2 complex. **FIG. 16F** provides the activity of an anti-IL-2 antibody-IL-2 complex.

[0034] FIG. 17A-F provide IL-2 activity of protein complexes comprising the structure depicted in **FIG. 14C** in wells coated with PD-1-Fc or an IgG1 control protein. Activity was measured as growth of a 630 nm signal from HEK-Blue™ IL-2 reporter cells. **FIG. 17B 17D** provide results for two PD-1/IL-2 DBA complexes comprising anti-PD-1 domains in the Fab arms and a PD-1/IL-2 DBA scFv on the Fc arm. **FIG. 17A, 17C, and 17E-H** provide results for control protein complexes.

[0035] FIG. 18 provides rates of serum concentration decreases in the blood of wild-type mice of a PD-1/IL-2 DBA-cytokine complex ('2B07 IL-2 mut') and two control complexes.

[0036] FIG. 19A-D provide CD8⁺ T cell and NK cell counts in blood and spleen tissue collected from wild-type mice 5 days following treatment with a PD-1/IL-2 DBA-cytokine complex ('2B07 IL-2 mut') and two control complexes.

[0037] FIG. 20 provides tumor volume measurements as a function of the number of days post tumor cell implant in mice. Mice received various intravenous doses of a PD-1/IL-2 DBA-IL-2 complex, a PD-1/IL-2 DBA complex lacking IL-2, or an isotype control.

[0038] FIG. 21A-F provide results for IFNAR2 binding in the presence (triangles) and absence (squares) of PD-L1 for six separate DBA PDL1-IFN variants.

[0039] FIG. 22A-H provide IFNAR2 binding by five PD-L1/IFN α DBA-cytokine complexes and three control complexes.

[0040] FIG. 23A-D provide ELISA measurements for PD-L1 and IL-15 binding by four separate anti-PD-L1 and anti-IL-15 DBAs.

[0041] FIG. 24A-F provide IL-15 activity as measured by HEK-Blue™ IL-2 reporter cell colorimetric responses for four scFv DBA-IL-15 complexes and two monospecific anti-IL-15 antibody IL-15 complexes.

[0042] FIG. 25A-D provide IL-15 activity as measured by HEK-Blue™ IL-2 reporter cell colorimetric responses for two DBA-IL-15 complexes and PDL1-IFN DBA control protein complexes.

[0043] FIG. 26 shows ELISA binding data for five dual-binding scFvs binding to CEA.

[0044] FIG. 27A-F demonstrate IFNAR2 binding by three DBA-cytokine protein complexes, an IFN α monospecific binding scFv, and two non-IFN α binding scFvs.

[0045] FIG. 28A provides ELISA binding data for six scFvs to LRRC15. Results from **FIG. 28A** are summarized in **FIG. 28B**.

[0046] FIG. 29A-F summarize IFNAR2 binding by four LRRC15-IFN- α DBA-IFN α complexes and two control complexes.

DETAILED DESCRIPTION

[0047] The present disclosure provides compositions of protein complexes and methods of use thereof. Promising therapeutics are often unable to be realized due to harmful side effects, or systemic on-target toxicity. Provided herein are protein complexes, which specifically exhibit therapeutic efficacy locally, where the relevant cells and targets are present. Moreover, protein complexes of the present disclosure are self-regulated, remaining inactive in the absence of a specific marker and activating in the presence of the specific marker. The protein complexes disclosed herein may include a sensor domain (e.g., an antibody or scFv) that is linked to a therapeutic domain (e.g., a cytokine, a therapeutic antibody domain, a receptor, a ligand) via a linker. The sensor domain may be a dual binding protein that has affinity for the therapeutic domain and a specific marker, such that the marker and the therapeutic domain compete for binding to the sensor domain. In some embodiments, the dual binding protein is a dual binding antibody. In the absence of the marker, the sensor domain binds the therapeutic domain, rendering the therapeutic domain unable to exert activity. When the sensor domain is bound to the marker, the therapeutic domain is unbound and may exert activity. In some embodiments, regulation of therapeutic activity by the complex may be reversible, that is, when the sensor domain disassociates from the marker, the sensor domain may bind the therapeutic domain, rendering the therapeutic domain once again unable to exert activity. Thus, the protein complexes of the present disclosure comprise sensor domains that regulate therapeutic domains in the presence of the marker, bind the marker, and render the therapeutic domain active. Various structures and compositions of protein complexes are disclosed herein, including pharmaceutical formulations. Also provided herein are methods for treating a subject in need thereof by administering the protein complex to the subject.

[0048] As used herein, a “marker” may refer to the moiety that is bound by the sensor domain of the protein complexes disclosed herein. Non-limiting examples of a “marker” include a protein, a protein modification, a carbohydrate, a metabolite, or any other molecule that can be bound by an antibody. A marker may also refer to a disease-specific marker, such as a molecular marker of a disease state (e.g., cancer).

[0049] As used herein, a “target” may refer to a molecule through which the therapeutic domain of the protein complexes disclosed herein may act. Non-limiting examples of a “target” include cytokine receptor, a cytokine, a ligand, an enzyme substrate, or any other molecule that, when contacted by the therapeutic domain, has a therapeutic impact on a subject (e.g., human or non-human animal) administered the protein complex.

[0050] As used herein, an “antibody” may refer to an antibody, an antibody derivative, or fragment(s) thereof that contains part or all of an antibody variable domain.

[0051] The term “recombinant nucleic acid” refers to synthetic nucleic acid having a nucleotide sequence that is not naturally occurring. A recombinant nucleic acid may be synthesized in the laboratory. A recombinant nucleic acid is prepared by using recombinant DNA technology by using enzymatic modification of DNA, such as enzymatic restriction digestion, ligation, and DNA cloning. A recombinant nucleic acid as used herein can be DNA, or RNA. A recombinant DNA may be transcribed in vitro, to generate a messenger RNA (mRNA), the recombinant mRNA may be isolated, purified and used to transfect a cell. A recombinant nucleic acid may encode a protein or a polypeptide. A recombinant nucleic acid, under suitable conditions, can be incorporated into a living cell, and can be expressed inside the living cell. As used herein, “expression” of a nucleic acid usually refers to transcription and/or translation of the nucleic acid. The product of a nucleic acid expression is usually a protein but can also be an mRNA. Detection of an mRNA encoded by a recombinant nucleic acid in a cell that has incorporated the recombinant nucleic acid, is considered positive proof that the nucleic acid is “expressed” in the cell.

[0052] The process of inserting or incorporating a nucleic acid into a cell can be via transformation, transfection or transduction. Transformation is the process of uptake of foreign nucleic acid by a bacterial cell. This process is adapted for propagation of plasmid DNA, protein production, and other applications. Transformation introduces recombinant plasmid DNA into competent bacterial cells that take up extracellular DNA from the environment. Some bacterial species are naturally competent under certain environmental conditions, but competence is artificially induced in a laboratory setting. Transfection is the forced introduction of small molecules such as DNA, RNA, or antibodies into eukaryotic cells. Just to make life confusing, ‘transfection’ also refers to the introduction of bacteriophage into bacterial cells. ‘Transduction’ is mostly used to describe the introduction of recombinant viral vector particles into target cells, while ‘infection’ refers to natural infections of humans or animals with wild-type viruses.

Protein Complexes

[0053] The present disclosure provides complexes that may self-regulate therapeutic activity. Protein complexes of the present disclosure may include a sensor domain and a therapeutic domain. The sensor domain and therapeutic domain may be linked by a linker. The sensor domain may regulate the activity of the therapeutic domain. Regulation of the activity of the therapeutic domain may include binding of the sensor domain to the therapeutic domain, rendering the therapeutic domain unable to exert therapeutic activity. Regulation of the activity of the therapeutic domain may further include unbinding, or release, of the therapeutic domain by the sensor domain upon binding of the sensor domain to a marker. The marker may be

expressed by a cell associated with a disease. For example, the disease may be cancer, the cell may be a tumor cell, and the marker may be a tumor-specific marker that is expressed on tumor cells. Thus, the protein complexes of the present disclosure are superior drug candidates as the sensor domain-dependent activity of the therapeutic domain allows for localized activity, even upon systemic administration of the protein complex. Compared to therapeutic domains administered on their own, the protein complexes of the present disclosure exhibit regulated therapeutic activity of the therapeutic domain. As a result, compared to free therapeutic domains administered on their own, the protein complexes of the present disclosure exhibit reduced systemic on-target toxicity.

[0054] The protein complexes of the present disclosure can have an Fc region. The protein complexes of the present disclosure can have a domain that improves kinetic properties. For example, the protein complexes of the present disclosure may be further coupled to a half-life extender, such as an Fc region, albumin, PEG, or another zwitterionic polymer. The protein complexes of the present disclosure may have two heavy chains and two light chains. The protein complexes of the present disclosure may have two heavy chains and one light chain. The protein complexes of the present disclosure may include multiple sensor domains and multiple therapeutic domains. For example, a protein complex of the present disclosure may include two sensor domains and two therapeutic domains, all of which are linked and in which the two therapeutic domains are bound to the two sensor domains. In some embodiments, a protein complex of the present disclosure may include two sensor domains and one therapeutic domain, all of which are linked and in which the therapeutic domain may bind to both sensor domains or only one of the two sensor domains.

[0055] In some embodiments, the marker may be a surface protein, such as a cell surface protein. The marker may also be soluble ATP. In some embodiments, the marker may be a secreted protein. For example, the secreted protein may be a protein that is released by proliferating tumor cells. In some embodiments, the marker may be expressed by a cancer cell. The marker may be expressed by an immune cell. The marker may be expressed by a stromal cell. The marker may be expressed by an endothelial cell. Exemplary markers include PD1, PD-L1, CEACAM5, FAP, LRRC15, a metabolite, adenosine, AMP, ADP, ATP, or kynurenine. Other markers may include CRIPTO, CD19, CD20, CD22, CD30, CD33, Glycoprotein NMB, CanAg, HER2 (ErbB2/Neu), CD56 (NCAM), CD70, CD79, CD138, PSCA, PSMA (prostate specific membrane antigen), BCMA, E-selectin, EphB2, Melanotransferin, Muc16 and TMEFF2, or any other marker described in US 10,561,739, incorporated herein by reference in its entirety. Other markers may also include BMPR1B, E16, STEAP1, 0772P, MPF, Napi3b, Sema 5b, PSCA hlg, ETBR, MSG783, STEAP2, TrpM4, CD21, CD79b, FcRH2, NCA, MDP,

IL20R α , Brevican, EphB2R, ASLG659, PSCA, GEDA, BAFF-R, CD79a, CXCR5, HLA-DOB, P2X5, CD72, FCRHI, IRTA2, or any other marker described in WO 2005/082023, incorporated herein by reference in its entirety.

[0056] In some embodiments, binding of the sensor domain to the therapeutic domain versus binding of the sensor domain to a marker is regulated by the relative affinity of the sensor domain for the therapeutic domain. In some embodiments, the sensor domain may have a dissociation constant (K_d) for the marker that is lower than the dissociation constant of the sensor domain for the therapeutic domain. Thus, the sensor may have a higher affinity (lower K_d) for the marker than for the therapeutic domain. The sensor domains of the present disclosure may be engineered, for example by affinity maturation, to have a higher affinity (lower dissociation constant) for the marker than the therapeutic domain. In the absence of the marker, the sensor domain of the present disclosure may have a sufficiently high affinity for the therapeutic domain such that the therapeutic domain is bound by the sensor domain. In the presence of the marker, the affinity of the sensor domain for the marker is sufficiently high (low dissociation constant), such that the marker outcompetes the therapeutic domain for binding to the sensor domain. As a result, the equilibrium binding shifts from a state in which the sensor domain is bound to the therapeutic domain to a state in which the therapeutic domain is unbound and the sensor domain binds to the marker.

[0057] The sensor domain may have an affinity for the marker that is at least 2-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 5-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 10-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 15-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 20-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 25-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 30-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 35-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 40-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 45-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 50-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is at least 60-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that

[illegible]

350-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 350 to 400-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 400 to 450-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 450 to 500-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 500 to 1000-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 10 to 80-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 30 to 70-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 40 to 60-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 20 to 50-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 10 to 1000-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 70 to 500-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 100 to 500-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 500 to 750-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 250 to 750-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 1000 to 100000-fold higher than an affinity for the therapeutic domain. The sensor domain may have an affinity for the marker that is from 2 to 100000-fold higher than an affinity for the therapeutic domain.

[0058] A protein complex of the present disclosure, or a fragment thereof, may comprise one or more complementary determining regions (CDRs) having at least 80% sequence identity to any one of the CDRs disclosed herein. For example, a protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 80% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 85% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 90% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 92% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20,

SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 95% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 97% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having at least 99% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. A protein complex of the present disclosure, or a fragment thereof, may comprise one or more CDRs having any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252.

[0059] A protein complex, or a fragment thereof, can have at least 80% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 85% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 90% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 92% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 95% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 97% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO:

210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex can have at least 99% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof. A protein complex is any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof.

[0060] A protein complex of the present disclosure may have at least 95% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293, or a fragment thereof and have one or more CDRs with at least 80% sequence identity to any one SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252. The protein complexes of the present disclosure can have CDRs selected from SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142-173, or SEQ ID NO: 238-252 arranged in any combination or order.

[0061] A fragment of any of the above may retain the functional binding domains of the sensor or any functional therapeutic domains of the therapeutic. For example, a dual binding antibody protein complex can include the entire antibody or a fragment having regions of the antibody that are capable of binding to a marker and the therapeutic domain. In the latter case, the fragment may be an scFv that can bind to a marker and the therapeutic domain. Exemplary sequence of protein complexes of the present disclosure is shown below in **TABLE 1**.

TABLE 1 – Exemplary Protein Complexes

SEQ ID NO	Sequence	Description
SEQ ID NO: 41	MSTSTCDLPQTHSLGSRRTLMLLAQMRRLSL FSCLKDRHDFGFPQEEFGNQFQKAETIPVLHE MIQQIFNLFSTKDSSAAWDETLLDKFYTELY QQLNDLEACVIQGVGVTTETPLMKEDSILAVR KYFQRITLYLKEKKYSPCAWEVVR AEIMRSF SLSTNLQESLRSKEGGGGSGGGGSGGGGSGG GGSQVQLVQSGAEVKKPGASVKV SCKASGY TFSNYYVHWVRQAPGQGLEWMGWMDPNS GGTGYAHQFQGRVTMTRDTSTSTVYME LSS LRSEDTAVYYCAKEVFSGWYDYWGQGTLV TVSSASGGGGSGGGGSGGGGSHASDIQMTQS	Protein complex comprising a DBA/cytokine complex having a PD-L1/IFN α scFv sensor domain and an IFN α therapeutic domain scFv_IFN-Heavy_GS20_PDL1

SEQ ID NO	Sequence	Description
	PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQSYSTPYTFGGQGTKVEIKGKPIPNPLLGLDST	- IFN_1A05_H_I39V_S58P_Q69H_K70Q
SEQ ID NO: 42	QVQLVQSGAEVKKPGASVKVSCKASGYTFTKNYMHWRQAPGQGLEWLGWVSPDSGYTG YAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCTDLLSLELDDAFDIWGQGTMTVTVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYAASLTQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQSYSTPLTFGGGTKLEIKPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLSCAVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMVSKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK	Protein complex comprising a DBA/cytokine complex having a PD-L1 antibody sensor domain and an IFN α therapeutic domain, where the DBA is an scFv PDL1- IFN_uIFN_2D10sc Fv_KiH_PDL1- IFN_1A05_H_N36 G_Pep1
SEQ ID NO: 43	CDLPQTHSLGSRRTLMMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFCTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFRITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEGGGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSGYIHWVRQAPGQGLEWMGMWDSNSGGTGYA QKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCAKEVFSGWYDYWGQGLTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVCVLPPEEEMTKKQVTLWCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK	First heavy chain of a protein complex comprising a DBA/cytokine complex having a PD-L1 binding domain and an IFN α therapeutic domain PDL1- IFN_uIFN_2D10sc Fv_KiH_PDL1- IFN_1A05_H_N36 G_Pep2
SEQ ID NO: 44	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQSYSTPYTFGGQGTKVEIKRADAAPTVSIFPPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	Light chain of a protein complex comprising a DBA/cytokine complex having a PD-L1 scFv sensor domain and an IFN α therapeutic domain

SEQ ID NO	Sequence	Description
		PDL1- IFN_uIFN_2D10sc Fv_KiH_PDL1- IFN_1A05_H_N36 G Pep3
SEQ ID NO: 303	QVQLVESGGGVVQPGRSLRLDCKASGITFSN SGMHWVRQAPGKGLEWVAVIWIYDGSKRYY ADSVKGRFTISRDN SKNTLFLQMNSLRAEDT AVYYCATNDDYWGQGT LVT VSSAKTTAPSV YPLAPVCGD TTGSSVTLGCLVKGYFPEPVTL TWN SGLSSGVHTFPAVLQSDLYTLSSSVTV TSSTWPSQSITCNVAHPASSTKVDKKIEPRGP TIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLM ISLSPIVTCVVVDVSEDDPDVQISW FVNNVEV HTAQTQTHREDYNSTLRVVSALPIQH QDWM SGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVYVLPPEKEMTKKQVSLTCLVKDFMPEDI YVEWTNNGKTELNYKNTEPV LKSDGSYFMY SKLTVEKKNWVERN SYSCSVVHEGLHNHHT TKSFSRTPGGGGGSGGGGSGGGGSGGGGSQ VQLVQSGAEVKKPGASVKV SCKASGDTFTR YYVHWVRQAPGQGLEWMGIINPSGGYASYA QKFQGRVTMTTRDTSTSTVYME LSSLRSEDTA VYYCAAGLFIWGQGT LVT VSSASGGGGSGG GGSGGGGSHASDIQMTQSPSSLSASVGDRVTI TCRASQSIGRWLAWYQQKPGKAPKLLIYSAS NLETGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYNRFPVTFGP GTKVDIK	PD1- IL2_3x_Cterm_Nivo _2B07_H_H37Y_L_ A107Y_S109R; AF4505_pep2
SEQ ID NO: 304	QVQLVESGGGVVQPGRSLRLDCKASGITFSN SGMHWVRQAPGKGLEWVAVIWIYDGSKRYY ADSVKGRFTISRDN SKNTLFLQMNSLRAEDT AVYYCATNDDYWGQGT LVT VSSAKTTAPSV YPLAPVCGD TTGSSVTLGCLVKGYFPEPVTL TWN SGLSSGVHTFPAVLQSDLYTLSSSVTV TSSTWPSQSITCNVAHPASSTKVDKKIEPRGP TIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLM ISLSPIVTCVVVDVSEDDPDVQISW FVNNVEV HTAQTQTHREDYNSTLRVVSALPIQH QDWM SGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVYVLPPEKEMTKKQVSLTCLVKDFMPEDI YVEWTNNGKTELNYKNTEPV LKSDGSYFMY SKLTVEKKNWVERN SYSCSVVHEGLHNHHT TKSFSRTPGGGGGSGGGGSGGGGSGGGGSQ VQLVQSGAEVKKPGASVKV SCKASGYTFTR YYMHWVRQAPGQGLEWMGIINPRAGYTSY ALKFQGRVTMTTRDTSTSTVYME LSSLRSED AVYYCTSGWDVWGQGT LVT VSSASGGGGG GGGGSGGGGSHASDIQMTQSPSSLSASVGDR VTITCRASQSISTWLAWYQQKPGKAPKLLIY	PD1- IL2_3x_Cterm_Niv o_704var AF4504_pep2

SEQ ID NO	Sequence	Description
	AASSLD SGVPSRFSGSGSGTDFLTISSLQPED FATYYCQQSYSPVTFGQGTKVEIK	
SEQ ID NO: 181	APTSSTKKTQLQLEHLLLDLQMILNGINNYK NPKLTDMLTFFFYMPKKATELKHLQCLEREL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLEL KGSETTFMCEYADETATIVEFLNRWITFCQSII STLTGGGGSGGGSGGGSGGGGSQVQLVQ SGAEVKKPGASVKVSCASGDTFTRYVHW VRQAPGQGLEWMGIINPSGGYASYAQKFQG RVTMTRDTSTSTVYMESSLRSED TAVYYCA AGLFIWGQGLTVTVSSAKTTAPSVYPLAPVC GDTTGSSVTLGCLVKGYFPEPVTLTWNSGSL SSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQ SITCNVAHPASSTKVDKKIEPRGPTIKPCPPCK CPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTC VVVDVSEDDPDVQISWVFNNEVHTAQTQT HREDYNSTLRVVSALPIQH QDWMMSGKEFKC KVNNKDLGAPIERTISKPKGSVRAPQVYVLPP PEEEMTKKQVTLTCMVTDFMPEDIYVEWTN NGKTELNYKNTEPVLDSDGSYFMYSDLRVE KKNWVERNSYSCSVVHEGLHNHHTTESFSR TPGK	PD1- IL2_3x_Asym_PD1 - IL2_2B07_H_H37Y _L_W38Y_A107Y
SEQ ID NO: 182	QVQLVQSGAEVKKPGASVKVSCASGDTFTRYVHWV RQAPGQGLEWMGIINPSGGYASYAQKFQGRVTMTRD TSTSTVYMESSLRSED TAVYYCAAGLFIWGQGLTVTVS SAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPV TLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPS QSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPN AAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDV QISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQ VYVLPPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNN GKTELNYKNTEPVLSKSDGSYFMYSKLTVEKKNWVERNS YSCSVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHH H	PD1- IL2_3x_Asym_PD1 - IL2_2B07_H_H37Y _L_W38Y_A107Y
SEQ ID NO: 183	APTSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTD MLTFFFYMPKKATELKHLQCLERELKPLEEVLNLAQSKNF HLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLN RWITFCQSIISTLTGGGGSGGGSGGGSGGGGSQVQ LVQSGAEVKKPGASVKVSCASGYTFTDYMHVVRQ APGQGLEWMGIINPRAGYTSYALKFQGRVTMTRDTST STVYMESSLRSED TAVYYCTSGWDVWGQGLTVTVSS AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTL TWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPS QSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPN AAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDV	PD1- IL2_3x_Asym_PD1 - IL2_7A04_H_M115 W_L_Q68D

SEQ ID NO	Sequence	Description
	QISWVFNNEVHTAQQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQ VYVLPPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNN GKTELNYKNTEPVLSDSGSYFMYSDLRVEKKNWVERN SYSCSVVHEGLHNHHTTESFSRTPGK	
SEQ ID NO: 184	QVQLVQSGAEVKKPGASVKVSCKASGYFTDYYMHW VRQAPGQGLEWMGIINPRAGYTSYALKFQGRVTMTR DTSTSTVYMESSLRSEDVAVYYCTSGWDVWGQGTLV TVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPE PVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSST WPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCP APNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSED DPDVQISWVFNNEVHTAQQTQTHREDYNSTLRVVSAL PIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVR APQVYVLPPPEKEMTKKQVSLTCLVKDFMPEDIYVEWT NNGKTELNYKNTEPVLKSDSGSYFMYSKLTVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGGSHH HHHH	PD1- IL2_3x_Asym_PD1 - IL2_7A04_H_M115 W_L_Q68D

A. Sensor Domains

[0062] Protein complexes of the present disclosure include sensor domains. A sensor domain may be any protein that is capable of sensing the presence of a first moiety and regulating a second moiety, where the first moiety is a marker (e.g., a tumor cell marker) and the second moiety is a therapeutic domain (e.g., a cytokine therapeutic domain). For example, the present disclosure provides a sensor domain that may be an antibody or antibody fragment capable of binding a first moiety and binding and blocking the activity of a second moiety, wherein the first moiety is a marker (e.g., a tumor marker) and the second moiety is a therapeutic domain (e.g., a cytokine therapeutic domain). In the absence of the first moiety, the sensor domain binds the second moiety. If the first moiety is introduced into the system, the sensor domain binds the first moiety and unbinds the second moiety. Thus, the binding and unbinding of the second moiety is reversible. The sensor domain inactivates or blocks the activity of the therapeutic domain by binding the therapeutic domain and preventing it from binding to its target (e.g., a receptor, a ligand, or a substrate). The sensor domain regulates the therapeutic domain by releasing it to act on its target upon binding of a marker.

[0063] In some embodiments, the sensor domain is a dual binding protein such as a dual binding antibody. A dual binding protein may be capable of binding the marker and the therapeutic domain. A dual binding protein of the present disclosure may be selected or engineered to bind the marker and the therapeutic domain. The dual binding protein may have a higher affinity for

the marker as compared to the therapeutic domain. The dual binding protein may be affinity matured to have a higher affinity for the marker as compared to the therapeutic domain.

[0064] In some embodiments, the sensor domain is an antibody. The sensor domain may also be a fragment of an antibody. A fragment of an antibody consistent with the sensor domains disclosed herein retains its ability to exhibit dual binding to both a marker and a therapeutic domain. One or both domains of a bispecific antibody may be sensor domains of the protein complexes of the present disclosure. In the instance that bispecific antibodies are used, the bispecific antibody may include a first antigen binding domain that may bind a therapeutic domain and a marker and may also include a second antigen binding domain capable of binding the marker. In some embodiments, the bispecific antibody may have a first antigen binding domain that binds a therapeutic domain and a first marker, and a second antigen binding domain that binds a second marker. In some embodiments, the bispecific antibody may have a first antigen binding domain that binds a therapeutic domain and a first marker, and a second antigen binding domain that binds a therapeutic domain and a second marker. In some embodiments the first and second antigen binding domains may bind to the same therapeutic domain (**FIG. 13**).

[0065] In some embodiments the two sensor domains may bind to a single IFN α domain attached by a linker to two antibody domains; a first antibody domain that may bind to CEA (a first marker) and to the IFN α domain, and a second antibody domain that may bind to ATP (a second marker), and to the IFN α domain such that the IFN α is able to bind its receptor only in the presence of CEA and ATP (**FIG. 13**).

[0066] In some embodiments, the sensor domain is an anti-PD1 or anti-PDL1 antibody or fragment thereof (e.g., an scFv that binds PD1 or PD-L1). In some embodiments, the sensor domain binds to a marker comprising a surface protein, such as a cell surface protein, soluble ATP, a secreted protein, PD1, PD-L1, CEACAM5, FAP, LRRC15, a metabolite, adenosine, AMP, ADP, ATP, or kynurenine, or CRIPTO, CD19, CD20, CD22, CD30, CD33, Glycoprotein NMB, CanAg, HER2 (ErbB2/Neu), CD56 (NCAM), CD70, CD79, CD138, PSCA, PSMA (prostate specific membrane antigen), BCMA, E-selectin, EphB2, Melanotransferin, Muc16 and TMEFF2, BMPR1B, E16, STEAP1, 0772P, MPF, Napi3b, Sema 5b, PSCA hlg, ETBR, MSG783, STEAP2, TrpM4, CD21, CD79b, FcRH2, NCA, MDP, IL20R α , Brevican, EphB2R, ASLG659, PSCA, GEDA, BAFF-R, CD79a, CXCR5, HLA-DOB, P2X5, CD72, FCRHI, IRTA2, a sialic acid, or any other marker described in US 10,561,739, incorporated herein by reference in its entirety or WO 2005/082023, incorporated herein by reference in its entirety.

[0067] In some embodiments, the sensor domain comprises a condition-dependent target affinity. Many cell types, including a range of cancer cell types, generate specific extracellular and tissue-specific microenvironments distinct from those of healthy cells. Recently, significant

attention has been placed on the link between extracellular sodium depletion and certain brain cancers. As a further example, some cancers generate low pH microenvironments which can affect changes in the membranome protonation and conformational patterns. Accordingly, a sensor domain may comprise enhanced affinity for a target marker in the presence of a particular condition. A sensor domain may be responsive to pH, temperature, salinity, osmotic pressure, or any combination thereof. For example, a sensor domain may comprise an order of magnitude greater affinity for a target molecule or an order of magnitude lower affinity for a therapeutic domain in the presence of a particular condition. The particular condition may affect the sensor (e.g., a charge or conformation of the sensor), the target (e.g., a charge or solubility of the target), or both.

B. Therapeutic Domains

[0068] Protein complexes of the present disclosure include therapeutic domains. A therapeutic domain of the present disclosure is linked to a sensor domain via a linker to form a protein complex. The therapeutic domain may exert therapeutic activity by binding to a target. For example, the therapeutic domain may be a cytokine and its target may be a receptor target. Upon binding of the cytokine to its receptor target, the cytokine may modulate cellular proliferation, activation, differentiation, and/or may exert anti-tumor or anti-viral activity. Therapeutic domains consistent with the protein complexes of the present disclosure include a cytokine, a chemokine, an antibody, an antibody fragment, a peptide agonist, a peptide antagonist, an enzyme, a soluble receptor, a growth factor, a protein toxin, a soluble ligand, a small molecule, or combinations thereof. In some embodiments, an antibody or antibody fragment comprises an IgG, an IgA, an IgD, an IgE, an IgM, an Fab, an F(ab)^{'2}, a single domain antibody fragment (e.g., a nanobody), a diabody, an scFab, an scFv, an (scFv)₂, or any fragment (e.g., an Fc domain or CH domain) or combination thereof.

[0069] In some embodiments, the protein complexes of the present disclosure comprise a therapeutic domain comprising an IL-2 receptor agonist, IL-12 receptor agonist, or IFN α , or variants or fusions of these cytokines. In some embodiments, the therapeutic domain may be IFN α , IFN γ , IL-12, IL-4, IL-8, IL-10, IL-15, IL-18, IL-21, TGF beta, an anti-CD3 antibody, an anti-CD28 antibody or ligand, an antibody to or ligand of CD40, GITR, OX40, CD137, CD27, or Death Receptors, the extracellular domain of TGFBR2, VEGF-C, kynureninase, IL-7, TNF, MICA, MICB, CD47, an anti-CTLA4 antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody. The therapeutic domain may also be a fragment of any of the above mentioned moieties. A fragment retains functional regions of the moiety needed for binding to its target (e.g., IL-2 receptor) and any functional regions needed for activity.

C. Linkers

[0070] A protein complex disclosed herein may comprise a linker. The linker may connect two domains, such as a sensor domain and a therapeutic domain. The linker may connect two portions of a sensor domain, for example a light chain variable domain and a heavy chain variable domain. Various linkers are consistent with the protein complexes of the present disclosure. In some embodiments, the linker may be an amino acid linker or a chemical linker.

[0071] The linker may be a stable linker. For example, a linker may maintain a connection between a therapeutic domain and a sensor domain even upon binding of the sensor domain to a marker and, thereby, unbinding of the therapeutic domain from the sensor domain. For example, although the sensor domain may unbind the therapeutic domain, the therapeutic domain may remain linked to the sensor domain via the linker. Examples of linkers that are consistent with this activity may include non-cleavable linkers.

[0072] The linker may also be a flexible linker. A flexible linker is a linker that is long enough to allow for the therapeutic domain to bind to its target, once it is unbound from the sensor domain. Flexibility of the linker may affect therapeutic efficacy. For example, upon binding of the sensor domain to a marker and unbinding of the therapeutic domain, the therapeutic domain needs to be able to encounter and bind its therapeutic target (e.g., a receptor on the same cell surface as the marker or a receptor on an adjacent cell surface to the marker). If the linker is not flexible enough to allow for the therapeutic domain to bind its therapeutic target, therapeutic efficacy may be reduced or not exerted. When the linker is flexible, therapeutic domains may be able to bind their therapeutic target and exert high therapeutic efficacy. Flexibility of a linker may arise from the length of the linker. For example, short linkers may sterically hinder the therapeutic domain from binding its target. Longer linkers may allow for the protein complex to be more flexible and allow for therapeutic domains to bind their target. In some embodiments, a linker that is too long may impact the ability of the sensor domain to bind the therapeutic domain and inhibit activity in the absence of the marker. In some embodiments, a linker that is too long may impact the stability of a protein therapeutic domain or the half-life of the protein therapeutic domain *in vivo*.

[0073] In some embodiments, the linker may be attached to a heavy chain of the sensor domain or a light chain of the sensor domain. A linker may be fused to the N-terminus or C-terminus of the sensor domain. In some embodiments, the linker may be attached to a heavy chain or light chain of the therapeutic domain or is fused with the N-terminus or C-terminus of the therapeutic domain. For example, a linker may be attached to an N-terminus or C-terminus of an scFV or an ScFab.

[0074] Amino Acid Linkers. An amino acid linker may comprise any amino acid residues. In some embodiments, favored amino acid residues are amino acid residues that are entropically flexible. Favored amino acid residues in an amino acid linker of the present disclosure may include glycine and serine. Other preferred amino acid residues may include alanine, proline, threonine, and glutamic acid. In preferred embodiments, the amino acid linker may comprise from 3 to 60 amino acid residues in length. In some embodiments, the amino acid linker may comprise 20 amino acid residues. In some embodiments, the amino acid linker may comprise 40 amino acid residues. In some embodiments, the amino acid linker may comprise 60 amino acid residues. In some embodiments, the amino acid linker may comprise 80 amino acid residues. An amino acid linker may comprise at least 5 amino acid residues. An amino acid linker may comprise at least 10 amino acid residues. An amino acid linker may comprise at least 15 amino acid residues. An amino acid linker may comprise at least 20 amino acid residues. An amino acid linker may comprise at least 25 amino acid residues. An amino acid linker may comprise at least 30 amino acid residues. An amino acid linker may comprise at least 35 amino acid residues. An amino acid linker may comprise at least 40 amino acid residues. An amino acid linker may comprise at least 45 amino acid residues. An amino acid linker may comprise at least 50 amino acid residues. An amino acid linker may comprise at least 55 amino acid residues. An amino acid linker may comprise at least 60 amino acid residues. An amino acid linker may comprise at least 65 amino acid residues. An amino acid linker may comprise at least 70 amino acid residues. An amino acid linker may comprise at least 75 amino acid residues. An amino acid linker may comprise at least 80 amino acid residues. An amino acid linker may comprise at least 85 amino acid residues. An amino acid linker may comprise at least 90 amino acid residues. An amino acid linker may comprise at least 95 amino acid residues. An amino acid linker may comprise at least 100 amino acid residues. An amino acid linker may comprise at least 110 amino acid residues. An amino acid linker may comprise at least 120 amino acid residues. An amino acid linker may comprise at least 130 amino acid residues. An amino acid linker may comprise at least 140 amino acid residues. An amino acid linker may comprise at least 150 amino acid residues. An amino acid linker may comprise at least 160 amino acid residues. An amino acid linker may comprise at least 170 amino acid residues. An amino acid linker may comprise at least 180 amino acid residues. An amino acid linker may comprise at least 190 amino acid residues. An amino acid linker may comprise at least 200 amino acid residues. An amino acid linker may comprise at least 300 amino acid residues. An amino acid linker may comprise at least 400 amino acid residues. An amino acid linker may comprise at least 500 amino acid residues. An amino acid linker may comprise from 5 to 10 amino acid residues. An amino acid linker may comprise from 10 to 15 amino acid residues. An amino acid

linker may comprise from 15 to 20 amino acid residues. An amino acid linker may comprise from 20 to 25 amino acid residues. An amino acid linker may comprise from 25 to 30 amino acid residues. An amino acid linker may comprise from 30 to 35 amino acid residues. An amino acid linker may comprise from 35 to 40 amino acid residues. An amino acid linker may comprise from 40 to 45 amino acid residues. An amino acid linker may comprise from 45 to 50 amino acid residues. An amino acid linker may comprise from 50 to 55 amino acid residues. An amino acid linker may comprise from 55 to 60 amino acid residues. An amino acid linker may comprise from 60 to 65 amino acid residues. An amino acid linker may comprise from 65 to 70 amino acid residues. An amino acid linker may comprise from 70 to 75 amino acid residues. An amino acid linker may comprise from 75 to 80 amino acid residues. An amino acid linker may comprise from 80 to 85 amino acid residues. An amino acid linker may comprise from 85 to 90 amino acid residues. An amino acid linker may comprise from 90 to 95 amino acid residues. An amino acid linker may comprise from 95 to 100 amino acid residues. An amino acid linker may comprise from 5 to 80 amino acid residues. An amino acid linker may comprise from 20 to 40 amino acid residues. An amino acid linker may comprise from 20 to 80 amino acid residues. An amino acid linker may comprise from 30 to 60 amino acid residues. An amino acid linker may comprise from 40 to 50 amino acid residues. An amino acid linker may comprise from 10 to 30 amino acid residues. An amino acid linker may comprise from 10 to 20 amino acid residues. An amino acid linker may comprise from 5 to 25 amino acid residues. An amino acid linker may comprise from 25 to 75 amino acid residues. An amino acid linker may comprise from 100 to 500 amino acid residues. An amino acid linker may comprise from 100 to 300 amino acid residues. An amino acid linker may comprise from 5 to 500 amino acid residues. An amino acid linker may comprise no more than 100 amino acid residues. An amino acid linker may comprise no more than 90 amino acid residues. An amino acid linker may comprise no more than 80 amino acid residues. An amino acid linker may comprise no more than 70 amino acid residues. An amino acid linker may comprise no more than 60 amino acid residues. An amino acid linker may comprise no more than 50 amino acid residues. An amino acid linker may comprise no more than 40 amino acid residues. An amino acid linker may comprise no more than 30 amino acid residues. An amino acid linker may comprise no more than 20 amino acid residues. An amino acid linker may comprise no more than 10 amino acid residues. An amino acid linker may comprise no more than 95 amino acid residues. An amino acid linker may comprise no more than 90 amino acid residues. An amino acid linker may comprise no more than 85 amino acid residues. An amino acid linker may comprise no more than 80 amino acid residues. An amino acid linker may comprise no more than 75 amino acid residues. An amino acid linker may comprise no more than 70 amino acid residues. An amino acid linker may comprise no more

than 65 amino acid residues. An amino acid linker may comprise no more than 60 amino acid residues. An amino acid linker may comprise no more than 55 amino acid residues. An amino acid linker may comprise no more than 50 amino acid residues. An amino acid linker may comprise no more than 45 amino acid residues. An amino acid linker may comprise no more than 40 amino acid residues. An amino acid linker may comprise no more than 35 amino acid residues. An amino acid linker may comprise no more than 30 amino acid residues. An amino acid linker may comprise no more than 25 amino acid residues. An amino acid linker may comprise no more than 20 amino acid residues. An amino acid linker may comprise no more than 15 amino acid residues. An amino acid linker may comprise no more than 10 amino acid residues. An amino acid linker may comprise no more than 200 amino acid residues. An amino acid linker may comprise no more than 300 amino acid residues. An amino acid linker may comprise no more than 400 amino acid residues. An amino acid linker may comprise no more than 500 amino acid residues.

Non-Cleavable Linkers.

[0075] A non-cleavable linker of the present disclosure may include a chemical linker that is stable. Examples of non-cleavable linkers consistent for use in protein complexes of the present disclosure to link the sensor domain and the therapeutic domain may include a thioether linker, an alkyl linker, a polymeric linker. A linker may be an SMCC linker or a PEG linker. In preferred embodiments, the linker may be a PEG linker.

[0076] A non-cleavable linker may also include a non-proteolytically cleavable peptide. A non-proteolytically cleavable peptide may be inert to proteases present in a given sample or organism. For example, a peptide may be inert to all human protease cleavage sequences, and thereby may comprise a high degree of stability within humans and human samples. Such a peptide may also comprise a secondary structure which renders a protease cleavage site inert or inaccessible to a protease. A non-cleavable linker of the present disclosure may comprise a half-life for cleavage of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 12 hours, at least 16 hours, at least 1 day, at least 2 days, at least 3 days, at least 1 week, at least 2 weeks, or at least 1 month in the presence of human proteases at 25 °C in pH 7 buffer.

D. Protein Complex Structures

[0077] The present disclosure provides a wide variety of protein complexes spanning a range of structures. A protein complex of the present disclosure may comprise a therapeutic domain and a sensor domain expressed as a single unit. A therapeutic domain may be expressed as an N-terminal extension of a sensor domain, as a C-terminal extension of a sensor domain, or disposed within a sensor domain. For example, a protein complex may comprise a peptide which

comprises, from N-terminus to C-terminus, a therapeutic domain, a peptide linker, an scFv domain, and optionally a tag, such as a purification tag (e.g., a V5 or myc tag) or a localization signal. Alternatively, a therapeutic domain and a sensor domain may be coupled (e.g., chemically coupled) subsequent to expression.

[0078] A protein complex may comprise a plurality of protein subunits. The plurality of protein subunits (e.g., a therapeutic domain and a sensor domain, two sensor domains, or two subunits of a sensor domain) may be chemically or physically coupled following expression. The plurality of protein subunits may comprise a plurality of sensor and/or therapeutic domains. A sensor and/or a therapeutic domain may be comprised of a single protein subunit, of multiple protein subunits, or by portions thereof. For example, a sensor domain may comprise an antibody Fab region comprising portions of an immunoglobulin light chain and an immunoglobulin heavy chain.

[0079] A plurality of protein subunits may comprise physical handles which facilitate their selective coupling. The physical handles may enable spontaneous, irreversible, and/or non-mediated (e.g., not requiring a chaperone protein or a catalytic complex) coupling between the protein subunits, thereby enabling complex and asymmetric protein complexes. For example, two distinct protein complex subunits expressed in a single Chinese hamster ovary (CHO) cell, may comprise physical handles which spontaneously and irreversibly couple prior to cellular export. Such physical handles may comprise a ‘knob-into-hole’ (KIH) construct or a charge-swap construct, in which two protein subunits comprise physical structures with mutual binding affinities and specificities. Such physical handles may comprise a covalently binding pair, such as a plurality of thiols configured to form disulfide bonds. Physical handles may enable facile production of protein complexes comprising identical or distinct domains.

[0080] A protein complex may comprise two or more identical domains. An example of such a protein complex is provided in **FIG. 14A**, which illustrates an antibody (multi-sensor domain) coupled to two IL-2 therapeutic domains. In this example, the protein complex comprises two protein immunoglobulin light chain subunits and two immunoglobulin heavy chain subunits complexed to form a competent antibody. The two immunoglobulin heavy chain subunits comprise N-terminal linkers coupled to IL-2 therapeutic domains. Each immunoglobulin heavy chain is coupled to an immunoglobulin light chain, such that the protein complex comprises two Fab regions, each separately coupled to a therapeutic domain by a linker.

[0081] While the above example provides a symmetric protein complex with two identical sensor domains and two identical therapeutic domains, a protein complex may also comprise a plurality of distinct sensor and/or therapeutic domains. Such a protein complex may comprise an immunoglobulin unit with a first arm comprised of a heavy chain-light chain pair, and a second

arm comprised of an antibody fragment such as an scFv, an scFab, a VH, or a fragment thereof. In such cases, the heavy chain, the antibody fragment, or the light chain may comprise an N-terminal extension with a linker and a therapeutic domain, as illustrated in **FIG. 9A, C, and F**, respectively. Alternatively, the heavy chain, the antibody fragment, or the light chain may comprise a C-terminal extension with a linker and a therapeutic domain. A protein complex may also comprise a symmetric immunoglobulin unit with a single therapeutic domain. For example, as shown in **FIG. 9B**, an immunoglobulin unit may comprise an N-terminal linker and therapeutic unit on a single heavy chain. Alternatively, an immunoglobulin unit may comprise an N-terminal linker and therapeutic unit on a single light chain. An immunoglobulin unit may also comprise a pair of antibody fragments coupled to a single Fc region. An immunoglobulin unit may comprise a nanobody. An immunoglobulin unit may comprise a diabody.

[0082] In some cases, a plurality of distinct sensor domains are associated with a plurality of distinct therapeutic domains. Such a plurality of sensor domains may comprise common targets. For example, a protein complex may comprise a first sensor domain associated with an IL-2 therapeutic domain and comprising affinities for IL-2 and PD-1, and a second sensor domain associated with an IFN α therapeutic domain and comprising an affinity for IFN α and PD-1. Alternatively, a plurality of sensor domains may comprise separate targets. For example, a protein complex may comprise a first sensor domain associated with an IL-2 therapeutic domain and comprising affinities for IL-2 and PD-1, and a second sensor domain associated with an IFN α therapeutic domain and comprising an affinity for IFN α and CEACAM5.

[0083] A protein complex may comprise a therapeutic domain targeted by one or more than one sensor domain. A protein complex comprising such a plurality of sensor domains may comprise a multi-target dependence for activity. This concept is illustrated in **FIG. 13**, which provides a protein complex comprising a therapeutic domain, a first sensor domain targeting the therapeutic domain and a first target ('Marker 1'), and a second sensor domain targeting the therapeutic domain and a second target ('Marker 2'). In this example, the presence of Marker 1 leads to therapeutic domain binding to DBA 2, while the presence of Marker 2 leads to therapeutic domain binding to DBA 1. However, the presence of Marker 1 and Marker 2 liberates the therapeutic domain, enhancing its activity. Accordingly, the activity of the protein complex is requisite upon the presence of both of its markers. An example of such a system may be a protein complex comprising a first sensor domain which targets IL-2 and PD-1, and a second sensor domain which targets IL-2 and CEACAM5, such that CEACAM5 and PD-1 are requisite for IL-2 activity by the protein complex. A protein complex may comprise a dependence for at least 2, at least 3, at least 4, or at least 5 target markers. A protein complex may comprise a dependence for at most 5, at most 4, at most 3, at most 2, or for a single target marker.

[0084] Multi-marker activity dependence may enhance the selectivity of a protein complex. Some cells, including many forms of cancerous cells, comprise minor variations in their surfaceomes relative to healthy cells, rendering monospecific targeting unfeasible for distinguishing diseased cells. Accordingly, selectively targeting a particular diseased cell or tissue may require targeting a plurality of markers. A protein complex of the present disclosure may target at least 2, at least 3, at least 4, or at least 5 markers. A protein complex of the present disclosure may target at most 5, at most 4, at most 3, or at most 2 markers. In some cases, at least one of the markers targeted by a protein complex is commonly shared between a target cell or tissue and a healthy cell or tissue. In some cases, all of the markers targeted by a protein complex are commonly shared between a target cell or tissue and a healthy cell or tissue.

[0085] A sensor domain of the present disclosure may target at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 markers and no therapeutic domain. A sensor domain of the present disclosure may target at most 2, at most 3, at most 4, at most 5, at most 6, at most 7, at most 8, at most 9, or at most 10 markers and no therapeutic domain. A sensor domain of the present disclosure may target a single therapeutic domain and at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 markers. A sensor domain of the present disclosure may target a single therapeutic domain and at most 1, at most 2, at most 3, at most 4, at most 5, at most 6, at most 7, at most 8, at most 9, or at most 10 markers. A sensor domain of the present disclosure may target at least two therapeutic domains and at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 markers. A sensor domain of the present disclosure may target at least two therapeutic domains and at most 1, at most 2, at most 3, at most 4, at most 5, at most 6, at most 7, at most 8, at most 9, or at most 10 markers.

[0086] Two sensor domains may comprise identical affinities for a therapeutic domain, or may comprise different affinities for the therapeutic domain. Two sensor domains may comprise affinities for a therapeutic domain differing by at least 1 order of magnitude, at least 2 orders of magnitude, at least 3 orders of magnitude, or at least 4 orders of magnitude for a therapeutic domain. Two sensor domains may comprise affinities for a therapeutic domain which differ by at most 4 orders of magnitude, at most 3 orders of magnitude, at most 2 orders of magnitude, or at most 1 order of magnitude. A combination of different therapeutic domain affinities by a plurality of sensor domains may enhance the affinity of a protein complex for a target marker. For example, a protein complex may comprise a first sensor domain which weakly targets a first cell surface marker and weakly targets a therapeutic domain, and a second sensor domain which strongly targets a second cell surface marker and strongly targets the therapeutic domain, such

that the protein complex exhibits weak activity in the presence of the cell surface second marker and strong activity in the presence of the first and the second cell surface markers.

[0087] Two sensor domains of a protein complex may also target separate therapeutic domains. For example, a protein complex may comprise a first sensor domain which targets IL-2 and PD-1, and a second sensor domain which targets IFN α and CEACAM5. A protein complex may comprise a sensor domain which does not target a therapeutic domain. Such a sensor domain may aid in target localization, or may enhance the activity of a separate sensor domain for a therapeutic domain. An example of a protein complex comprising a sensor domain which does not target a therapeutic domain is provided in **FIG. 14C**. This system comprises a monospecific anti-PD-1 antibody, wherein a first heavy chain comprises a C-terminal linker coupled to a therapeutic domain, and a second heavy chain comprises a C-terminal linker coupled to a sensor domain with dual specificity for the therapeutic domain and for a target marker.

[0088] A protein complex may comprise a single target, 2 targets, 3 targets, 4 targets, or more than 4 targets. A protein complex may comprise at least 2 targets, at least 3 targets, or at least 4 targets. A protein complex may comprise at most 4 targets, at most 3 targets, or at most 2 targets. A protein complex may comprise a single sensor domain, 2 sensor domains, 3 sensor domains, 4 sensor domains, or more than 4 sensor domains. A protein complex may comprise at least 2 sensor domains, at least 3 sensor domains, or at least 4 sensor domains. For example, a protein complex may comprise an IgM antibody comprising Fab region sensor domains, or an IgA antibody comprising 4 Fab region sensor domains.

[0089] A protein complex may comprise a range of sensor-to-therapeutic domain ratios. A protein complex may comprise equal numbers of sensor domains and therapeutic domains, examples of which are provided by **FIG. 14A**, which illustrates a protein complex with 2 sensor domains and 2 therapeutic domains, and **FIG. 8**, which illustrates a protein complex with a single sensor domain and a single therapeutic domain. A protein complex may comprise a greater number of sensor domains than therapeutic domains, such as the protein complexes of **FIGS. 9A, 9B, 9C, 9F, and 14B**, which each comprise two sensor domains and one therapeutic domain. In such cases, a therapeutic domain may be capable of interacting with multiple sensor domains, or may be constrained from interacting with more than one sensor domain. The number of therapeutic domains with which a sensor domain may interact may depend on its linker. A linker may be sufficiently short so as to prevent a therapeutic domain from interacting with a sensor domain, or may be sufficiently long so as to allow a therapeutic domain to interact with multiple sensor domains.

[0090] In specific cases, a protein complex may comprise an antibody with Fc-coupled therapeutic and sensor domains. As illustrated in **FIG. 14C**, a protein complex may comprise an

antibody with a first heavy chain C-terminal extension comprising a linker and a therapeutic domain, and a second heavy chain C-terminal extension comprising a linker and a sensor domain. An antibody of this design may comprise common targets across its Fab and C-terminal extension sensor domain. For example, the antibody Fab regions and C-terminal extension sensor domain may each target PD-1. Conversely, an antibody of this design may comprise separate targets across its Fab regions and C-terminal extension sensor domain.

[0091] In some embodiments, an amino acid in the protein complex described herein may comprise a conservative substitution. A conservative substitution may comprise a substitution of one amino acid with a different amino acid with similar biochemical properties (e.g. charge, hydrophobicity, and size). Examples of conservative substitutions, as well as substitutions that may be, but are not necessarily, preferred, are provided in TABLE 33.

TABLE 33 – Exemplary Conservative Substitutions

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Lys; Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro; Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Leu; Val; Ile; Ala; Tyr	Leu
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr

Original Residue	Exemplary Substitutions	Preferred Substitutions
Thr (T)	Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

[0092] In some embodiments, the present disclosure describes a recombinant nucleic acid that encodes the protein complex disclosed herein. In some embodiments, the recombinant nucleic acid comprises a plasmid or a vector that encodes the entire protein complex. In some embodiments, the recombinant nucleic acid comprises plasmids or vectors that encode the therapeutic domain, the sensor domain, and the linker respectively. In some embodiments, the recombinant nucleic acid comprises plasmids or vectors that encode any two of the therapeutic domain, the sensor domain, and the linker together.

Pharmaceutical Formulations

[0093] A protein complex or a recombinant nucleic acid encoding the protein complex of the present disclosure may be formulated as a pharmaceutical composition. A pharmaceutical composition may comprise a pharmaceutically acceptable carrier or excipient. As used herein “pharmaceutically acceptable” or “pharmacologically acceptable” includes molecular entities and compositions that do not produce an adverse, allergic or other untoward reaction when administered to a subject, as appropriate. “Pharmaceutically acceptable carrier” includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients are often also incorporated into the compositions.

Applications

[0094] A protein complex of the present disclosure may be used for various therapeutic applications. A protein complex of the present disclosure may be used as a therapeutic to administer to a subject in need thereof. The subject may be a human or non-human mammal. The subject may have a disease. The disease may be cancer. The cancer may be acute lymphoblastic leukemia (ALL); acute myeloid leukemia (AML); cancer in adolescents; adrenocortical carcinoma; aids-related cancers; kaposi sarcoma (soft tissue sarcoma); aids-related lymphoma (lymphoma); primary cns lymphoma (lymphoma); anal cancer; appendix

cancer - see gastrointestinal carcinoid tumors; astrocytomas, childhood (brain cancer); atypical teratoid/rhabdoid tumor, childhood, central nervous system (brain cancer); basal cell carcinoma of the skin - see skin cancer; bile duct cancer; bladder cancer; bone cancer (includes ewing sarcoma and osteosarcoma and malignant fibrous histiocytoma); brain tumors; breast cancer; bronchial tumors (lung cancer); burkitt lymphoma - see non-hodgkin lymphoma; carcinoid tumor (gastrointestinal); carcinoma of unknown primary; cardiac (heart) tumors, childhood; central nervous system; atypical teratoid/rhabdoid tumor, childhood (brain cancer); medulloblastoma and other cns embryonal tumors, childhood (brain cancer); germ cell tumor, childhood (brain cancer); primary cns lymphoma; cervical cancer; childhood cancers; cancers of childhood, unusual; cholangiocarcinoma - see bile duct cancer; chordoma, childhood (bone cancer); chronic lymphocytic leukemia (CLL); chronic myelogenous leukemia (CML); chronic myeloproliferative neoplasms; colorectal cancer; craniopharyngioma, childhood (brain cancer); cutaneous t-cell lymphoma - see lymphoma (mycosis fungoides and sézary syndrome); ductal carcinoma in situ (DCIS) - see breast cancer; embryonal tumors, medulloblastoma and other central nervous system, childhood (brain cancer); endometrial cancer (uterine cancer); ependymoma, childhood (brain cancer); esophageal cancer; esthesioneuroblastoma (head and neck cancer); ewing sarcoma (bone cancer); extracranial germ cell tumor, childhood; extragonadal germ cell tumor; eye cancer; intraocular melanoma; retinoblastoma; fallopian tube cancer; fibrous histiocytoma of bone, malignant, and osteosarcoma; gallbladder cancer; gastric (stomach) cancer; gastrointestinal carcinoid tumor; gastrointestinal stromal tumors (GIST) (soft tissue sarcoma); germ cell tumors; childhood central nervous system germ cell tumors (brain cancer); childhood extracranial germ cell tumors; extragonadal germ cell tumors; ovarian germ cell tumors; testicular cancer; gestational trophoblastic disease; hairy cell leukemia; head and neck cancer; heart tumors, childhood; hepatocellular (liver) cancer; histiocytosis, langerhans cell; hodgkin lymphoma; hypopharyngeal cancer (head and neck cancer); intraocular melanoma; islet cell tumors, pancreatic neuroendocrine tumors; kaposi sarcoma (soft tissue sarcoma); kidney (renal cell) cancer; langerhans cell histiocytosis; laryngeal cancer (head and neck cancer); leukemia; lip and oral cavity cancer (head and neck cancer); liver cancer; lung cancer (non-small cell, small cell, pleuropulmonary blastoma, and tracheobronchial tumor); lymphoma; male breast cancer; malignant fibrous histiocytoma of bone and osteosarcoma; melanoma; melanoma, intraocular (eye); merkel cell carcinoma (skin cancer); mesothelioma, malignant; metastatic cancer; metastatic squamous neck cancer with occult primary (head and neck cancer); midline tract carcinoma with nut gene changes; mouth cancer (head and neck cancer); multiple endocrine neoplasia syndromes; multiple myeloma/plasma cell neoplasms; mycosis fungoides (lymphoma); myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms;

myelogenous leukemia, chronic (CML); myeloid leukemia, acute (AML); myeloproliferative neoplasms, chronic; nasal cavity and paranasal sinus cancer (head and neck cancer); nasopharyngeal cancer (head and neck cancer); neuroblastoma; non-hodgkin lymphoma; non-small cell lung cancer; oral cancer, lip and oral cavity cancer and oropharyngeal cancer (head and neck cancer); osteosarcoma and malignant fibrous histiocytoma of bone; ovarian cancer; pancreatic cancer; pancreatic neuroendocrine tumors (islet cell tumors); papillomatosis (childhood laryngeal); paraganglioma; paranasal sinus and nasal cavity cancer (head and neck cancer); parathyroid cancer; penile cancer; pharyngeal cancer (head and neck cancer); pheochromocytoma; pituitary tumor; plasma cell neoplasm/multiple myeloma; pleuropulmonary blastoma (lung cancer); pregnancy and breast cancer; primary central nervous system (CNS) lymphoma; primary peritoneal cancer; prostate cancer; rectal cancer; recurrent cancer; renal cell (kidney) cancer; retinoblastoma; rhabdomyosarcoma, childhood (soft tissue sarcoma); salivary gland cancer (head and neck cancer); sarcoma; childhood rhabdomyosarcoma (soft tissue sarcoma); childhood vascular tumors (soft tissue sarcoma); ewing sarcoma (bone cancer); kaposi sarcoma (soft tissue sarcoma); osteosarcoma (bone cancer); soft tissue sarcoma; uterine sarcoma; Sézary syndrome (lymphoma); skin cancer; small cell lung cancer; small intestine cancer; soft tissue sarcoma; squamous cell carcinoma of the skin - see skin cancer; squamous neck cancer with occult primary, metastatic (head and neck cancer); stomach (gastric) cancer; t-cell lymphoma, cutaneous - see lymphoma (mycosis fungoides and Sèzary syndrome); testicular cancer; throat cancer (head and neck cancer); nasopharyngeal cancer; oropharyngeal cancer; hypopharyngeal cancer; thymoma and thymic carcinoma; thyroid cancer; tracheobronchial tumors (lung cancer); transitional cell cancer of the renal pelvis and ureter (kidney (renal cell) cancer); unknown primary carcinoma; unusual cancers of childhood; ureter and renal pelvis, transitional cell cancer (kidney (renal cell) cancer); urethral cancer; uterine cancer, endometrial; uterine sarcoma; vaginal cancer; vascular tumors (soft tissue sarcoma); vulvar cancer; Wilms tumor and other childhood kidney tumors; or cancer in young adults or any cancer mentioned at <https://www.cancer.gov/types>.

[0095] In addition to the treatment of cancer, the protein complexes of the present disclosure have potential applications in a variety of other settings where targeted, conditional activity may be advantageous. In autoimmune and inflammatory disease, therapeutics that act through global immune suppression have the disadvantage of leaving patients more susceptible to a variety of opportunistic infections. Additionally, the short half-life and lack of accumulation in disease tissues may limit the efficacy of immune-dampening recombinant cytokines. The protein complexes of the present disclosure may address these shortcomings by allowing targeted delivery of immune modulators including IL-4, IL-10, TGF- β , and TNFR2 selectively to

affected anatomical locations while remaining silent in the periphery. Additional applications may include cell type-specific therapeutic targeting, such Treg cell-directed IL-2. Targeted, conditional activation of opioid agonists in specific organs or in the presence of markers of inflammation may reduce the addictive risk of pain control.

[0096] A protein complex may be administered as a pharmaceutical composition. A pharmaceutical composition of the disclosure can be a combination of any protein complex described herein with other chemical components, such as carriers, stabilizers, diluents, dispersing agents, suspending agents, thickening agents, and/or excipients. The pharmaceutical composition facilitates administration of a protein complex described herein to an organism. Pharmaceutical compositions can be administered in therapeutically-effective amounts as pharmaceutical compositions by various forms and routes including, for example, intravenous, subcutaneous, intramuscular, rectal, aerosol, parenteral, ophthalmic, pulmonary, transdermal, vaginal, optic, nasal, oral, inhalation, dermal, intra-articular, intrathecal, intranasal, and topical administration. A pharmaceutical composition can be administered in a local or systemic manner, for example, via injection of the protein complex described herein directly into an organ, optionally in a depot.

[0097] Parenteral injections can be formulated for bolus injection or continuous infusion. The pharmaceutical compositions can be in a form suitable for parenteral injection as a sterile suspension, solution or emulsion in oily or aqueous vehicles, and can contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Pharmaceutical formulations for parenteral administration include aqueous solutions of a protein complex described herein in water-soluble form. Suspensions of protein complexes described herein can be prepared as oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions can contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. The suspension can also contain suitable stabilizers or agents which increase the solubility and/or reduces the aggregation of such protein complexes described herein to allow for the preparation of highly concentrated solutions. Alternatively, the protein complexes described herein can be lyophilized or in powder form for re-constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use. In some embodiments, a purified protein complex is administered intravenously. A protein complex of the present disclosure may comprise a sufficiently long serum half life (e.g., as demonstrated in EXAMPLE 17) to enable dosing regimens comprising daily, alternating day, twice weekly, weekly, biweekly, or monthly dosing frequencies. A protein complex of the present disclosure may comprise a serum half-life of at least 12 hours, at least 24 hours, at least 36 hours, at least

48 hours, at least 72 hours, at least 96 hours, at least 120 hours, at least 168 hours, at least 250 hours, at least 320 hours, or at least 400 hours. The serum half-life may be a human serum half-life, a murine serum half-life, a porcine serum-half life, a bovine serum half-life, a canine serum half-life, a feline serum half-life, or a leporine serum half-life.

[0098] A protein complex of the disclosure can be applied directly to an organ, or an organ tissue or cells, during a surgical procedure, or via transdermal, subcutaneous, intramuscular, intratumoral, intrathecal, topical, or local delivery. In some embodiments, a protein complex of the present disclosure may be injected directly into the synovium (e.g., for administration of a protein complex comprising IL-10 for rheumatoid arthritis). In some embodiments, a protein complex may be applied directly to a cancerous tissue (e.g., a tumor). The protein complexes described herein can be administered topically and can be formulated into a variety of topically administrable compositions, such as solutions, suspensions, lotions, gels, pastes, medicated sticks, balms, creams, and ointments. Such pharmaceutical compositions can contain solubilizers, stabilizers, tonicity enhancing agents, buffers and preservatives.

[0099] In practicing the methods of treatment or use provided herein, therapeutically-effective amounts of the protein complex described herein are administered in pharmaceutical compositions to a subject suffering from a condition. In some instances the pharmaceutical composition will affect the physiology of the animal, such as the immune system, inflammatory response, or other physiologic affect. In some embodiments, the subject is a mammal such as a human. A therapeutically-effective amount can vary widely depending on the severity of the disease, the age and relative health of the subject, the potency of the compounds used, and other factors.

[0100] Pharmaceutical compositions can be formulated using one or more physiologically-acceptable carriers comprising excipients and auxiliaries, which facilitate processing of the active compounds into preparations that can be used pharmaceutically. Formulation can be modified depending upon the route of administration chosen. Pharmaceutical compositions comprising a protein complex described herein can be manufactured, for example, by expressing the protein complex in a recombinant system, purifying the protein complex, lyophilizing the protein complex, mixing, or dissolving. The pharmaceutical compositions can include at least one pharmaceutically acceptable carrier, diluent, or excipient and compounds described herein as free-base or pharmaceutically-acceptable salt form.

[0101] Methods for the preparation of protein complexes described herein include formulating the protein complex described herein with one or more inert, pharmaceutically-acceptable excipients or carriers to form a solid, semi-solid, or liquid composition. Solid compositions include, for example, powders, tablets, dispersible granules, capsules, cachets, and suppositories.

These compositions can also contain minor amounts of nontoxic, auxiliary substances, such as wetting or emulsifying agents, pH buffering agents, and other pharmaceutically-acceptable additives.

[0102] Certain methods described herein comprise administering to the subject an intravenous pharmaceutical composition comprising a protein complex of the present disclosure, for example, as described herein. Intravenous pharmaceutical compositions of protein complexes include any formulation suitable for administration to a subject via any intravenous method, including a bolus, an infusion which occurs over time or any other intravenous method known in the art. In some aspects, the rate of infusion is such that the dose is administered over a period of less than five minutes, more than five minutes but less than 15 minutes or greater than 15 minutes. In other aspects, the rate of infusion is such that the dose is administered over a period of less than 5 minutes. In other aspects, the rate of infusion is such that the dose is administered over a period of greater than 5 minutes and less than 15 minutes. In some other aspects, the rate of infusion is such that the dose is administered over a period of greater than 15 minutes.

[0103] “Product” or “dosage form” as used herein refers to any solid, semi-solid, lyophilized, aqueous, liquid or frozen formulation or preparation used for administration. Upon administration, the rate of release of an active moiety from a product is often greatly influenced by the excipients and/or product characteristics which make up the product itself. For example, an enteric coat on a tablet is designed to separate that tablet's contents from the stomach contents to prevent, for example, degradation of the stomach which often induces gastrointestinal discomfort or injury. According to the currently accepted conventional understanding, systemic exposure of the active moiety will be relatively insensitive to the small formulation changes.

[0104] Non-limiting examples of pharmaceutically-acceptable excipients can be found, for example, in Remington: The Science and Practice of Pharmacy, Nineteenth Ed (Easton, Pa.: Mack Publishing Company, 1995); Hoover, John E., Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pennsylvania 1975; Liberman, H. A. and Lachman, L., Eds., Pharmaceutical Dosage Forms, Marcel Dekker, New York, N.Y., 1980; and Pharmaceutical Dosage Forms and Drug Delivery Systems, Seventh Ed. (Lippincott Williams & Wilkins 1999), each of which is incorporated by reference in its entirety.

[0105] A protein complex of the present disclosure may be administered to a patient in an effective amount. The term “effective amount,” as used herein, can refer to a sufficient amount of an agent or a compound being administered which will relieve to some extent one or more of the symptoms of the disease or condition being treated. The result can be reduction and/or alleviation of the signs, symptoms, or causes of a disease, or any other desired alteration of a biological system. Compositions containing such agents or compounds can be administered for

prophylactic, enhancing, and/or therapeutic treatments. An appropriate “effective” amount in any individual case can be determined using techniques, such as a dose escalation study.

[0106] The methods, compositions, and kits of this disclosure can comprise a method to prevent, treat, arrest, reverse, or ameliorate the symptoms of a condition. The treatment can comprise treating a subject (e.g., an individual, a domestic animal, a wild animal or a lab animal afflicted with a disease or condition) with a protein complex of the disclosure. Protein complexes of the present disclosure may be administered to treat a disease in a subject. The subject can be a human. A subject can be a human; a non-human primate such as a chimpanzee, or other ape or monkey species; a farm animal such as a cattle, horse, sheep, goat, swine; a domestic animal such as a rabbit, dog, and cat; a laboratory animal including a rodent, such as a rat, mouse and guinea pig, or the like. A subject can be of any age. A subject can be, for example, an elderly adult, adult, adolescent, pre-adolescent, child, toddler, infant, or fetus in utero.

[0107] Treatment can be provided to the subject before clinical onset of disease. Treatment can be provided to the subject after clinical onset of disease. Treatment can be provided to the subject after 1 day, 1 week, 6 months, 12 months, or 2 years or more after clinical onset of the disease. Treatment may be provided to the subject for more than 1 day, 1 week, 1 month, 6 months, 12 months, 2 years or more after clinical onset of disease. Treatment may be provided to the subject for less than 1 day, 1 week, 1 month, 6 months, 12 months, or 2 years after clinical onset of the disease. Treatment can also include treating a human in a clinical trial. A treatment can comprise administering to a subject a pharmaceutical composition, such as one or more of the pharmaceutical compositions described throughout the disclosure. A treatment can comprise a once daily dosing. A treatment can comprise delivering a protein complex of the disclosure to a subject, either intravenously, subcutaneously, intramuscularly, by inhalation, dermally, intra-articular injection, orally, intrathecally, transdermally, intranasally, via a peritoneal route, or directly onto or into a diseased tissue, e.g., via topical, intra-articular injection route or injection route of application.

[0108] In some embodiments, the present disclosure provides a method for treating a cancer, the method comprising administering to a subject in need thereof an effective amount of a protein complex of the present disclosure.

[0109] In some embodiments, the present disclosure provides a method for treating a cancer, the method comprising administering to a patient in need thereof an effective amount of a pharmaceutical composition comprising a protein complex of the present disclosure and a pharmaceutically acceptable carrier.

Kits

[0110] A protein complex of the present disclosure may be provided in various kits. In some embodiments, pharmaceutical compositions comprising a protein complex of the present disclosure may be supplied as a kit. A kit may comprise a container that comprises a protein complex. Therapeutic protein complexes can be provided in the form of an injectable solution for single or multiple doses, or as a sterile powder that will be reconstituted before injection. Alternatively, such a kit can include a dry-powder disperser, liquid aerosol generator, or nebulizer for administration of a therapeutic protein complexes. Such a kit may further comprise written information on indications and usage of the pharmaceutical composition.

[0111] Unless otherwise defined, all technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used in this specification and the appended claims, the singular forms “a,” “an,” and “the” include plural references unless the context clearly dictates otherwise. Any reference to “or” herein is intended to encompass “and/or” unless otherwise stated.

[0112] Whenever the term “at least,” “greater than,” or “greater than or equal to” precedes the first numerical value in a series of two or more numerical values, the term “at least,” “greater than” or “greater than or equal to” applies to each of the numerical values in that series of numerical values. For example, greater than or equal to 1, 2, or 3 is equivalent to greater than or equal to 1, greater than or equal to 2, or greater than or equal to 3.

[0113] Whenever the term “no more than,” “less than,” “less than or equal to,” or “at most” precedes the first numerical value in a series of two or more numerical values, the term “no more than,” “less than” or “less than or equal to,” or “at most” applies to each of the numerical values in that series of numerical values. For example, less than or equal to 3, 2, or 1 is equivalent to less than or equal to 3, less than or equal to 2, or less than or equal to 1.

[0114] Where values are described as ranges, it will be understood that such disclosure includes the disclosure of all possible sub-ranges within such ranges, as well as specific numerical values that fall within such ranges irrespective of whether a specific numerical value or specific sub-range is expressly stated.

EXAMPLES

[0115] The following examples are illustrative and non-limiting to the scope of the devices, methods, systems, and kits described herein.

EXAMPLE 1**Selection of IFN α and PD-L1 Specific Dual Binding Antibodies (DBAs)**

[0116] This example describes isolation of sensor domains of the present disclosure, specifically, selection of IFN α and PD-L1 specific dual binding antibodies (DBAs). Anti-PD-L1 and anti-IFN α DBAs were isolated from a Tumbler antibody phage display library (Distributed Bio, Inc.). The antibody phage display library was constructed to incorporate the heavy chain CDR1, heavy chain CDR2, and light chain diversity of the Superhuman 2.0 antibody library combined with 10 heavy chain (“HC”) CDR3 sequences (SEQ ID NO: 1 – SEQ ID NO: 10) from the PD-L1 binding antibodies described, as shown below in **TABLE 2**.

TABLE 2 – HC-CDR3 of PD-L1 binders

SEQ ID NO	Sequence	Description
SEQ ID NO: 1	CARDRIAVAGFDYW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 2	CAKEVFSGWYDYW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 3	CTDLLSLELDDAFDIW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 4	CARSLFPTIFGVEVAFDIW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 5	CARDSYYYDSFDYW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 6	CARHGEWGSGWPFDYW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 7	CARDLLPAIFSGEVNDAFDIW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 8	CARETIAVAGFDPW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 9	CARDVLPTIFGVVSDAFDIW	HC-CDR3 of PD-L1 binder
SEQ ID NO: 10	CARGDYGDYFDYW	HC-CDR3 of PD-L1 binder

[0117] The library was subjected to four rounds of selection alternating between PD-L1 (to develop the PD-L1 binding, where PD-L1 serves as a marker) and IFN α (to develop IFN α binding, where IFN α is the therapeutic domain regulated by the sensor domain). Each round the phage library was incubated with the antigen (PD-L1 or IFN α), captured on magnetic beads, washed on a Kingfisher magnetic particle processor, eluted from the magnetic beads, and amplified by passaging in *E. coli*. In Round 1, the phage library was incubated with 50 nM of a human PD-L1-Fc fusion (R&D Systems, Prod. Num. 156-B7) and captured on protein G magnetic beads. In Round 2, the phage library was incubated with 100 nM of biotinylated human IFN α (Genscript, Prod. Num. Z03003, biotinylated using standard protocols) and captured on streptavidin magnetic beads. In Round 3, the phage library was incubated with 50 nM of a cynomolgus PD-L1-Fc fusion and captured on protein G magnetic beads. In Round 4, the phage library was incubated with 50 nM of biotinylated human IFN α and captured on streptavidin magnetic beads. The final selection was plated as single colonies and 380 colonies were picked for Sanger sequencing. Forty-one unique clones were chosen for expression. The scFv sequence for each clone was codon-optimized for *E. coli* expression and the corresponding DNA sequences synthesized as gBlocks (Integrated DNA Technologies, Inc.) with a T7

promoter, a translation initiation site, a Myc tag, the scFv sequence, a V5 tag sequence, and a T7 terminator. If the framework sequence of the antibody variable regions differed from the germline sequence, a second version of the clone was synthesized with the germline sequence. An exemplary sequence of a gBlock expression fragment is shown in **FIG. 3** (SEQ ID NO: 40, GCGAATTAATACGACTCACTATAGGGCTTAAGTATAAGGAGAATAATATATGTCTA CTTCAACAGAACAAAAGTTAATTAGTGAAGAAGATTTACAGGTCCAGTTGGTTCAG TCAGGCGCAGAAGTCAAAAAGCCGGGAGCGAGTGTCAAAGTATCTTGTAAGCGA GCGGTGGTACTTTTAGTAGTTATGCGATTTCTGGGTTCGCCAAGCCCCGGGACAGG GTCTGGAATGGATGGGTATTATTGACCCTTCCGTGACTTACACCCGCTACGCTCAGA AATTCCAGGGACGTGTTACCATGACCCGCGATACCAGCACCAAGTACCGTTTACATG GAACTTTCTCCCTGAGATCGGAAGACACGGCCGTGTATTATTGCGCTCGCTCACTC TTTCCGACCATCTTCGGCGTTGAAGTCGCCTTCGACATCTGGGGCCAGGGCACGCTG GTTACGGTAAGTTCCGCAAGTGGCGGTGGTGGTAGTGGTGGAGGTGGATCAGGAGG AGGTGGTTCTCACGCATCAGACATTCAAATGACACAGAGTCCATCATCCCTTTCTGC CTCCGTGGGTGACCGGGTGACGATAACCTGCCAAGCTAGCCAAGACATTAGCAACT ATCTGAACTGGTACCAGCAAAAAGCCTGGGAAAGCTCCGAAACTATTGATTTACGGT GCGTCGACTCTCCAGAGTGGGGTACCTAGTCGTTTTTCCGGTTCAGGGTCGGGTACA GATTTTACCCTTACTATTTCTCTCTGCAGCCAGAAGACTTTGCTACTTATTACTGCC AACAGACTTATTCGACTCCGATTACGTTTGGCCAGGGAACCAAAGTCGAAATCAAA GGCAAGCCGATCCCGAACCCTCTGCTGGGATTAGACAGCACGTAAGTACTAGCATAACC CCTCTCTAAACGGAGGGGTTT). Proteins from each of the gBlock fragments were expressed using a cell-free transcription/translation system (Cosmo Bio USA, Inc., PUREfrex2.1, Product # GFK-PF213 with DS Supplement, Prod. # GFK-PF005).

[0118] The cell-free expression samples containing V5-tagged scFvs were serially diluted in a 384-well plate. Alexa Fluor 647-labeled anti-V5 antibody was added to each well along with Eu-labeled IFN α 2a or PD-L1. Plates were incubated at room temperature for 2 hours and the HTRF signal was read on an Envision (Perkin Elmer) equipped with an HTRF laser module. To examine the ability of DBA binding domains to block Interferon alpha Receptor 2 (IFNAR2) binding to IFN α , V5-tagged DBA scFvs were synthesized using the PUREfrex 2.1 *in vitro* translation system and serially diluted in a 384 well plate. Eu-labeled IFN α was added to each well along with IFNAR2-Fc and an APC-labeled anti-Fc antibody. Plates were incubated at room temperature for 2 hours, and the HTRF signal was read on an Envision (Perkin Elmer) as a measure of IFN α :IFNAR2 binding. Fluorescence signal values from the binding and inhibition curves is summarized in **TABLE 4** and binding curves for IFN α and PD-L1 are shown in **FIG. 4** and **FIG. 5**, respectively. IFNAR2 blocking curves are shown in **FIG. 6**. DBAs having

sequences of SEQ ID NO: 21 – SEQ ID NO: 27 were able to bind both IFN α (**FIG. 4**) and PD-L1 (**FIG. 5**). SEQ ID NO: 24 blocked binding of IFN α to IFNAR2, and SEQ ID NO: 26 reduced binding of IFN α to IFNAR2 (**FIG. 6**).

TABLE 3 – DBAs and Controls

SEQ ID NO	Sequence	Description
SEQ ID NO: 21	QVQLVQSGAEVKKPGASVKVSCKASGYTF SNYYIHWVRQAPGQGLEWMGWMDSNSG GTGYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAKEVFSGWYDYWGQGT LTVSSASGGGGSGGGGSGGGGSHASDIQM TQSPSSLSASVGDRVTITCRASQSISSYLNW YQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSYSTPY TFGQGTKVEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 22	QVQLVQSGAEVKKPGASVKVSCKASGGTF SSYAISWVRQAPGQGLEWVGWMDPKSGN TGYYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARSLFPTIFGVEVAFDIWGQ GTLVTVSSASGGGGSGGGGSGGGGSHASD IQMTQSPSSLSASVGDRVTITCQASQDINNY LNWYQQKPGKAPKLLIYKASSLEPGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQKSN VPFTFGQGTKVEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 23	QVQLVQSGAEVKKPGASVKVSCKASGGTF SSYYMHWVRQAPGQGLEWMGWMNPNSG NTGYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARSLFPTIFGVEVAFDIWG QGTLLTVSSASGGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVTITCQASQDITN YLNWYQQKPGKAPKLLIYAASSLESGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQSY SIPITFGQGTRLEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 24	QVQLVQSGAEVKKPGASVKVSCKASGGTF TGYYMHWVRQAPGQGLEWMGWVNPNSG NTGYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARSLFPTIFGVEVAFDIWG QGTLLTVSSASGGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVTITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQS YSPPTFGQGTKLEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 25	QVQLVQSGAEVKKPGASVKVSCKASGNTF TDYYMHWVRQAPGQGLEWMGWMNPNS GNTGYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARSLFPTIFGVEVAFDIW GQGTLLTVSSASGGGGSGGGGSGGGGSHA SDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVP	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain

SEQ ID NO	Sequence	Description
	SRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYSTPPTFGQGTRLEIK	
SEQ ID NO: 26	QVQLVQSGAEVKKPGASVKVSCASGGTF SSYAISWVRQAPGQGLEWMGIIDPSVTYTR YAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARSLFPTIFGVEVAFDIWGQGT LTVSSASGGGGSGGGGSGGGGSHASDIQ MTQSPSSLSASVGDRVTITCQASQDISNYL NWKYQQKPGKAPKLLIYGASTLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYCQQTYST PITFGQGTKVEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 27	QVQLVQSGAEVKKPGASVKVSCASGGTF SSYAISWVRQAPGQGLEWMGWMDANNG NTGYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARSLFPTIFGVEVAFDIWG QGT LTVSSASGGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVTITCRASQSVSS YLNWKYQQKPGKAPKLLIYKASSLESGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQSS STPLSFGGGTKVEIK	DBA capable of binding a PD-L1 marker and IFN α therapeutic domain
SEQ ID NO: 28	EVQLVESGGGLVQPGGSLRLSCAASGFNIK DTYIHWVRQAPGKGLEWVARIYPTNGYTR YADSVKGRFTISADTSKNTAYLQMNSLRA EDTAVYYCSRWGGDGFYAMDYWGQGT L VTVSSASGGGGSGGGGSGGGGSHASDIQM TQSPSSLSASVGDRVTITCRASQDVNTAVA WYQQKPGKAPKLLIYSASFLYSGVPSRFSG SRSGTDFTLTISSLQPEDFATYYCQQHYTTP PTFGQGTKVEIK	Anti-HER2 control
SEQ ID NO: 29	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DSWIHWVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVYYCARRHWPGGFDYWGQGT LVT VSSAASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQDVSTAVAW YQQKPGKAPKLLIYSASFLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYLYHP ATFGQGTKVEIK	Anti-PD-L1 control
SEQ ID NO: 30	EVQLVESGGGLVQPGGSLRLSCATSGYTFT EYIIHWVRQAPGKGLEWVASINPDYDITNY NQRFKGRFTISLDKSKRTAYLQMNSLRAED TAVYYCASWISDFFDYWGQGT LTVSSAS GGGGSGGGGSGGGGSHASDIQMTQSPSSL SASVGDRVTITCRASQSVSTSSYSYMHY QQKPGKAPKVLISYASNLESGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQHSWGIPRT FGQGTKVEIK	Anti-IFN α control

TABLE 4 - Fluorescence Signal Values from Binding and Inhibition Curves

Name	PDL1 Binding	IFNα Binding	IFNAR2- IFN binding
PDL1-IFN-R01-A03	2,715	20,447	42,528
PDL1-IFN-R01-A04	2,377	10,890	45,590
PDL1-IFN-R01-A05 (SEQ ID NO: 21)	3,113	7,115	50,505
PDL1-IFN-R01-A06 (SEQ ID NO: 22)	2,781	8,563	44,019
PDL1-IFN-R01-A07	3,010	4,496	52,343
PDL1-IFN-R01-A08	2,274	19,905	40,314
PDL1-IFN-R01-A09	1,628	6,585	50,070
PDL1-IFN-R01-A09V2	1,894	5,264	49,709
PDL1-IFN-R01-A10	1,969	6,105	48,781
PDL1-IFN-R01-A11 (SEQ ID NO: 23)	2,965	14,613	41,796
PDL1-IFN-R01-A12	2,133	9,478	53,273
PDL1-IFN-R01-B01	3,172	7,460	44,230
PDL1-IFN-R01-B02	2,695	7,190	42,135
PDL1-IFN-R01-B03	2,383	4,072	44,076
PDL1-IFN-R01-B04	2,518	12,736	42,948
PDL1-IFN-R01-B04V2	2,703	12,952	43,748
PDL1-IFN-R01-B05	2,074	3,480	50,563
PDL1-IFN-R01-B06	3,084	17,212	43,958
PDL1-IFN-R01-B07	2,897	6,271	40,647
PDL1-IFN-R01-B07V2	2,907	6,111	42,880
PDL1-IFN-R01-B08	2,924	4,042	46,089
PDL1-IFN-R01-B09 (SEQ ID NO: 24)	1,378	35,717	31,232
PDL1-IFN-R01-B10	899	4,118	46,508
PDL1-IFN-R01-B11	2,525	14,580	43,204
PDL1-IFN-R01-B12 (SEQ ID NO: 25)	2,977	9,230	44,505
PDL1-IFN-R01-C01	2,780	6,975	47,032
PDL1-IFN-R01-C02	2,923	4,123	49,398
PDL1-IFN-R01-C03	2,671	6,522	46,323
PDL1-IFN-R01-C04	2,917	7,761	48,699
PDL1-IFN-R01-C05	2,802	3,427	47,470
PDL1-IFN-R01-C06	399	4,380	49,878
PDL1-IFN-R01-C06V2	391	4,130	47,685
PDL1-IFN-R01-C07	2,139	24,494	43,262
PDL1-IFN-R01-C08 (SEQ ID NO: 26)	2,746	45,175	14,739
PDL1-IFN-R01-C08V2	2,812	55,319	16,753
PDL1-IFN-R01-C09	2,388	4,346	48,696
PDL1-IFN-R01-C10	2,489	12,727	43,275
PDL1-IFN-R01-C10V2	2,665	11,972	43,576
PDL1-IFN-R01-C11 (SEQ ID NO: 27)	3,043	7,730	40,503
PDL1-IFN-R01-C12	1,006	13,135	44,871
PDL1-IFN-R01-D01	582	7,018	39,109

Name	PDL1 Binding	IFN α Binding	IFNAR2-IFN binding
PDL1-IFN-R01-D03	2,904	6,084	42,638
PDL1-IFN-R01-D05	2,325	6,402	49,246
PDL1-IFN-R01-D06	2,907	8,326	45,581
PDL1-IFN-R01-D07	414	4,974	38,164
anti-Her2 control (SEQ ID NO: 28)	425	4,275	52,922
Anti-PD-L1 control (SEQ ID NO: 29)	2,445	1,803	39,121
Anti-IFN control (SEQ ID NO: 30)	416	19,098	51,190
No DNA control	422	4,135	45,042

EXAMPLE 2

Isolation of a set of dual-binding antibodies (DBAs) that bind human PD-1 and human IL-

2

[0119] This example describes the isolation of sensor domains of the present disclosure, specifically, a set of DBAs that bind human PD-1 and human IL-2. Anti-PD-1 and anti-IL-2 DBAs were isolated from a Tumbler antibody phage display library (Distributed Bio, Inc.). The antibody phage display library was constructed to incorporate the heavy chain CDR1, heavy chain CDR2, and light chain diversity of the Superhuman 2.0 antibody library combined with 10 heavy chain CDR3 sequences from PD-1 binding antibodies (SEQ ID NO: 11 – SEQ ID NO: 20).

TABLE 5 – HC-CDR3 of PD-1 binders

SEQ ID NO	Sequence	Description
SEQ ID NO: 11	CAAGLFIW	HC-CDR3 of PD-1 binder
SEQ ID NO: 12	CAGGWLDW	HC-CDR3 of PD-1 binder
SEQ ID NO: 13	CARDHLGGSYQPW	HC-CDR3 of PD-1 binder
SEQ ID NO: 14	CARDLVGVSPGINYVPRYYYY YYGMDVW	HC-CDR3 of PD-1 binder
SEQ ID NO: 15	CARDTGLGYYYGSGDFDYW	HC-CDR3 of PD-1 binder
SEQ ID NO: 16	CARSGYSYGYFYDYW	HC-CDR3 of PD-1 binder
SEQ ID NO: 17	CARTGGYPAIDSW	HC-CDR3 of PD-1 binder
SEQ ID NO: 18	CASGWDVW	HC-CDR3 of PD-1 binder
SEQ ID NO: 19	CASSPLQWVDVW	HC-CDR3 of PD-1 binder
SEQ ID NO: 20	CTSGMDVW	HC-CDR3 of PD-1 binder

[0120] This library was subjected to four rounds of selection with standard protocols. In brief, the phage library was incubated with the antigen, then captured on magnetic beads and washed on a Kingfisher magnetic particle processor, eluted from the magnetic beads and amplified by passaging in *E. coli*. Round 1 was incubated with 50 nM human PD-1-His fusion (R&D

Systems, Prod. Num. 8986-PD) and captured with TRIS NTA Biotin (Sigma-Aldrich Prod. Num. 75543) and streptavidin magnetic beads. Round 2 was incubated with 100 nM biotinylated IL-2 (Creative Biomart, Prod. Num. IL2-501H, biotinylated using standard protocols) and captured on streptavidin magnetic beads. Round 3 was incubated with 50 nM cynomolgus PD-1-Fc fusion (R&D Systems, Prod. Num. 8578-PD) and captured on protein G magnetic beads. Round 4 was incubated with 50 nM biotinylated human IL-2 and captured on streptavidin magnetic beads. The final selection was plated as single colonies and 380 colonies picked for Sanger sequencing. One hundred and fifty-one unique clones were chosen for expression. The scFv sequence for each clone was codon-optimized for *E. coli* expression and the corresponding DNA sequences sent to Integrated DNA Technologies, Inc. (IDT) for synthesis as gBlocks with a T7 promoter, a translation initiation site and a T7 terminator (see an exemplary gBlock sequence in **FIG. 3**). Protein from each gBlock encoding an scFv was expressed using the PURExpress *In vitro* Protein Synthesis Kit (New England Biolabs, Inc., Prod. Num. E6800). The PURExpress scFv proteins were used directly in HTRF binding assays and cell-based functional assays. Each scFv was tested for binding to PD-1 and to human IL-2. Eighty-one of the antibodies showed dual-binding activity for both PD-1 and IL-2 and a summary of fluorescence signal values of binding curves is shown in **TABLE 7**. To examine the ability of DBA binding domains to block IL-2 receptor binding, V5-tagged DBA scFvs were serially diluted in a 384 well plate. Europium-labeled Streptavidin, biotin-labeled IL-2 (Acro Biosystems, Prod. Num. IL2-H82E4), IL-2 Receptor beta (Fc-IL2RB) (Acro Biosystems, Prod. Num. ILB-H5253), and APC-labeled anti-Fc antibody. Plates were incubated at room temperature for 2 hours, and the HTRF signal was read on an Envision (Perkin Elmer) as a measure of IL-2:IL2RB binding. Four scFvs (SEQ ID NO: 31 – SEQ ID NO: 34) bound PD-1, bound IL-2 and blocked binding of IL-2 to IL-2RB (**TABLE 7**).

TABLE 6 – DBAs and Controls

SEQ ID NO	Sequence	Description
SEQ ID NO: 31	QVQLVQSGAEVKKPGVSVKVSCKASGYTF PRSYIHWVRQAPGQGLEWMGWINPHSGDT YYAQNFGQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARDTGLGYYYGSGDFDYWG QGTLVTSSASGGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVTITCRASQSISR YLNWYQKPKGKAPKLLIYTASSLQSGVPSR FSGSGSGTDFTLTISLQPEDFATYYCQQAN RFPLTFGPGTKVDIK	DBA capable of binding a PD-1 marker and IL-2 therapeutic
SEQ ID NO: 32	QVQLVQSGAEVKKPGASVKVSCKASGYTF PRYHIHWVRQAPGQGLEWMGMINPSGGTT TYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARDTGLGYYYGSGDFDYWG	DBA capable of binding a PD-1 marker and IL-2 therapeutic

SEQ ID NO	Sequence	Description
	QGTLVTVSSASGGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVITITCRASQSISS WLAWYQQKPGKAPKLLIYAASSLQSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQS HSFPLTFGGGTKVEIK	
SEQ ID NO: 33	QVQLVQSGAEVKKPGASVKVSCKASGYTF TRYIIHWVRQAPGQGLEWMGWINAYNGD TNYAQKLQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDSEYDYSFDYWGGTL VTVSSASGGGGSGGGGSGGGGSHASDIQM TQSPSSLSASVGDRVITITCRASQTITDWLA WYQQKPGKAPKLLIYGASNLQGGVPSRFS GSGSGTDFTLTISSLQPEDFATYYCQQYYSS WTFGGGTKVEIK	DBA capable of binding a PD-1 marker and IL-2 therapeutic
SEQ ID NO: 34	QVQLVQSGAEVKKPGASVKVSCKASGYTF TSYYMHWVRQAPGQGLEWMGIINPSDGST TYAQSFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCASGWDVWGGTLVTVSSASG GGGSGGGGSGGGGSHASDIVMTQSPDSL VSLGERATINCKSSQSVFSSANNKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYYCQQYFGTP VTFGGGTKVEIK	DBA capable of binding a PD-1 marker and IL-2 therapeutic

TABLE 7

Name	PD1 Binding	IL2 Binding	IL2RB Blocking
No DNA	5	6	1,490
PD1-IL2-R01-H08	576	-9	1,829
PD1-IL2-R01-H09	1,015	131	1,772
PD1-IL2-R02-A03	1,508	635	1,714
PD1-IL2-R02-A04	909	978	1,618
PD1-IL2-R02-A05	1,557	23	1,735
PD1-IL2-R02-A06	357	515	1,772
PD1-IL2-R02-A08	995	520	1,612
PD1-IL2-R02-A09	1,421	1,470	1,495
PD1-IL2-R02-A10	500	838	1,847
PD1-IL2-R02-A11	1,625	1,559	1,783
PD1-IL2-R02-A12	1,725	130	1,586
PD1-IL2-R02-B01	746	1,077	1,516
PD1-IL2-R02-B02	1,740	1,107	1,849
PD1-IL2-R02-B04	11	2,346	1,536
PD1-IL2-R02-B05	1,665	2,489	1,613
PD1-IL2-R02-B06	1,527	32	1,605
PD1-IL2-R02-B07	1,685	628	1,814
PD1-IL2-R02-B08	1,446	92	1,680

Name	PD1 Binding	IL2 Binding	IL2RB Blocking
PD1-IL2-R02-B10	211	343	1,607
PD1-IL2-R02-B11	1,426	915	1,509
PD1-IL2-R02-B12	1,264	316	1,762
PD1-IL2-R02-C01	1,463	296	1,743
PD1-IL2-R02-C02 (SEQ ID NO: 31)	1,299	298	1,069
PD1-IL2-R02-C03 (SEQ ID NO: 32)	1,383	293	1,211
PD1-IL2-R02-C04	1,622	575	1,857
PD1-IL2-R02-C06	1,376	34	1,684
PD1-IL2-R02-C07	34	87	1,607
PD1-IL2-R02-C08	1,468	619	1,671
PD1-IL2-R02-C10	174	256	1,757
PD1-IL2-R02-C12	1,367	340	1,723
PD1-IL2-R02-D01	1,421	68	1,614
PD1-IL2-R02-D02	1,473	539	1,726
PD1-IL2-R06-A10	1,269	9	1,796
PD1-IL2-R06-A11	1,376	34	1,762
PD1-IL2-R06-A12	1,305	7	1,681
PD1-IL2-R06-B01	10	2,109	1,307
PD1-IL2-R06-B02	1,666	15	1,799
PD1-IL2-R06-B03	923	4	1,661
PD1-IL2-R06-B04	1,782	28	1,666
PD1-IL2-R06-B06	1,223	17	1,648
PD1-IL2-R06-B08	1,777	1,160	1,738
PD1-IL2-R06-B10	13	31	1,847
PD1-IL2-R06-B11	1,534	24	1,699
PD1-IL2-R06-B12	822	1,125	1,604
PD1-IL2-R06-C02	1,667	26	1,671
PD1-IL2-R06-C04	1,491	7	1,759
PD1-IL2-R06-C08	1,448	8	1,693
PD1-IL2-R06-C09	1,158	1,525	1,602
PD1-IL2-R06-C11	1,879	-2	1,785
PD1-IL2-R06-C12	1,669	1,998	1,033
PD1-IL2-R06-D02	280	432	1,677
PD1-IL2-R06-D03	9	93	1,606
PD1-IL2-R06-D05	505	-3	1,786
PD1-IL2-R06-D07	1,577	24	1,820
PD1-IL2-R06-D10	1,751	49	1,719
PD1-IL2-R06-D11	405	593	1,576
PD1-IL2-R06-D12	1,024	1,423	1,649
PD1-IL2-R06-E01	1,628	3	1,724
PD1-IL2-R06-E02	1,554	16	1,598

Name	PD1 Binding	IL2 Binding	IL2RB Blocking
PD1-IL2-R06-E04 (SEQ ID NO: 33)	50	247	1,108
PD1-IL2-R06-E05	1,364	14	1,734
PD1-IL2-R06-E06	1,627	15	1,735
PD1-IL2-R06-E07	1,801	12	1,698
PD1-IL2-R06-E09	1,467	11	1,511
PD1-IL2-R06-E11	1,805	294	1,767
PD1-IL2-R06-E12	4	-7	1,735
PD1-IL2-R06-F01	196	280	1,629
PD1-IL2-R06-F03	1,377	28	1,642
PD1-IL2-R06-F04	26	779	1,726
PD1-IL2-R06-F05	1,493	18	1,625
PD1-IL2-R06-F06	1,577	46	1,595
PD1-IL2-R06-F07	1,544	335	1,682
PD1-IL2-R06-F08	1,570	9	1,780
PD1-IL2-R06-F09	30	41	1,776
PD1-IL2-R06-F10	1,745	24	1,607
PD1-IL2-R06-F11	1,586	12	1,574
PD1-IL2-R06-F12	623	8	1,645
PD1-IL2-R06-G01	130	184	1,640
PD1-IL2-R06-G02	1,754	20	1,623
PD1-IL2-R06-G04	1,348	13	1,596
PD1-IL2-R06-G05	1,382	10	1,846
PD1-IL2-R06-G06	1,383	4	1,744
PD1-IL2-R06-G08	1,708	124	1,533
PD1-IL2-R06-G09	557	756	1,527
PD1-IL2-R06-G10	1,595	35	1,703
PD1-IL2-R06-G11	1,469	17	1,709
PD1-IL2-R06-G12	1,281	1,479	1,713
PD1-IL2-R06-H01	381	4	1,647
PD1-IL2-R06-H02	1,501	20	1,748
PD1-IL2-R06-H03	1,132	1,449	1,617
PD1-IL2-R06-H04	355	1	1,677
PD1-IL2-R06-H05	1,409	21	1,561
PD1-IL2-R06-H06	1,491	23	1,650
PD1-IL2-R06-H07	12	13	1,701
PD1-IL2-R06-H08	847	1,118	1,746
PD1-IL2-R06-H09	1,732	22	1,662
PD1-IL2-R06-H10	830	1,151	1,569
PD1-IL2-R07-A03	1,786	28	1,511
PD1-IL2-R07-A04	730	973	1,613
PD1-IL2-R07-A05	477	663	1,327
PD1-IL2-R07-A08	1,628	841	1,618

Name	PD1 Binding	IL2 Binding	IL2RB Blocking
PD1-IL2-R07-A09 (SEQ ID NO: 34)	1,235	2,040	910
PD1-IL2-R07-A10	1,716	63	1,518
PD1-IL2-R07-B01	1,397	32	1,565
PD1-IL2-R07-B02	192	321	1,634
PD1-IL2-R07-B03	65	202	1,604
PD1-IL2-R07-B04	1,862	410	1,527
PD1-IL2-R07-B05	965	351	1,389
PD1-IL2-R07-B06	1,882	44	1,497
PD1-IL2-R07-B07	6	2,549	1,517
PD1-IL2-R07-B08	906	1,047	1,475
PD1-IL2-R07-B09	1,788	27	1,384
PD1-IL2-R07-B10	18	19	1,635
PD1-IL2-R07-B11	1,765	9	1,641
PD1-IL2-R07-C01	230	367	1,536
PD1-IL2-R07-C02	236	304	1,500
PD1-IL2-R07-C03	20	1,347	1,536
PD1-IL2-R07-C07	15	275	1,665
PD1-IL2-R07-C10	1,064	317	1,550
PD1-IL2-R07-C11	1,523	642	1,460
PD1-IL2-R07-C12	1,377	49	1,707
PD1-IL2-R07-D01	1,541	79	1,657
PD1-IL2-R07-D03	1,483	33	1,481
PD1-IL2-R07-D04	923	1,104	1,517
PD1-IL2-R07-D06	1,664	416	1,734
PD1-IL2-R07-D07	6	835	1,512
PD1-IL2-R07-D10	1,580	193	1,572
PD1-IL2-R07-D11	1,401	798	1,614
PD1-IL2-R07-E02	1,473	992	1,830
PD1-IL2-R07-E03	1,459	422	1,683
PD1-IL2-R07-E05	512	913	1,513
PD1-IL2-R07-E06	1,483	1,178	1,526
PD1-IL2-R07-E07	1,181	1,060	1,524
PD1-IL2-R07-E08	1,604	472	1,717
PD1-IL2-R07-E09	1,733	23	1,569
PD1-IL2-R07-E10	1,472	251	1,545
PD1-IL2-R07-E11	1,146	56	1,777
PD1-IL2-R07-E12	1,698	106	1,764
PD1-IL2-R07-F01	3	17	1,529
PD1-IL2-R07-F02	348	752	1,537
PD1-IL2-R07-F03	1,788	520	1,750
PD1-IL2-R07-F04	1,416	145	1,767
PD1-IL2-R07-F06	1,422	438	1,579

Name	PD1 Binding	IL2 Binding	IL2RB Blocking
PD1-IL2-R07-F09	1,589	17	1,456
PD1-IL2-R07-F10	24	19	1,778
PD1-IL2-R07-F12	505	196	1,553
PD1-IL2-R07-G01	4	214	1,560
PD1-IL2-R07-G02	1,610	61	1,735
PD1-IL2-R07-G04	82	147	1,600
PD1-IL2-R07-G05	981	216	1,475
PD1-IL2-R07-G06	860	512	1,655
PD1-R04-C10	1,552	4	1,550
PD1-R07-A05	653	19	1,730
PD1-R07-A10	484	25	2,290
PD1-R07-C09	1,911	20	2,080
PD1-R07-D03	1,733	22	2,208
PD1-R07-D05	1,760	16	1,578
PD1-R07-D06	1,997	22	1,749
PD1-R07-E05	633	24	2,246
PD1-R07-G12	907	11	1,577
PD1-R15-B02	1,671	28	1,797
PDL1-DB03-H02	18	11	1,725
Anti-Her2 (SEQ ID NO: 28)	4	20	1,636

EXAMPLE 3

Competitive Binding for Targets of Dual Binding Antibodies (DBAs)

[0121] This example describes competitive binding between the marker and the therapeutic domain of dual binding antibodies (DBAs). To test the ability of PD-L1 (marker) to compete with IFN α (therapeutic) for binding to the DBA binding domains, V5-tagged DBA or control scFvs were synthesized using the PUREfrex 2.1 *in vitro* translation system and added to a 384 well plate at a single dilution. Eu-labeled PD-L1 and Alexa Fluor 647-labeled anti-V5 antibody were added to all wells and incubated for 30 minutes at room temperature. Titrated concentrations of IFN α were added to all wells and the plate was incubated for 1 hour at room temperature. The HTRF signal was read on Envision (Perkin Elmer). As shown in FIG. 7, IFN α competed with PD-L1 for binding to DBA clones B09 (SEQ ID NO: 24) and C08 (SEQ ID NO: 26), whereas the binding of an anti-PD-L1 mono-specific antibody was unaffected by the concentration of IFN α .

EXAMPLE 4**Screening Dual Binding Antibodies (DBAs) for Improved Binding Affinity**

[0122] This example illustrates screening dual binding antibodies (DBAs) for improved binding affinity. The sequences for each DBA were aligned with the parental, single specificity antibody from which it was derived and with other DBAs derived from the same parental, single specificity antibody. Using this sequence information, variants with amino acid substitutions in and adjacent to the CDR regions were designed to test for altered binding to either antigen. Additionally, consideration was given to sequence variants that may improve stability. Representative variants are shown in **TABLE 8** and **TABLE 9**. CDR sequences provided in **TABLE 8** and **TABLE 9** correspond to HCDR1 – HCDR2 – HCDR3, with substitutions underlined and in bold. Sequences of dual binding PD-L1 and IFN α variants are provided in **TABLE 10**.

TABLE 8 - Heavy chain CDR regions of anti-PDL1 02_A08, DBA PDL1-IFN_1A05, and variants

SEQ ID NO	Description	CDR Sequence
SEQ ID NO: 305	Parental monospecific antibody PDL1_02_A08	CKASGYTFSGYMHW - WMGWMDPNSGYTGYAHQFQGRV - CAKEVFSGWYDYWGQ
SEQ ID NO: 306	Dual-binding antibody (DBA) PDL1-IFN R01 A05	CKASGYTFSNYYIHW - WMGWMDSNSGGTGYAQKFQGRV - CAKEVFSGWYDYWGQ
SEQ ID NO: 307	DBA variant H_N36G	CKASGYTFS <u>G</u> YYIHW - WMGWMDSNSGGTGYAQKFQGRV - CAKEVFSGWYDYWGQ
SEQ ID NO: 308	DBA variant H_I39V_S58P_Q69H_K70Q	CKASGYTFSNYY <u>V</u> HW - WMGWMD <u>P</u> NSGGTGYA <u>H</u> QFQGRV - CAKEVFSGWYDYWGQ
SEQ ID NO: 309	DBA variant H_G64Y_Q69H	CKASGYTFSNYYIHW - WMGWMDSNSG <u>Y</u> TGYA <u>H</u> KFQGRV - CAKEVFSGWYDYWGQ

TABLE 9 - Light chain CDR regions of anti-PDL1 02_A08, DBA PDL1-IFN_1A05, and variants

SEQ ID NO	Construct	CDR Sequence
SEQ ID NO: 310	Parental monospecific antibody PDL1 02 A08	CRASQTISSYLNWY - IYAASLTESGVPSR - YYCQQGYSTPITFGPGTKVDIK

SEQ ID NO	Construct	CDR Sequence
SEQ ID NO: 311	Dual-binding antibody (DBA) PDL1-IFN_R01_A05	CRASQSISSYLNWY - IYAASSLQSGVPSR - YYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 312	L_Q68E	CRASQSISSYLNWY - IYAASSLESGVPSR - YYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 313	L_Q68E_E125D	CRASQSISSYLNWY - IYAASSLESGVPSR - YYCQQSYSTPYTFGQGGTKV DIK

TABLE 10 – Sequences of dual binding PD-L1 and IFN α variants

SEQ ID NO	Variant	Sequence
SEQ ID NO: 35	H_N36G	QVQLVQSGAEVKKPGASVKVSCASGYTFSGYIIHW VRQAPGQGLEWMGWMDSNSGGTGYAQKFQGRVTMT RDTSTSTVYMESSLRSED ¹ AVYYCAKEVFSGWYDY WGQGT ² LVTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 36	H_I39V_S 58P_Q69H _K70Q	QVQLVQSGAEVKKPGASVKVSCASGYTFSNYYVHW VRQAPGQGLEWMGWMDPNSSGGTGYAHQFQGRVTMT RDTSTSTVYMESSLRSED ¹ AVYYCAKEVFSGWYDY WGQGT ² LVTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 37	H_G64Y_ Q69H	QVQLVQSGAEVKKPGASVKVSCASGYTFSNYYIIHW VRQAPGQGLEWMGWMDSNSGYTGYAHKFQGRVTMT RDTSTSTVYMESSLRSED ¹ AVYYCAKEVFSGWYDY WGQGT ² LVTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 38	L_Q68E	QVQLVQSGAEVKKPGASVKVSCASGYTFSNYYIIHW VRQAPGQGLEWMGWMDSNSGGTGYAQKFQGRVTMT RDTSTSTVYMESSLRSED ¹ AVYYCAKEVFSGWYDY WGQGT ² LVTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYAASSLESGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 39	L_Q68E_E 125D	QVQLVQSGAEVKKPGASVKVSCASGYTFSNYYIIHW VRQAPGQGLEWMGWMDSNSGGTGYAQKFQGRVTMT RDTSTSTVYMESSLRSED ¹ AVYYCAKEVFSGWYDY WGQGT ² LVTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYAASSLESGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSTPYTFGQGGTKV DIK

[0123] The scFv sequence for each variant was codon-optimized for *E. coli* expression and the corresponding DNA sequences synthesized as gBlocks (Integrated DNA Technologies, Inc.) with a T7 promoter, a translation initiation site, a Myc tag, the scFv sequence, a V5 tag sequence and a T7 terminator. Proteins encoded by the gBlock fragments were expressed using a cell-free transcription/translation system (Cosmo Bio USA, Inc., PUREfrex2.1, Product # GFK-PF213 with DS Supplement, Prod. # GFK-PF005). The cell-free expression samples were assayed for PD-L1 and IFN α binding as described in **EXAMPLE 1**.

[0124] Variants with different binding affinities may also be generated by display methods, such as phage display and mRNA display. Libraries for use in these methods may be created from the parental antibody by varying CDRs with random amino acid changes or by varying positions in the CDRs identified as suitable for change.

EXAMPLE 5

Binding Affinity of Dual Binding Antibodies (DBAs)

[0125] This example describes binding affinity of protein complexes, specifically, dual binding antibodies (DBAs). Variants were synthesized as V5-tagged scFvs using the PUREfrex 2.1 *in vitro* translation system and diluted 1:30 in 1X kinetics buffer (KB, forteBIO) for testing. Biotinylated anti-V5 antibody (clone SV5-Pk1 BioRad, biotinylated using EZ-Link® Sulfo-NHS-LC-Biotin, THERMO) was diluted to 80 nM in 1X KB, then loaded onto streptavidin biosensor tips (SA, forteBIO) on an OctetRED96e instrument. These tips were then loaded with scFv for 240 seconds. The loaded tips were transferred to 1X KB for 60 seconds to establish baseline, then dipped into 160 nM ACRO human PDL1-his for 150 seconds to measure association, then into 1X KB for 180 seconds to measure dissociation. Immediately following this dissociation, baseline signal in 1X KB was measured, the tips were dipped into 5,000 nM IFN α 2b (GenScript) for 150 seconds to measure association, then into 1X KB for 240 seconds to measure dissociation. Data were fit to a 1:1 kinetics model. Response for binding of IFN α 2b was qualitative negative or positive. Sequences of the DBA variants used in **TABLE 11** are provided in **TABLE 8** and **TABLE 9**.

TABLE 11 - Kinetics of binding of DBA variants

	KD (PD-L1, nM)	IFNα binding (@5uM)
H G64Y Q69H	13	+/-
H I39V S58P Q69H K70Q	8	-
H N36G	37	+
L Q68E	21	+
L Q68E E125D	21	+
PDL1-IFN_R01_A05	120	Not tested

[0126] The affinity of the DBA in this or other antibody formats may be measured in a similar manner to generate quantitative or semi-quantitative measurements using standard methods of measurement of protein interaction, including biolayer interferometry (e.g., Octet, Molecular Devices LLC.) surface plasmon resonance (e.g., BiaCore, GE Healthcare Life Sciences), kinetic exclusion (KinExA, Sapidyn Instruments, Inc.), or other biophysical methods. In addition, apparent affinity of a target for the DBA in the covalently linked construct may be measured with these methods by competition for a nonlinked binding agent.

EXAMPLE 6

Dual Binding Antibody (DBA)-Cytokine Protein Complexes

[0127] This example describes dual binding antibody (DBA)-cytokine protein complexes of the present disclosure. Various DBA-cytokine protein complexes of the present disclosure were designed to include a cytokine, a linker, and one or more dual binding antibody domains. An exemplary protein complex is shown in **FIG. 8** (at left) and its amino acid sequence is shown in **FIG. 8** (at right). Pictorial representations of other exemplary constructs are shown in **FIG. 9** (SEQ ID NO: 42 – SEQ ID NO: 54 and SEQ ID NO: 77 – SEQ ID NO: 79).

[0128] A series of DBA-cytokine protein complexes may be designed with two marker binding domains and one therapeutic domain. The DBAs used in this series, provided in **TABLE 13** with sequences provided in **TABLE 14**, exhibit a range of affinities for the marker and the therapeutic domain. Exemplary DBA complexes are provided in **TABLE 12**, **TABLE 15**, and **TABLE 16**.

TABLE 12 – Exemplary DBA Cytokine Protein Complexes

SEQ ID NO	Sequences	Description
SEQ ID NO: 42	QVQLVQSGAEVVKPGASVKVSCKASGYTFT KNYMHWVRQAPGQGLEWLGWVSPDSGYTG YAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVYYCTTDLLELDDAFDIWGQGTMTVVS SASGGGSGGGGSGGGGSHASDIQMTQSPSS LSASVGDRVTITCRASQSISSWLAWYQQKPG KAPKLLIYAASLTQSGVPSRFSGSGSGTDFTLT ISSLPEDFATYYCQQSYSTPLTFGGGKLEIK PRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIK DVLMSLSPIVTCVVVDVSEDDPDVQISWVFN NVEVHTAQQTTHREDYNSTLRVVSALPIHQ DWMSGKEFKCKVNNKDLGAPIERTISKPKGS VRAPQVYVLPPEEEMTKKQVTLSCAVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSY FMVSKLRVEKKNWVERNSYSCSVVHEGLHN HHTTKSFSRTPGK	PD-L1/IFN α protein complexes having a DBA sensor domain capable of binding a PD-L1 marker and IFN α therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 43	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD RHDFGFPPQEEFGNQFQKAETIPVLHEMIQQIF	PD-L1/IFN α protein complexes

SEQ ID NO	Sequences	Description
	NLFSTKDSSAAWDETL LDKFCTEL YQQLNDL EACVMQEERVGETPLMNADSI LAVKKYFRRI TLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQ ERLRRKEGGGGSGGGGSGGGGSGGGGSQVQ LVQSGAEVKKPGASVKV SCKASGYTFSGYYI HWVRQAPGQGLEWMGWMDSNSGGTGYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAV YYCAKEVFSGWYDYWGQGT LVTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPV TLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVT VTSSTWPSQSITCNVAHPASSTKVDKKIEPRG PTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISW FVNNVE VHTAQQTQTHREDYNSTLRVVSALPIQH QDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVR APQVCVLPPPEEEMTKKQVTLWCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYF MYSKLRVEKKNWVERNSYSCSVVHEGLHNH HTTKSFSRTPGK	having a DBA sensor domain capable of binding a PD-L1 marker and IFN α therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 44	DIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYAASSLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPYT FGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGA SVVCFLNNFYPKDINVKWKIDG SERQNGVLN SWTDQDSKDYSTYSMSSTLT LTKDEYERHNSY TCEATHKTSTSPIVKSFN RNEC	PD-L1/IFN α protein complexes having a DBA sensor domain capable of binding a PD-L1 marker and IFN α therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 45	QVQLVQSGAEVKKPGASVKV SCKASGGTFSS YAIWVRQAPGQGLEWMGIIDPSVTYTRYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAV YYCARSLFPTIFGVEVAFDIWGQGT LVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGY FPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTL SSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIK DVL MISLSPIVTCVVVDVSEDDPDVQISW FVN NVEVHTAQQTQTHREDYNSTLRVVSALPIHQ DWMSGKEFKCKVNNKDLGAPIERTISKPKGS VRAPQVYVLPPEEEMTKKQVTLSCAVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSY FMVSKLRVEKKNWVERNSYSCSVVHEGLHN HHTTKSFSRTPGK	PD-L1/IFN α protein complexes having a DBA sensor domain capable of binding a PD-L1 marker and IFN α therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 46	CDLPQTHSLGSRRTLM LLAQMRRISLFSCLKD RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIF NLFSTKDSSAAWDETL LDKFCTEL YQQLNDL EACVMQEERVGETPLMNADSI LAVKKYFRRI TLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQ ERLRRKEGGGGSGGGGSGGGGSGGGGSQVQ LVQSGAEVKKPGASVKV SCKASGGTFSSY AIS	PD-L1/IFN α protein complexes having a DBA sensor domain capable of binding a PD-L1 marker and IFN α

SEQ ID NO	Sequences	Description
	WVRQAPGQGLEWMGIIDPSVTYTRYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDNAVYYC ARSLFPTIFGVEVAFDIWGQGTLLTVSSAKTT APSVYPLAPVCGDITGSSVTLGCLVKGYFPEP VTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSV TVTSSTWPSQSITCNVAHPASSTKVDKKIEPR GPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWVFNNV EVHTAQQTTHREDYNSTLRVVSALPIQHQQDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVR APQVCVLPPPEEEMTKKQVTLWCMVTDMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYF MYSKLRVEKKNWVERNYSYSCSVVHEGLHNH HTTKSFSRTPGK	therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 47	DIQMTQSPSSLSASVGDRVTITCQASQSSINYL AWYQQKPGKAPKLLIYKASSLESGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQTSTPITF GQGTKVEIKRADAAPTVSIFPPSSEQLTSGGAS VVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSYMSSTLTTLTKDEYERHNSYT CEATHKTSTSPIVKSFNRNEC	PD-L1/IFN α protein complexes having a DBA sensor domain capable of binding a PD-L1 marker and IFN α therapeutic domain and having an IFN α therapeutic activity
SEQ ID NO: 48	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIF NLFSTKDSSAAWDETLLDKFCTELYQQLNDL EACVMQEERVGETPLMNADSILAVKKYFRRI TLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQ ERLRRKEGGGGSGGGGSGGGGSGGGGSQVQ LVQSGAEVKKPGASVKVSCASGGTFSSYAIS WVRQAPGQGLEWMGIIDPSVTYTRYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDNAVYYC ARSLFPTIFGVEVAFDIWGQGTLLTVSSASGG GGSGGGGSGGGGSHASDIQMTQSPSSLSASV GDRVTITCQASQDISNYLNWYQQKPGKAPKL LIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQ EDFATYYCQQTSTPITFGQGTKVEIKAKTTA PSVYPLAPVCGDITGSSVTLGCLVKGYFPEPV TLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVT VTSSTWPSQSITCNVAHPASSTKVDKKIEPRG PTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWVFNNV EVHTAQQTTHREDYNSTLRVVSALPIQHQQDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVR APQVYVLPCEEEMTKKQVTLSCAVTDFMPE DIYVEWTNNGKTELNYKNTEPVLDSDGSYFM VSKLRVEKKNWVERNYSYSCSVVHEGLHNHH TTKSFSRTPGK	ExemplarySeq_C_ Pep1 Asymmetric DBA- Cytokine Complex scFv-IgG format
SEQ ID NO: 49	QVQLVQSGAEVKKPGASVKVSCASGYTFSG YYIHWVRQAPGQGLEWMGWMDSNSGGTGY	ExemplarySeq_C_ Pep2

SEQ ID NO	Sequences	Description
	AQKFQGRVTMTRDTSTSTVYMESSLRSED AVYYCAKEVFSGWYDYWGQGLTVTVSSAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPE PVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEP RGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKD VLMISLSPIVTCVVVDVSEDDPDVQISWVFN VEVHTAQTTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGS VRAPQVCVLPPEEEMTKKQVTLWCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDG SYFMYSKLRVEKKNWVERNYSYSCSVVHEGL HNNHTTKSFSRTPGK	Asymmetric DBA- Cytokine Complex scFv-IgG format
SEQ ID NO: 50	DIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYAASSLQSGVPSRFSG SGSGTDFLTISSLQPEDFATYYCQQSYSTPYT FGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGA SVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSYSTYMSSTLTTLTKDEYERHNSY TCEATHKTSTSPIVKSFNNEC	Exemplary Seq_C_ Pep3 Asymmetric DBA- Cytokine Complex scFv-IgG format
SEQ ID NO: 51	QVQLVQSGAEVKKPGASVKVSCKASGYTFST YYHWVRQAPGQGLEWMGIINPSGGGTVYA QKFQGRVTMTRDTSTSTVYMESSLRSED TA VYYCAAGLFIWGQGLTVTVSSAKTTAPSVY PLAPVCGDTTGSSVTLGCLVKGYFPEPVT LTWNSGSLSSGVHTFPAVLQSDLYTLSSSVT VTSSTWPSQSITCNVAHPASSTKVDKKIEP RGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWV FNNVEVHTAQTTQTHREDYNSTLRVVSALPI QHQDWMSGKEFKCKVNNKDLGAPIERTISKPK GSVRAPQVYVLPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDG SYFMYSKLRVEKKNWVERNYSYSCSVVHEGL HNNHTTKSFSRTPGK	PD1- IL2_6C12_N36T_S ym_L_Long_Pep1 Symmetric DBA- Cytokine Complex IgG format
SEQ ID NO: 52	APTSSSTKKTKLQLEHLLLDLQMLNGINNYK NPKLTRMLTFKFYMPKKATELKHLQCLEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLEL KGSETTFMCEYADETATVEFLNRWITFCQSII STLTVPGVGVPGAGVPGVGVPGGGVPGVGV PGGGVPGAGVPGGGVPGVGVPGAGVPGVGV PGGGDIQMTQSPSSLSASVGDRVTITCRASQY ISSGLAWYQQKPGKAPKLLIYKASSLDNGVPS RFSGSGSGTDFLTISSLQPEDFATYYCQQYE RLPLTFGGGTKVEIKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQ NGVLNSWTDQDSKDSYSTYMSSTLTTLTKDEYE RHNSYTCEATHKTSTSPIVKSFNNEC	PD1- IL2_6C12_N36T_S ym_L_Long_Pep2 Symmetric DBA- Cytokine Complex IgG format
SEQ ID NO: 53	APTSSSTKKTKLQLEHLLLDLQMLNGINNYK NPKLTRMLTFKFYMPKKATELKHLQCLEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLEL	PD1- IL2_6C12_N36T_

SEQ ID NO	Sequences	Description
	KGSETTFMCEYADETATIVEFLNRWITFCQSII STLTGGGGSGGGGSGGGGSGGGGSGVQLVQ SGAEVKKPGASVKVSCASGYTFSTYYIHWV RQAPGQGLEWMGIINPSGGGTVYAQKFQGR VTMTRDTSTSTVYMESSLRSEDNAVYYCAA GLFIWGQGTLLTVSSAKTTAPSVYPLAPVCG DTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKPCPPCKCP APNAAGGPSVFIFPPKIKDVLMISSLPIVTCVV VDVSEDDPDVQISWVFNNEVHTAQTQTHRE DYNSTLRVVSALPIQHQQDWMSGKEFKCKVN NKDLGAPIERTISKPKGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDFMPEDIYVEWTNNGKT ELNYKNTEPVLDSGYSFYMSKLRVEKKNW VERNSYSCSVVHEGLHNHHTTKSFSRTPGK	D68E_Sym_H_Short_Pep1 Symmetric DBA-Cytokine Complex IgG format
SEQ ID NO: 54	DIQMTQSPSSLSASVGRVTITCRASQYISSGL AWYQQKPGKAPKLLIYKASSLENGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQYERLPLT FGGGTKVEIKRADAAPTVISIFPPSSEQLTSGGA SVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDYSTYSMSSTLTTLTKDEYERHNSY TCEATHKTSTSPIVKSFNRECE	PD1-IL2_6C12_N36T_D68E_Sym_H_Short_Pep2 Symmetric DBA-Cytokine Complex IgG format
SEQ ID NO: 77	QVQLVQSGAEVKKPGASVKVSCASGYTFST YYVHWVRQAPGQGLEWMGIINPSGGSTSYA QNFQGRVTMTRDTSTSTVYMESSLRSEDNAV YYCASGWDVWGQGTITVTVSSAKTTAPSVY PLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTS STWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSL SPIVTCVVVDVSEDDPDVQISWVFNNEVHT AQTQTHREDYNSTLRVVSALPIQHQQDWMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEEMTKKQVTLTCMVTDFMPEDIYV EWTNNGKTELNYKNTEPVLDSGYSFYMSD LRVEKKNWVERNSYSCSVVHEGLHNHHTTE SFSRTPGK	PD1-IL2_L_7A05scFv_PD1-R07-A05_Pep1 Asymmetric DBA-Cytokine Complex IgG-scFv format
SEQ ID NO: 78	QVQLVQSGAEVKKPGASVKVSCASGYTFST YYVHWVRQAPGQGLEWMGIINPSGGSTSYA QNFQGRVTMTRDTSTSTVYMESSLRSEDNAV YYCASGWDVWGQGTITVTVSSASGGGGSG GGGGSGGGGSHASEIVMTQSPATLSVSPGERAT LSCRASQSVNTYLAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYGSSPVTFGQGTREIKPRGPTIKPCPP CKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIV TCVVVDVSEDDPDVQISWVFNNEVHTAQT QTHREDYNSTLRVVSALPIQHQQDWMSGKEFK CKVNNKDLGAPIERTISKPKGSVRAPQVYVLP	PD1-IL2_L_7A05scFv_PD1-R07-A05_Pep2 Asymmetric DBA-Cytokine Complex IgG-scFv format

SEQ ID NO	Sequences	Description
	PPEKEMTKKQVSLTCLVKDFMPEDIYVEWTN NGKTELNYKNTEPVLSKSDGSYFMYSKLTVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTP GGGGSGGGSHHHHHH	
SEQ ID NO: 79	APTSSSTKKTQLQLEHLLDLQMLNGINNYK NPKLTDMLTFKFYMPKKATELKHLQCLEEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLEL KGSETTFMCEYADETATIVEFLNRWITFCQSII STLTGGGGSGGGGSGGGGSGGGGSEIVMTQS PATLSVSPGERATLSCRASQSVNTYLAWYQQ KPGQAPRLLIYGASTRATGIPARFSGSGSGTEF TLTISSLQSEDFAVYYCQQYGGSSPVTFGQGTR LEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFL NNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTTLTKDEYERHNSYTCEAT HKTSTSPIVKSFNRNEC	PD1- IL2_L_7A05scFv_ PD1-R07- A05_Pep3 Asymmetric DBA- Cytokine Complex IgG-scFv format

TABLE 13 – Dual-Binding Antibodies (DBAs)

Dual- Binding Antibody	Marker	Therapeutic	HV* SEQ ID NO:	LV** SEQ ID NO:	HV_cdr1 SEQ ID NO:	HV_cdr2 SEQ ID NO:	HV_cdr3 SEQ ID NO:	LV_cdr1 SEQ ID NO:	LV_cdr2 SEQ ID NO:	LV_cdr3 SEQ ID NO:
AB001718	PD-1	IL-2	127	135	142	148	154	157	163	168
AB001744	PD-1	IL-2	128	136	143	148	154	158	163	169
AB002022	PD-1	IL-2	129	137	144	149	154	159	164	170
AB001609	PD-L1	IFN α	130	138	145	150	155	160	165	171
AB001638	PD-L1	IFN α	130	139	145	150	155	161	165	172
AB001843	PD-L1	IFN α	131	140	146	151	156	162	166	173
AB001866	PD-L1	IFN α	132	140	147	152	156	162	166	173
AB001875	PD-L1	IFN α	133	140	143	153	156	162	166	173
AB001909	PD-L1	IFN α	134	141	143	151	156	162	167	173

*HV refers to the heavy chain variable region of the respective antibodies

**LV refers to the light chain variable region of the respective antibodies

TABLE 14 – Sequences of DBA Protein Components

SEQ ID NO:	DBA Protein Component	Sequence
SEQ ID NO: 127	AB001718_HV	QVQLVQSGAEVKKPGASVKVSCKASG DTFSTYYVHWVRQAPGQGLEWMGIINP SGGGTVYAQKFQGRVTMTRDTSTSTVY MELSSLRSED TAVYYCAAGLFIWGQGT LTVVSS
SEQ ID NO: 128	AB001744_HV	QVQLVQSGAEVKKPGASVKVSCKASG YTFSNYYIHWRQAPGQGLEWMGIINP SGGGTVYAQKFQGRVTMTRDTSTSTVY MELSSLRSED TAVYYCAAGLFIWGQGT LTVVSS

SEQ ID NO:	DBA Protein Component	Sequence
SEQ ID NO: 129	AB002022_HV	QVQLVQSGAEVKKPGASVKVSCKASG DTFTRHYVHWVRQAPGQGLEWMGIIN PSGGYASYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDNAVYYCAAGLFIWGQG TLVTVSS
SEQ ID NO: 130	AB001609_HV	QVQLVQSGAEVKKPGASVKVSCKASG GTFSSYAIWVRQAPGQGLEWMGIIDPS VTYTRYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCARSLFPTIFGVE VAFDIWGQGTTLVTVSS
SEQ ID NO: 131	AB001843_HV	QVQLVQSGAEVKKPGASVKVSCKASG YTFSGYYIHWVRQAPGQGLEWMGWM DSNSGGTGYAQKFQGRVTMTRDTSTST VYMELSSLRSEDNAVYYCAKEVFSGW YDYWGQGTTLVTVSS
SEQ ID NO: 132	AB001866_HV	QVQLVQSGAEVKKPGASVKVSCKASG YTFSNYYVHWVRQAPGQGLEWMGWM DPNSGGTGYAHQFQGRVTMTRDTSTST VYMELSSLRSEDNAVYYCAKEVFSGW YDYWGQGTTLVTVSS
SEQ ID NO: 133	AB001875_HV	QVQLVQSGAEVKKPGASVKVSCKASG YTFSNYYIHWVRQAPGQGLEWMGWM DSNSGYTGYAQQFQGRVTMTRDTSTST VYMELSSLRSEDNAVYYCAKEVFSGW YDYWGQGTTLVTVSS
SEQ ID NO: 134	AB001909_HV	QVQLVQSGAEVKKPGASVKVSCKASG YTFSNYYIHWVRQAPGQGLEWMGWM DSNSGGTGYAQKFQGRVTMTRDTSTST VYMELSSLRSEDNAVYYCAKEVFSGW YDYWGQGTTLVTVSS
SEQ ID NO: 135	AB001718_LV	DIQMTQSPSSLSASVGDRVTITCRASQYI SSGLAWYQQKPGKAPKLLIYKASSLDN GVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYERLPLTFGGGKVEIK
SEQ ID NO: 136	AB001744_LV	DIQMTQSPSSLSASVGDRVTITCRASQSI GTGLAWYQQKPGKAPKLLIYKASSLDN GVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYNRAPLTFGGGKVEIK
SEQ ID NO: 137	AB002022_LV	DIQMTQSPSSLSASVGDRVTITCRASQSI GRWLAWYQQKPGKAPKLLIYSASNLET GVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYESFPVTFGPGTKVDIK
SEQ ID NO: 138	AB001609_LV	DIQMTQSPSSLSASVGDRVTITCRASQSI SNRLAWYQQKPGKAPKLLIYKASSLES GVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSNSTPFTFGQGKVEIK
SEQ ID NO: 139	AB001638_LV	DIQMTQSPSSLSASVGDRVTITCQASQSI SNYLAWYQQKPGKAPKLLIYKASSLES GVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQTYSTPITFGQGKVEIK

SEQ ID NO:	DBA Protein Component	Sequence
SEQ ID NO: 140	AB001843 LV	DIQMTQSPSSLSASVGDRVTITCRASQSI SSYLNWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQSYSTPYTFGQGGTKVEIK
SEQ ID NO: 141	AB001909 LV	DIQMTQSPSSLSASVGDRVTITCRASQSI SSYLNWYQQKPGKAPKLLIYAASSLES GVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQSYSTPYTFGQGGTKVDIK
SEQ ID NO: 142	AB001718 HV_cdr1	GDTFSTYYVH
SEQ ID NO: 143	AB001744 HV_cdr1	GYTFSNYYIH
SEQ ID NO: 144	AB002022 HV_cdr1	GDTFTRHYVH
SEQ ID NO: 145	AB001609 HV_cdr1	GGTFSSY AIS
SEQ ID NO: 146	AB001843 HV_cdr1	GYTFSGYYIH
SEQ ID NO: 147	AB001866 HV_cdr1	GYTFSNYYVH
SEQ ID NO: 148	AB001718 HV_cdr2	IINPSGGGT VYAQKFQG
SEQ ID NO: 149	AB002022 HV_cdr2	IINPSGGYAS YAQKFQG
SEQ ID NO: 150	AB001609 HV_cdr2	IIDPSVTYTRYA QKFQG
SEQ ID NO: 151	AB001843 HV_cdr2	WMDSNSGGTGYA QKFQG
SEQ ID NO: 152	AB001866 HV_cdr2	WMDPNSSGGTGYA HQFQG
SEQ ID NO: 153	AB001875 HV_cdr2	WMDSNSGYTGYA QQFQG
SEQ ID NO: 154	AB001718 HV_cdr3	AAGLFI
SEQ ID NO: 155	AB001609 HV_cdr3	ARSLFPTIFGVEVAFDI
SEQ ID NO: 156	AB001843 HV_cdr3	AKEVFSGWYDY
SEQ ID NO: 157	AB001718 LV_cdr1	RASQYISSGLA
SEQ ID NO: 158	AB001744 LV_cdr1	RASQSIGTGLA
SEQ ID NO: 159	AB002022 LV_cdr1	RASQSIGRWLA
SEQ ID NO: 160	AB001609 LV_cdr1	RASQSI SNRLA
SEQ ID NO: 161	AB001638 LV_cdr1	QASQSI SNYLA
SEQ ID NO: 162	AB001843 LV_cdr1	RASQSISSYLN
SEQ ID NO: 163	AB001718 LV_cdr2	KASSLDN
SEQ ID NO: 164	AB002022 LV_cdr2	SASNLET
SEQ ID NO: 165	AB001609 LV_cdr2	KASSLES
SEQ ID NO: 166	AB001843 LV_cdr2	AASSLQS
SEQ ID NO: 167	AB001909 LV_cdr2	AASSLES
SEQ ID NO: 168	AB001718 LV_cdr3	QQYERLPL
SEQ ID NO: 169	AB001744 LV_cdr3	QQYNRAPL
SEQ ID NO: 170	AB002022 LV_cdr3	QQYESFPV
SEQ ID NO: 171	AB001609 LV_cdr3	QQSNSTPF
SEQ ID NO: 172	AB001638 LV_cdr3	QQTYSTPI
SEQ ID NO: 173	AB001843 LV_cdr3	QQSYSTPY

TABLE 15 – Exemplary DBA-Cytokine Protein Complexes

Name	DBA / Therapeutic	DBA	Type	DBA domains	Therapeutic domains	2nd Ab domain	Heavy Chain 1 SEQ ID NO:	Heavy Chain 2 SEQ ID NO:	Heavy Chain 3 SEQ ID NO:
AF00 3229	PD-1 / IL-2	AB001 718	FIG. 9b	2	1	N/A	80	97	114
AF00 3230	PD-1 / IL-2	AB001 744	FIG. 9b	2	1	N/A	81	98	115
AF00 3232	PD-1 / IL-2	AB002 022	FIG. 9b	2	1	N/A	82	99	116
AF00 3250	PD-1 / IL-2	AB001 718	FIG. 9a	1	1	anti-PD-1	83	100	117
AF00 3251	PD-1 / IL-2	AB001 744	FIG. 9a	1	1	anti-PD-1	84	101	118
AF00 3253	PD-1 / IL-2	AB002 022	FIG. 9a	1	1	anti-PD-1	85	102	119
AF00 3103	PD-L1 / IFN α	AB001 609	FIG. 9b	2	1	N/A	86	103	120
AF00 3104	PD-L1 / IFN α	AB001 909	FIG. 9b	2	1	N/A	87	104	126
AF00 3105	PD-L1 / IFN α	AB001 843	FIG. 9b	2	1	N/A	88	105	122
AF00 3106	PD-L1 / IFN α	AB001 875	FIG. 9b	2	1	N/A	89	106	123
AF00 3217	PD-L1 / IFN α	AB001 609	FIG. 9a	1	1	anti-PD- L1	90	107	124
AF00 3218	PD-L1 / IFN α	AB001 843	FIG. 9a	1	1	anti-PD- L1	91	108	125
AF00 3219	PD-L1 / IFN α	AB001 909	FIG. 9a	1	1	anti-PD- L1	92	109	126
AF00 2618	PD-L1 / IFN α	AB001 609	FIG. 9d	2	2	N/A	93		110
AF00 2639	PD-L1 / IFN α	AB001 875	FIG. 9d	2	2	N/A	94		111
AF00 2645	PD-L1 / IFN α	AB001 609	FIG. 9c	2	2	N/A	95		112
AF00 2666	PD-L1 / IFN α	AB001 875	FIG. 9e	2	2	N/A	96		277

TABLE 16 – Sequences of Peptides in TABLE 15

SEQ ID NO:	DBA	Sequence
SEQ ID NO: 80	AF003229 _Pep1	APTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTF KFYMPKKATELKHLQCLEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKP GASVKVSCASGDTFSTYYVHWVRQAPGQGLEWMGIINPS GGGTVYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGD TTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMI SLPIVTCVVVDV SEDDPDVQISW FVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTE LNYKNTEPVLDSDGSYFMYSDLRVEKKNWVERNSYSCSVV HEGLHNHHTTESFSRTPGK

SEQ ID NO:	DBA	Sequence
SEQ ID NO: 81	AF003230_Pep1	APTSSSTKKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKP GASVKVSCKASGYTFSNYYIHWVRQAPGQGLEWMGIINPS GGGTVYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLSPVTCVVVDV SEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTE LNYKNTEPVLDSDGSYFMYSDLRVEKKNWVERNSYSCSVV HEGLHNHHTTESFSRTPGK
SEQ ID NO: 82	AF003232_Pep1	APTSSSTKKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKP GASVKVSCKASGDTFTRHYVHWVRQAPGQGLEWMGIINPS GGYASYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLSPVTCVVVDV SEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTE LNYKNTEPVLDSDGSYFMYSDLRVEKKNWVERNSYSCSVV HEGLHNHHTTESFSRTPGK
SEQ ID NO: 83	AF003250_Pep1	APTSSSTKKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKP GASVKVSCKASGDTFSTYYVHWVRQAPGQGLEWMGIINPS GGGTVYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLSPVTCVVVDV SEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTE LNYKNTEPVLDSDGSYFMYSDLRVEKKNWVERNSYSCSVV HEGLHNHHTTESFSRTPGK
SEQ ID NO: 84	AF003251_Pep1	APTSSSTKKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKP GASVKVSCKASGYTFSNYYIHWVRQAPGQGLEWMGIINPS

SEQ ID NO:	DBA	Sequence
		GGGTVYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDNAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGDGTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLPIVTCVVVDV SEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTE LNYKNTEPVLDSGGSYFMYSDLRVEKKNWVERNNSYSCSVV HEGLHNHHTTESFSRTPGK
SEQ ID NO: 85	AF003253_Pep1	APTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTF KFYMPKKATELKHLCLEELKPLEEVLNLAQSKNFHLRPR DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQ SIISTLTGGGGSGGGSGGGSGGGSGQVQLVQSGAEVKKP GASVKVSCKASGDTFTRHYVHWVRQAPGQGLEWMGIINPS GGYASYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDNAVY YCAAGLFIWGQGLTVTVSSAKTTAPSVYPLAPVCGDGTGSS VTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLPIVTCVVVDV SEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALP IQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTE LNYKNTEPVLDSGGSYFMYSDLRVEKKNWVERNNSYSCSVV HEGLHNHHTTESFSRTPGK
SEQ ID NO: 86	AF003103_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGSGGGSGGGSGQVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAIWVRQAPGQGLEWMGIIDPSVTYTRYA QKFQGRVTMTRDTSTSTVYMELSSLRSEDNAVYYCARSLFP TIFGVEVAFDIWGQGLTVTVSSAKTTAPSVYPLAPVCGDGT GSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSLPIVTCVVV DVSEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVS ALPIHQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVCVLPPPEEEMTKKQVTLWCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSGGSYFMYSKLRVEKKNWVERNNSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 87	AF003104_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGSGGGSGGGSG QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIHWVRQA PGQGLEWMGWMDSNSGGTGYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDNAVYYCAKEVFSGWYDYWGQGLTVTVSS AKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTW

SEQ ID NO:	DBA	Sequence
		NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFP PKIKDVLMISSLPIVTCVVVDVSEDDPDVQISWVFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNK DLGAPIERTISKPKGSVRAPQVCVLPPPEEEMTKKQVTLWC MVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMY SKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 88	AF003105_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGGSGGGGSGGGGSSQVQLVQSGAEVKKPGASVKV SCKASGYTFSGYIHWVRQAPGQGLEWMGWMDSNSGGTG YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKE VFSGWYDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGS SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLY TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVD VSEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVCVLPPPEEEMTKKQVTLWCMVTDFMPEDIYVEWTNNG KTELNYKNTEPVLDSGGSYFMYSKLRVEKKNWVERNYSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 89	AF003106_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGGSGGGGSGGGGSSQVQLVQSGAEVKKPGASVKV SCKASGYTFSNYYIHWVRQAPGQGLEWMGWMDSNSGYTG YAQQFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKE VFSGWYDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGS SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLY TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVD VSEDDPDVQISWVFVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVCVLPPPEEEMTKKQVTLWCMVTDFMPEDIYVEWTNNG KTELNYKNTEPVLDSGGSYFMYSKLRVEKKNWVERNYSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 90	AF003217_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGGSGGGGSGGGGSSQVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAIWVRQAPGQGLEWMGIIDPSVTYTRYA QKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSLFP TIFGVEVAFDIWGQGTLLTVSSAKTTAPSVYPLAPVCGDTT GSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVV

SEQ ID NO:	DBA	Sequence
		DVSEDDPDVQISWVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVCVLPPEEEMTKKQVTLWCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSGDSYFMYSKLRVEKKNWVERNYSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 91	AF003218_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGGSGGGGSGGGGSSQVQLVQSGAEVKKPGASVKV SCKASGYTFSGYIHWVRQAPGQGLEWMGWMDSNSGGTG YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDNAVYYCAKE VFSGWYDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGS SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLY TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVD VSEDDPDVQISWVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVCVLPPEEEMTKKQVTLWCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSGDSYFMYSKLRVEKKNWVERNYSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 92	AF003219_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF CTELYQQLNDLEACVMQEERVGETPLMNADSILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIVRSLSLSTNLQERLRRKEG GGGSGGGGSGGGGSGGGGSSQVQLVQSGAEVKKPGASVKV SCKASGYTFSNYIHWVRQAPGQGLEWMGWMDSNSGGTG YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDNAVYYCAKE VFSGWYDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGS SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLY TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVD VSEDDPDVQISWVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVCVLPPEEEMTKKQVTLWCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSGDSYFMYSKLRVEKKNWVERNYSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 93	AF002618_Pep1	QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYAISWVRQA PGQGLEWMGIIDPSVTYTRYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCARSLFPTIFGVEVAFDIWGQGTLLTV SSAKTTAPSVYPLAPVCGDTTGS SVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFI FPPKIKDVLMISSLPIVTCVVVDVSEDDPDVQISWVNNVEV HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN NKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLT CMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGDSYFM YSKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPG K

SEQ ID NO:	DBA	Sequence
SEQ ID NO: 94	AF002639_Pep1	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIHWVRQA PGQGLEWMGWMDSNSGYTGAAQQFQGRVTMTRDTSTSTV YMELSSLRSEDТАVYYCAKEVFSGWYDYWGQGTLVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTNW SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPP KIKDVLMISSLPIVTCVVVDVSEDDPDVQISWVFNNEVHT AQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNK DLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCM VTDMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 95	AF002645_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF YTELYQQLNDLEACVIQGVGVTTETPLMKEDSILAVRKYFQR ITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEVP GVGVPGAGVPGVGVPGGGVPGVGVPGGGVPGAGVPGGGV PGVGVPGAGVPGVGVPGGGQVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAIWVRQAPGQGLEWMGIIDPSVTYTRYA QKFQGRVTMTRDTSTSTVYMELSSLRSEDТАVYYCARSLFP TIFGVEVAFDIWGQGTЛTVSSAKTTAPSVYPLAPVCGDTT GSSVTLGCLVKGYFPEPVTLTNWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVV DVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 96	AF002666_Pep1	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF YTELYQQLNDLEACVIQGVGVTTETPLMKEDSILAVRKYFQR ITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEVP GVGVPGAGVPGVGVPGGGVPGVGVPGGGVPGAGVPGGGV PGVGVPGAGVPGVGVPGGGQVQLVQSGAEVKKPGASVKV SCKASGYTFSNYYIHWVRQAPGQGLEWMGWMDSNSGYTG YAAQQFQGRVTMTRDTSTSTVYMELSSLRSEDТАVYYCAKE VFSGWYDYWGQGTЛTVSSAKTTAPSVYPLAPVCGDTTG SVTLGCLVKGYFPEPVTLTNWNSGSLSSGVHTFPAVLQSDLY TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIK PCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVV VDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNG KTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSC SVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 97	AF003229_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGDTFSTYYVHWVRQ APGQGLEWMGIINPSGGGTVYAAQKFQGRVTMTRDTSTSTV YMELSSLRSEDТАVYYCAAGLFIWGQGTЛTVSSAKTTAP SVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTNWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS

SEQ ID NO:	DBA	Sequence
		TKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQT HREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAP IERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFM PEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLTVE KKNWVERNNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGG SHHHHHH
SEQ ID NO: 98	AF003230_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIHWVRQA PGQGLEWMGIINPSGGGTVYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCAAGLFIWGQGTLLTVSSAKTTAPSV YPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASST KVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTH REDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPI ERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFM PEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLTVE KKNWVERNNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGG SHHHHHH
SEQ ID NO: 99	AF003232_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGDTFTRHYVHWVRQ APGQGLEWMGIINPSGGYASYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDNAVYYCAAGLFIWGQGTLLTVSSAKTTAPS VYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS TKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQT HREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAP IERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFM PEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLTVE KKNWVERNNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGG SHHHHHH
SEQ ID NO: 100	AF003250_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYVHWVRQ APGQGLEWMGIINPSGGSTSYAQNFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCASGWDVWGQGTTLTVSSASGGGGS GGGGSGGGGSHASEIVMTQSPATLSVSPGERATLSCRASQS VNTYLAWEYQKPGQAPRLLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDAVYYCQYQYSSPVTFGQGTREIKPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVV DVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNG KTELNYKNTEPVLKSDGSYFMYSKLTVEKKNWVERNNSYSC SVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
SEQ ID NO: 101	AF003251_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYVHWVRQ APGQGLEWMGIINPSGGSTSYAQNFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCASGWDVWGQGTTLTVSSASGGGGS GGGGSGGGGSHASEIVMTQSPATLSVSPGERATLSCRASQS VNTYLAWEYQKPGQAPRLLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDAVYYCQYQYSSPVTFGQGTREIKPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVV

SEQ ID NO:	DBA	Sequence
		DVSEDDPDVQISWVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQDWMMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNG KTELNYKNTEPVLKSDGSYFMYSKLTVEKKNWVERNSYSC SVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
SEQ ID NO: 102	AF003253_Pep2	QVQLVQSGAEVKKPGASVKVSCASGYFTFTYYVHWVRQ APQGQGLEWMGIINPSGGSTSYAQNFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCASGWDVWGQGTITVTVSSASGGGGG GGGGSGGGGSHASEIVMTQSPATLSVSPGERATLSCRASQS VNTYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDAVYYCQQYGSSPVTFTGQGRTRLEIKPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLSPIVTCVVV DVSEDDPDVQISWVNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQDWMMSGKEFKCKVNNKDLGAPIERTISKPKGSVRA PQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNG KTELNYKNTEPVLKSDGSYFMYSKLTVEKKNWVERNSYSC SVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
SEQ ID NO: 103	AF003103_Pep2	QVQLVQSGAEVKKPGASVKVSCASGGTFSSYAISWVRQA PGQGLEWMGIIDPSVTYTRYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDNAVYYCARSLFPTIFGVEVAFDIWGQGTLVTV SSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFI FPPKIKDVLMLSPIVTCVVVDVSEDDPDVQISWVNNVEV HTAQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKVN NKDLGAPIERTISKPKGSVRAPQVYVLPPECEEMTKKQVTL CAVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFM VSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG KHHHHHHH
SEQ ID NO: 104	AF003104_Pep2	QVQLVQSGAEVKKPGASVKVSCASGYTFSNYYIHWVRQA PGQGLEWMGWMDSNSGGTGYYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDNAVYYCAKEVFSGWYDYWGQGTITVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPP KIKDVLMLSPIVTCVVVDVSEDDPDVQISWVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKVNNK DLGAPIERTISKPKGSVRAPQVYVLPPECEEMTKKQVTLSCA VTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMVS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGKH HHHHHH
SEQ ID NO: 105	AF003105_Pep2	QVQLVQSGAEVKKPGASVKVSCASGYTFSGYIHWVRQA PGQGLEWMGWMDSNSGGTGYYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDNAVYYCAKEVFSGWYDYWGQGTITVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPP KIKDVLMLSPIVTCVVVDVSEDDPDVQISWVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKVNNK DLGAPIERTISKPKGSVRAPQVYVLPPECEEMTKKQVTLSCA

SEQ ID NO:	DBA	Sequence
		VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMVS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGKH HHHHH
SEQ ID NO: 106	AF003106_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIHWRQA PGQGLEWMGWMDSNSGYTGYYAQFQGRVTMTRDTSTSTV YMELSSLRSEDVAVYYCAKEVFSGWYDYWGQGLTLTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTNW SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPP KIKDVLMISSLPIVTCVVVDVSEDDPDVQISWVFNNEVHT AQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNK DLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLSCA VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMVS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGKH HHHHH
SEQ ID NO: 107	AF003217_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTKNYMHWRQA APGQGLEWLGWVSPDSGYTGYYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDVAVYYCTDILLSELDLDAFDIWGQGTMT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYAASLTQSGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLTFGGGTK LEIKPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSL PIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDY NSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTIS KPKGSVRAPQVYVLPPEEEMTKKQVTLSCAVTDFMPEDIY VEWTNNGKTELNYKNTEPVLDSGGSYFMVSKLRVEKKNW VERNSYSCSVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 108	AF003218_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTKNYMHWRQA APGQGLEWLGWVSPDSGYTGYYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDVAVYYCTDILLSELDLDAFDIWGQGTMT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYAASLTQSGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLTFGGGTK LEIKPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSL PIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDY NSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTIS KPKGSVRAPQVYVLPPEEEMTKKQVTLSCAVTDFMPEDIY VEWTNNGKTELNYKNTEPVLDSGGSYFMVSKLRVEKKNW VERNSYSCSVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 109	AF003219_Pep2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTKNYMHWRQA APGQGLEWLGWVSPDSGYTGYYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDVAVYYCTDILLSELDLDAFDIWGQGTMT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYAASLTQSGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLTFGGGTK LEIKPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMISSL PIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDY NSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTIS KPKGSVRAPQVYVLPPEEEMTKKQVTLSCAVTDFMPEDIY

SEQ ID NO:	DBA	Sequence
		VEWTNNGKTELNYKNTEPVLDSDGSYFMVSKLRVEKKNW VERNSYSCSVVHEGLHNHHTTKSFSRTPGK
SEQ ID NO: 110	AF002618_Pep2	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF YTELYQQNLNDEACVIQGVGVTTETPLMKEDSILAVRKYFQR ITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGG GGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQSISNRLAWYQQKPGKAPKLLIYKASSLESVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSNSTPFTFGQGTKVEIKR ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI DGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDEYERHN SYTCEATHKTSTSPIVKSFNNEC
SEQ ID NO: 111	AF002639_Pep2	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKF YTELYQQNLNDEACVIQGVGVTTETPLMKEDSILAVRKYFQR ITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGG GGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGQGTKVEIK RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWK IDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDEYERHN SYTCEATHKTSTSPIVKSFNNEC
SEQ ID NO: 112	AF002645_Pep2	DIQMTQSPSSLSASVGDRVTITCRASQSISNRLAWYQQKPGK APKLLIYKASSLESVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSNSTPFTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN NEC
SEQ ID NO: 114	AF003229_Pep3	DIQMTQSPSSLSASVGDRVTITCRASQYISSGLAWYQQKPGK APKLLIYKASSLDNGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYERLPLTFGGGTKVEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNNEC
SEQ ID NO: 115	AF003230_Pep3	DIQMTQSPSSLSASVGDRVTITCRASQSIGTGLAWYQQKPGK APKLLIYKASSLDNGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQYNRAPLTFGGGTKVEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNNEC
SEQ ID NO: 116	AF003232_Pep3	DIQMTQSPSSLSASVGDRVTITCRASQSIGRWLAWYQQKPG KAPKLLIYSASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQYESFPVTFGPGTKVDIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNNEC
SEQ ID NO: 126	AF003219_Pep3	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGK APKLLIYAASSLESVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYSTPYTFGQGTKVDIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS

SEQ ID NO:	DBA	Sequence
		KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

EXAMPLE 7**Reduced Type I IFN α Reporter Activation by a PD-L1/IFN α Protein Complex**

[0129] This example demonstrates reduced Type I IFN α reporter activation by a PD-L1/IFN α protein complex of the present disclosure, specifically a PD-L1/IFN α DBA/cytokine complexes, relative to unregulated antibody-IFN α immune cytokines. The DBA-cytokine protein complexes and control immune cytokines used in this experiment were IgG proteins with IFN α fused to the N-terminus of the heavy chain through a linker composed of 4 repeats of “GGGGS,” as

exemplified in **FIG. 9E**. The genes for two DBA-cytokine complexes, C08 IFN α (CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEM IQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVTTETPLMKEDSILAV RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSCASGGTFSSYAIWVRQAPGQGLEWMGII DPSVTYTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARS LFPTIFGVEVA FDIWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISW FVNNVE VHTAQ TQTHREDYNSTLRVVSALPIQH QDWM SKEFKCKVNNKDLGAPIERTISKPKG SVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLD SDGSYFMYSKLRVEKKNWVERN SYSCSVVHEGLHNHHTTKSFSRTPGK; SEQ ID NO: 57 and

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYGASTLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPITFGQGTKVEIKRADAAPT VSI FPPSS EQLTSGGASVVCFLNNFY PKDINVKWKIDG SERQNGVLNSWTDQDSKDSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC; SEQ ID NO: 58) and

B09 IFN α

(CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEM IQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVTTETPLMKEDSILAV RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSCASGGTFTGYMHVVRQAPGQGLEWM GWVNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARS LFPTIFG VEVAFDIWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW

NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGP
TIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFFVN
NVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISK
PKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEP
VLDSGDGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK; SEQ ID

NO: 59 and

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISLQPEDFATYYCQQSYSPPTFGQGTKLEIKRADAAPTVSIFPPSS
EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT
LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC; SEQ ID NO: 60), and

two control immune-cytokines, anti-Her2 IFN α

(CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEM
IQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVTTETPLMKEDSILAV
RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGGGGSGGG
GSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGGTFSSYAISWVRQAPGQGLEWMG
WINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSLFPTIFGVE
VAFDIWGQGTTVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS
GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTI
KPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFFVNN
VEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISK
KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEP
VLDSGDGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK; SEQ ID
NO: 61 and

DIQMTQSPSSLSASVGDRVTITCRASQSIIDRLAWYQQKPGKAPKLLIYKASSLESQVPSR
FSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVDIKRADAAPTVSIFPPSSE
QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT
TKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC; SEQ ID NO: 62) and anti-PD-L1 IFN α
(CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEM
IQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVTTETPLMKEDSILAV
RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGGGGSGGG
GSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARI
YPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMD
YWGGQGTLVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSL
SSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPC
PPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFFVNNVEV

HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGS
VRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDS
DGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK; SEQ ID NO: 63
and
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVP
SRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRADAAPTIVSIFPPS
SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYMSSTL
TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC; SEQ ID NO: 64) were synthesized,
expressed in HEK293 cells and Protein A purified (GenScript). Titrated concentrations of the
DBA-cytokine complexes and antibody-cytokine controls were added to a 96-well plate along
with 50,000 type I IFN α reporter cells (InvivoGen) in complete DMEM (+10% FBS, 2 mM L-
glutamine, sodium pyruvate). Plates were incubated at 37 °C overnight and developed by adding
20 μ L of culture supernatant to 180 μ L QUANTI-Blue Solution (InvivoGen). After a 30 minute
incubation at room temperature, plates were read on an Envision (Perkin Elmer) at 630 nm. In
the absence of PD-L1, the IFN α tethered PD-L1-IFN α DBA complexes C08 and B09 show
decreased reporter activation compared to equimolar amounts of the control anti-PD-L1 or anti-
HER2 IFN α immunocytokines (FIG. 10).

EXAMPLE 8

Reduced CD8⁺ T cell STAT5 phosphorylation by a PD-1/IL-2 Dual Binding Antibody (DBA) Cytokine Complexes

[0130] This example describes CD8⁺ T-cell STAT5 phosphorylation by PD-1/IL-2 DBA-cytokine complexes of the present disclosure. Genes for the PD-1/IL-2 DBAs shown in TABLE 17 were synthesized and expressed in HEK293 as IgG proteins with IL-2 fused to the N-terminus of the heavy or light chain through a linker (Genscript). Although only two of the antibodies blocked IL-2 binding to IL-2RB as scFvs, over 30 of the antibodies were able to reduce IL-2 signaling by a linked IL-2 domain. An exemplary set of these DBAs were chosen for analysis and compared to a control anti-HER2-IL-2 immunocytokine (TABLE 17).

TABLE 17 – IgG PD-1/IL-2 DBA protein complexes

Name	Heavy Chain Sequence SEQ ID NO	Light Chain Sequence SEQ ID NO
Anti-HER2	(SEQ ID NO: 65) EVQLVESGGGLVQPGGSLRLSCAA SGFNKDTYIHWRQAPGKGLEWV ARIYPTNGYTRYADSVKGRFTISAD TSKNTAYLQMNSLRAEDTAVYYCS	(SEQ ID NO: 66) APTSSSTKKKTQLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLQCLEEELKPL EEVLNLAQSKNFHLRPRDLISNI

Name	Heavy Chain Sequence SEQ ID NO	Light Chain Sequence SEQ ID NO
	RWGGDGFYAMDYWGQGTLLTVSS AKTTAPSVYPLAPVCGDTTGSSVTL GCLVKGYFPEPVTLTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVTSST WPSQSITCNVAHPASSTKVDKKIEP RGPTIKPCPPCKCPAPNAAGGPSVFI FPPKIKDVLMLISLSPIVTCVVVDVSE DDPDVQISWVFNNEVHTAQTQTH REDYNSTLRVVSALPIQHQQDWMMSG KEFKCKVNNKDLGAPIERTISKPKG SVRAPQVYVLPPEEEMTKKQVTL TCMVTDMPEDIYVEWTNNGKTEL NYKNTEPVLDSDGSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHH TTKSFSRTPGK	NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPAGVPGVGVPGGGVPG VGVPGGGVPGAGVPGGGVPGV GVPAGVPGVGVPGGGDIQMT QSPSSLSASVGDRVTITCRASQD VNTAVAWYQQKPGKAPKLLIY SASFLYSGVPSRFSGSRSGTDFT LTISSLQPEDFATYYCQQHYTTP PTFGQGTKVEIKRADAAPTVSIF PPSSEQLTSGGASVVCFLNFPY KDINVKWKIDGSRQNGVLNS WTDQDSKDSYMSSTLTTLTKD EYERHNSYTCEATHKTSTSPIVK SFNRNEC
2-A08	(SEQ ID NO: 67) QVQLVQSGAEVKKPGASVKVSCK VSGYTFTSYDINWVRQAPGQGLEW MGWINPNSGDTGYAQKFQGRVTM TRDTSTSTVYMELSSLRSEDAVYY CARDTGLGYYYGSGDFDYWGQGT LTVSSAKTTAPSVYPLAPVCGDTT GSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSV TVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNAA GGPSVFIFPPKIKDVLMLISLSPIVTCV VVDVSEDDPDVQISWVFNNEVHT AQTQTHREDYNSTLRVVSALPIQH QDWMMSGKEFKCKVNNKDLGAPIE RTISKPKGSVRAPQVYVLPPEEEM TTKQVTLTCMVTDMPEDIYVEWT NNGKTELNYKNTEPVLDSDGSYFM YSKLRVEKKNWVERNSYSCSVVHE GLHNHHTTKSFSRTPGK	(SEQ ID NO: 68) APTSSSTKKTKLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLCLEELKPL EEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPAGVPGVGVPGGGVPG VGVPGGGVPGAGVPGGGVPGV GVPAGVPGVGVPGGGDIQMT QSPSSLSASVGDRVTITCQASQD IHNYLNWYQQKPGKAPKLLIYD VSNLETGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQAISFPLT FGGGTKVEIKRADAAPTVSIFPP SSEQLTSGGASVVCFLNFPYK DINVKWKIDGSRQNGVLNSW TDQDSKDSYMSSTLTTLTKDE YERHNSYTCEATHKTSTSPIVKS FNRNEC
2-A11	(SEQ ID NO: 69) QVQLVQSGAEVKKPGASVKVSCK ASGHTFTRYMHVVRQAPGQGLE WMGIINPSGGYATYAQKFQGRVTM TRDTSTSTVYMELSSLRSEDAVYY CASGWDVWGQGTLLTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVK GYFPEPVTLTWNSGSLSSGVHTFPA VLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKD VLMISLSPIVTCVVVDVSEDDPDVQ ISWVFNNEVHTAQTQTHREDYNS	(SEQ ID NO: 70) APTSSSTKKTKLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLCLEELKPL EEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPAGVPGVGVPGGGVPG VGVPGGGVPGAGVPGGGVPGV GVPAGVPGVGVPGGGDIQMT QSPSSLSASVGDRVTITCRASQSI NSWLAWYQQKPGKAPKLLIYA TSTLESVPSRFSGSGSGTDFTL

Name	Heavy Chain Sequence SEQ ID NO	Light Chain Sequence SEQ ID NO
	TLRVVSALPIQHQDWMMSGKEFKCK VNNKDLGAPIERTISKPKGSVRAPQ VYVLPPEEEMTKKQVTLTCMVT FMPEDIYVEWTNNGKTELNYKNTE PVLDSGDSYFMYSKLRVEKKNWV ERNYSYSCSVVHEGLHNHHTTKSFSR TPGK	TISSLQPEDFATYYCQQSYSFPP TFGQGTKVEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPK DINVKWKIDGSERQNGVLNSW TDQDSKDSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKS FNRNEC
2-B05	(SEQ ID NO: 71) QVQLVQSGAEVKKPGASVKVSCK ASGYTFTNYYIHWVRQAPGQGLE WMGIINPRAGYTSYALKFQGRVTM TRDTSTSTVYMELSSLRSEDVAVYY CAGGWLWDWGQGLTVTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVK GYFPEPVTLTWNSSGLSSGVHTFPA VLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKD VLMISLSPIVTCVVVDVSEDDPDVQ ISWVFNNEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMMSGKEFKCK VNNKDLGAPIERTISKPKGSVRAPQ VYVLPPEEEMTKKQVTLTCMVT FMPEDIYVEWTNNGKTELNYKNTE PVLDSGDSYFMYSKLRVEKKNWV ERNYSYSCSVVHEGLHNHHTTKSFSR TPGK	(SEQ ID NO: 72) APTSSSTKKKTQLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLQCLEEELKPL EEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPGAGVPGVGVPGGGVPG GVVPGGGVPGAGVPGGGVPGV GVPGAGVPGVGVVPGGGDIQMT QSPSSLSASVGDRVITTCRASQSI SSWLAWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSFTMPI TFGQGTRLEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPK DINVKWKIDGSERQNGVLNSW TDQDSKDSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKS FNRNEC
2-B07	(SEQ ID NO: 73) QVQLVQSGAEVKKPGASVKVSCK ASGDTFTRHYVHWVRQAPGQGLE WMGIINPSGGYASYAQKFQGRVTM TRDTSTSTVYMELSSLRSEDVAVYY CAAGLFIWGQGLTVTVSSAKTTAPS VYPLAPVCGDTTGSSVTLGCLVKG YFPEPVTLTWNSSGLSSGVHTFPAV LQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPC PPCKCPAPNAAGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQIS WVFNNEVHTAQTQTHREDYNST LRVVSALPIQHQDWMMSGKEFKCKV NKNKDLGAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDF MPEDIYVEWTNNGKTELNYKNTEP VLDSGDSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRT PGK	(SEQ ID NO: 74) APTSSSTKKKTQLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLQCLEEELKPL EEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPGAGVPGVGVVPGGGVPG GVVPGGGVPGAGVPGGGVPGV GVPGAGVPGVGVVPGGGDIQMT QSPSSLSASVGDRVITTCRASQSI GRWLAWYQQKPGKAPKLLIYS ASNLETGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQANSFPV TFGPGTKVDIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPK DINVKWKIDGSERQNGVLNSW TDQDSKDSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKS FNRNEC
7-A04	(SEQ ID NO: 75)	(SEQ ID NO: 76)

Name	Heavy Chain Sequence SEQ ID NO	Light Chain Sequence SEQ ID NO
	QVQLVQSGAEVKKPGASVKVSCK ASGYTFTDYMHWRQAPGQGLE WMGIINPRAGYTSYALKFQGRVTM TRDTSTSTVYMELSSLRSEDTAVYY CTSGMDVWGQGLTVTVSSAKTTAP SVYPLAPVCGDTTGSSVTLGCLVK GYFPEPVTLTWNSGSLSSGVHTFPA VLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKP CPPCKCPAPNAAGGPSVFIFPPKIKD VLMISLSPIVTCVVVDVSEDDPDVQ ISWVFNNEVHTAQTQTHREDYNS TLRVVSALPIQHQQDWMMSGKEFKCK VNNKDLGAPIERTISKPKGSVRAPQ VYVLPPEEEMTKKQVTLTCMVD FMPEDIYVEWTNNGKTELNYKNTE PVLDSGDSYFMYSKLRVEKKNWV ERNSYSCSVVHEGLHNHHTTKSFSR TPGK	APTSSSTKKTQLQLEHLLLDLQ MILNGINNYKNPKLTRMLTFKF YMPKKATELKHLQCLEEELKPL EEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADET ATIVEFLNRWITFCQSIISTLTVP GVGVPGAGVPGVGPVGGGVPG VGVPGGGVPGAGVPGGGVPGV GVPGAGVPGVGPVGGGGDIQMT QSPSSLSASVGDRVTITCRASQSI STWLAWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQQSYSPV TFGQGTKVEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPK DINVKWKIDGSEKQNGVLNSW TDQDSKDSYMSSTLTTLTKDE YERHNSYTCEATHKTSTSPIVKS FNRNEC

[0131] The PD-1/IL-2 DBA-cytokine complexes were serially diluted in complete RPMI (+10% FBS, 2 mM L-glutamine, sodium pyruvate) and added to a 96-well plate. 2×10^5 human PBMCs were added to each well and plates were incubated at 37 °C for 20 minutes. An equal volume prewarmed fixation buffer (Biolegend) was then added to each well and plates were incubated at 37 °C for 10 minutes. Cells were then fixed in pre-chilled Perm Buffer III (BD Biosciences) for 30 minutes at 4 °C. Cells were washed with FACS wash buffer (PBS +2% FBS, 2 mM EDTA) and stained with fluorophore labeled antibodies directed against CD3, CD4, CD8, (BioLegend) and phospho-STAT5 (BD Biosciences) diluted 1:20 in FACS wash buffer. Cells were incubated 1 hour at 4 °C, washed with FACS wash buffer, and analyzed on a SA3800 Spectral Analyzer. In the absence of PD-1, the PD-1/IL-2 DBA/cytokine complexes induced less STAT5 phosphorylation in T cells compared to the monospecific control anti-HER2 IL-2 immunocytokine (**FIG. 11**).

EXAMPLE 9

Regulated Interferon Receptor Binding by a PD-L1/IFN α Dual Binding Antibody (DBA) Cytokine Complex

This example describes regulated interferon receptor binding by a PD-L1/IFN α DBA-cytokine complex. DBA-cytokine complexes of SEQ ID NO: 41 and SEQ ID NO: 55 (MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTTETPLMKE DSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGG

GGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGNTFTDYYMHWRQAPGQ
GLEWMGWMNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMEISSLRSEDVAVYYCARS
LFPTIFGVEVAFDIWGQGLVTVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSAS
VGDRVITITCQASQDISNYLNWYQQKPKGKAPKLLIYAASSLESVPSRFSGSGSGTDFTLT
ISSLQPEDFATYYCQQSYSTPPTFGQGTRLEIKGKPIPNNLLGLDST) were chosen for
analysis with a negative control with a similar structure based on a HER2 binding scFv (SEQ ID
NO: 56,

MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPV
LHEMIQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVTTETPLMKED
SILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGSGGG
GSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLE
WVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGDDG
FYAMDYWGQGLVTVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVIT
TCRASQDVNTAVAWYQQKPKGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISLQPE
DFATYYCQQHYTTPPTFGQGTKVEIKGKPIPNNLLGLDST). The proteins were expressed
using a cell-free transcription/translation system (Cosmo Bio USA, Inc., PUREfrex2.1, Product
GFK-PF213 with DS Supplement, Prod. # GFK-PF005). 96-well ELISA plates were coated
with anti-V5 antibody (SV5-pk1) at 50 ng/well overnight at 4° C. The plates were washed twice
by adding 200ul/well of SuperBlock with 0.05% Tween 20 (SBT), and the final SBT wash was
incubated for 15 min at room temperature before aspiration. A dilution series of the protein for
each construct in SBT was then added to the anti-V5-coated plates at 50 µl/well and incubated
for 1 hour at room temperature. Each plate was then washed three times with PBS with 0.05%
Tween 20 (PBST). Bound constructs were then probed with either anti-IFN α , IFNAR2-Biotin,
PDL1-hFc-Avi or the combination of IFNAR2-Biotin and PDL1-hFc-Avi in SBT at 50ul/well
for 1 hour at room temperature. Plates were washed 3x with PBST. Goat anti-mIgG-HRP or
Streptavidin-HRP was added at 50ul/well and incubated for 30 min at room temperature
followed by 3x wash with PBST. Plates were developed by adding 50 ul/well of TMB and the
reaction was terminated with an equal volume of ELISA stop solution. As shown in **FIG. 12**
(top left), IFNAR2 binding to the DBA-IFN α complex (SEQ ID NO: 41) increased in a dose
dependent manner with the addition of PD-L1. IFNAR2 binding to a control HER2-specific
antibody-IFN α complex (SEQ ID NO: 56) was unaffected by the addition of PD-L1 (**FIG. 12**
top right). IFNAR2 binding to a DBA-IFN α complex containing SEQ ID NO: 55, was not
affected by addition of PD-L1 at these concentrations (**FIG. 12** bottom). The protein complex of
SEQ ID NO: 55 is similar to the protein complex of SEQ ID NO: 41, except that the sensor
domain of SEQ ID NO: 55 has a higher affinity for IFN α than the sensor domain of SEQ ID
NO: 41. Protein complexes of the present invention may need the correct balance between their
affinity for the marker and their affinity for the therapeutic domain.

EXAMPLE 10

PD-L1/IFN α Protein Complexes for PD-L1 Dependent IFN α Activity In Vitro

[0132] This example describes PD-L1/IFN α protein complexes for PD-L1 dependent IFN α
activity *in vitro*. PD-L1/IFN α protein complexes comprise a DBA capable of binding PD-L1
marker and an IFN α therapeutic domain where the protein complex is linked to the IFN α
therapeutic cytokine via a linker. In the absence of PD-L1, the PD-L1 sensor domain binds the
IFN α therapeutic domain, rendering the IFN α therapeutic inert. In the presence of PD-L1 (e.g.,
PD-L1 is expressed on a cell, such as a tumor cell or immune cell), the PD-L1 sensor domain
binds PD-L1, thereby unbinding the IFN α therapeutic domain and allowing for IFN α to exhibit
therapeutic activity.

[0133] PD-L1/IFN α protein complexes are designed and recombinantly expressed or chemically synthesized. PD-L1/IFN α protein complexes are administered *in vitro* to a cell (e.g., in cell culture). In the absence of the PD-L1 marker, the IFN α domain remains bound to the PD-L1 sensor domain and no therapeutic effect is observed. The cell may express PD-L1 endogenously or after activation, or following introduction of a gene encoding PD-L1. If the cell is a tumor cell expressing a PD-L1 marker, the therapeutic effect may be inhibition of cell growth or induction of IFN α -responsive genes. Where the cell is an immune cell, the therapeutic effect may be cell growth, activation or induction of IFN-responsive genes. Where the cell is part of a mixture of cell types, any of these changes may be monitored for a responding cell population in the mixture.

EXAMPLE 11

PD-L1 Dependent IFN α Activity *In Vivo*

[0134] This example describes PD-L1/IFN α protein complexes for PD-L1 dependent IFN α activity *in vivo*. PD-L1/IFN α protein complexes comprise a PD-L1 sensor domain (e.g., an anti-PD-L1 antibody or an anti-PD-L1 scFv) linked to an IFN α cytokine via a linker, where the IFN α cytokine is a therapeutic. In the absence of PD-L1, the PD-L1 sensor domain binds the IFN α therapeutic domain, rendering the IFN α therapeutic inert. In the presence of PD-L1 (e.g., PD-L1 is expressed on a cell, such as a tumor cell or immune cell), the PD-L1 sensor domain binds PD-L1, thereby unbinding the IFN α therapeutic domain and allowing for IFN α to exhibit therapeutic activity.

[0135] PD-L1/IFN α protein complexes are recombinantly expressed or chemically synthesized. PD-L1/IFN α protein complexes are administered *in vivo* to a subject in need thereof. Administration is performed intravenously, intramuscularly, subcutaneously, intradermally, intraperitoneally, or mucosally. In the absence of PD-L1, the IFN α therapeutic domain remains bound to the PD-L1 sensor domain and no therapeutic efficacy is observed (e.g., cell proliferation in the subject is uninhibited). In the presence of PD-L1, the PD-L1 sensor domain binds PD-L1 and unbinds the IFN α therapeutic domain. Therapeutic efficacy is observed (e.g., cell proliferation is inhibited or immune cell activation occurs). The cell is a tumor cell expressing PD-L1. The subject is a human or non-human animal in need thereof. The subject has a disease. The disease is cancer.

EXAMPLE 12

PD-1 Dependent IL-2 Activity In Human Cells

[0136] This example describes PD-1/IL-2 protein complexes for PD-1 dependent IL-2 activity in human cells, *in vitro* and *in vivo*. PD-1/IL-2 protein complexes comprise a PD-1 sensor

domain (e.g., an anti-PD-1 antibody or an anti-PD-1 scFv) linked to an IL-2 cytokine therapeutic domain via a linker, where the IL-2 cytokine is a therapeutic. In the absence of PD-1, the PD-1 sensor domain binds the IL-2 therapeutic domain, rendering the IL-2 therapeutic inert. In the presence of PD-1 (e.g., PD-1 is expressed on a cell, such as an immune cell), the PD-1 sensor domain binds PD-1, thereby unbinding the IL-2 therapeutic domain and allowing for IL-2 to exhibit therapeutic activity.

[0137] PD-1/IL-2 protein complexes are recombinantly expressed or chemically synthesized. PD-1/IL-2 protein complexes are administered *in vitro* to a human cell or *in vivo* to a mouse or to a human subject in need thereof. The human cell is a cell expressing PD-1. Administration to a mouse or to a human subject is performed intravenously, intramuscularly, subcutaneously, intradermally, intraperitoneally, or mucosally. In the absence of PD-1, the IL-2 therapeutic domain remains bound to the PD-1 sensor domain and no therapeutic efficacy is observed (e.g., cell activation *in vitro* and in the subject is unaltered). In the presence of PD-1, the PD-1 sensor domain binds PD-1 and unbinds the IL-2 therapeutic domain. Therapeutic efficacy is observed (e.g., cell activation is observed *in vitro* and, in the subject, *in vivo*). The subject has a disease. The disease is cancer. The cell may express PD-1 endogenously or after activation, or following introduction of a gene encoding PD-1. The therapeutic effect may be cell growth, differentiation, activation or induction of IL2-responsive genes. *In vitro*, if the cell is part of a mixture of cell types, any of these changes may be monitored for a responding cell population in the mixture.

EXAMPLE 13

Bioactivity in Tumor Tissues

[0138] This example describes bioactivity in tumor tissues. A protein complex of the present disclosure is recombinantly expressed or chemically synthesized. The protein complex includes a sensor domain linked to a therapeutic domain. The linker is a peptide linker. The sensor domain is capable of binding to the therapeutic and a marker. In the absence of the marker, the sensor domain binds the therapeutic domain, rendering the therapeutic domain unable to bind to its target and unable to exert therapeutic activity. In the presence of the marker, the sensor domain binds the marker rendering the therapeutic domain free to bind to its target and able to exert therapeutic activity. The protein complex is administered *in vitro* to a cell or *in vivo* to a subject in need thereof. The cell expresses the marker to which the sensor domain binds. The cell is a tumor cell or immune cell. The subject is a human or non-human animal. The subject has a disease. The disease is cancer. Administration to a subject is performed intravenously, intramuscularly, subcutaneously, intradermally, intraperitoneally, or mucosally.

[0139] Upon administration of the protein-complex, the sensor domain binds the marker *in vitro* or *in vivo* in the subject and unbinds the therapeutic domain. Therapeutic efficacy is observed *in vitro* or *in vivo* in the subject, for example, cell proliferation of tumor cells is slowed down or completely halted and tumor cells are eliminated.

EXAMPLE 14

Activity in Tumor Models of Protein Complexes

[0140] This example describes activity in tumor models. The tumor models assess the efficacy and systemic on-target effects of the protein complexes. The tumor model assesses the ability of a protein complex of the present disclosure to exhibit sensor domain regulated activity of the therapeutic domain.

[0141] A protein complex of the present disclosure is recombinantly expressed or chemically synthesized. The protein complex includes a sensor domain linked to a therapeutic domain. The linker is a peptide linker. The sensor domain is capable of binding to the therapeutic domain and a marker. In the absence of the marker, the sensor domain binds the therapeutic domain rendering the therapeutic domain unable to bind to its target and unable to exert therapeutic activity. In the presence of the marker, the sensor domain binds the marker rendering the therapeutic domain free to bind to its target and able to exert therapeutic activity. The protein complex is administered in a tumor model, *in vitro* or *in vivo*. The tumor cells or the immune cells in the tumor model express the marker to which the sensor domain binds. Administration *in vivo* is performed intravenously, intramuscularly, subcutaneously, intradermally, intraperitoneally, or mucosally.

[0142] **Tumor measurement.** Prior to administration of the protein-complex, or in a control sample where the protein-complex is not administered, measurements of the tumor indicate that the tumor is continuing to proliferate. For example, a solid tumor in a tumor model (e.g., a mouse model of a tumor) is measured using calipers. Prior to administration of the protein-complex, or in a control sample where the protein-complex is not administered, the solid tumor continues to grow in size, as indicated by increasing measurements of tumor size with calipers. Upon administration of the protein-complex, over time, the sensor domain binds the marker expressed on the tumor and the therapeutic domain is unbound, thus, resulting in therapeutic efficacy. Therapeutic efficacy is validated by observing decreasing measurements of tumor size with calipers over time.

[0143] **Immune activation.** Prior to administration of the protein-complex, or in a control sample where the protein-complex is not administered, the solid tumor continues to grow in size, as indicated by increasing measurements of tumor size with calipers. Upon administration of the

protein-complex, over time, the sensor domain binds the marker and the therapeutic domain is unbound, thus, resulting in therapeutic efficacy. Therapeutic efficacy is validated by observing differences in the immune cells in the tumor, lymph node or systemically, when compared to the control sample. The differences may be immune cell phenotypes, activation state, differentiation state or specificity.

[0144] Systemic induction of cytokine markers. No induction of cytokine markers or reduced systemic induction of cytokine markers, when compared to the control, is observed upon administration of the protein complex.

[0145] Weight loss. No weight loss or reduced weight loss, when compared to the control, is observed upon administration of the protein complex.

EXAMPLE 15

PD-1/IL-2 DBA Cytokine Complex Induction of STAT5 Phosphorylation in a Lymphocyte Cell Line

[0146] This example describes PD-1/IL-2 DBA-cytokine complex induction of STAT5 phosphorylation in a lymphocytic cell line. To assess the dependence of PD-1/IL-2 DBA-cytokine complex activity on binding to PD-1, a PD-1-expressing variant is generated of an IL-2R⁺ T cell line such as Hut78 or Jurkat E6.1. The PD-1⁺ and PD-1⁻ variant cell lines are treated with titrating concentrations of a PD-1/IL-2 DBA-cytokine complex of this disclosure, and STAT5 phosphorylation is assessed by phospho-flow, TR-FRET, or other assays for measuring IL-2 signaling.

[0147] A HEK 293 IL-2 reporter cell line is engineered to express PD-1. The PD-1⁺ and PD-1⁻ variant cell lines are treated with titrating concentrations of PD-1/IL-2 DBA-cytokine complexes, and reporter activity is assessed as a measurement of IL-2 signaling. The PD-1/IL-2 DBA-cytokine complex exhibits increased potency on PD-1⁺ variant cell lines.

EXAMPLE 16

PD-1/IL-2 DBA Cytokine Complex Induction of STAT5 Phosphorylation and Other Markers of Activation, and Proliferation in Primary Lymphocytes

[0148] This example describes PD-1/IL-2 DBA-cytokine complex induction of STAT5 phosphorylation and other markers of activation and proliferation in primary lymphocytes. PBMCs are labeled with cell proliferation dye and incubated for 4 days with titrating concentrations of a PD-1/IL-2 DBA-cytokine complex of the present disclosure. PBMCs are stained with antibodies directed against immune cell phenotyping markers to distinguish CD4⁺ and CD8⁺ T cells, Treg cells, and natural killer (NK) cells and markers of cell activation, such

as CD25. Dye dilution on immune cell subsets is examined by flow cytometry as a measurement of proliferation.

[0149] Total T cells are isolated from PBMCs using immunomagnetic negative selection (STEMCELL) and stimulated with plate-bound anti-CD3 and soluble anti-CD28 for 72 hours to induce expression of PD-1. The PD-1+ T cells are incubated for 20 minutes with titrating concentrations of PD-1/IL-2 DBA-cytokine complexes. STAT5 phosphorylation is measured in fixed and permeabilized T cells by flow cytometry. In some experiments, PD-1 may be blocked on T cells with anti-PD-1 prior to treatment with PD-1/IL-2 DBA-cytokine complexes to assess the dependence of PD-1/IL-2 DBA-cytokine complex activity on binding to PD-1. The PD-1/IL-2 DBA-cytokine complex induces minimal STAT5 phosphorylation when PD-1 is blocked, showing activity that is conditional on its ability to bind PD-1.

EXAMPLE 17

In Vivo PD-1/IL-2 DBA Cytokine Complex Signaling in Non-Tumor Peripheral Tissues

[0150] This example describes PD-1/IL-2 DBA-cytokine complex pharmacokinetics in the blood of wild-type mice and the signaling of the complex in non-tumor peripheral tissue. The serum half-lives and peripheral tissue activities of PD-1/IL-2 DBA-cytokine complexes and suitable non-regulated controls such as anti-PD-1, anti-HER2-IL-2, or anti-PD-1-IL-2 were measured in mice dosed intravenously (i.v.) with the complexes. Blood, spleens, or both were collected at various timepoints after treatment and stained to identify CD8+ T cells and NK cells.

[0151] To examine the half-life of PD-1/IL-2 DBA-cytokine complex in circulation, wild-type C57BL/6 mice received a single 2.5 milligrams per kilogram intravenous dose of a PD-1/IL-2 DBA-cytokine complex (2B07 IL-2 mut; SEQ ID NO: 205-206), anti-HER2/IL-2-cytokine complex (Always-on IL-2 mut; SEQ ID NO: 64 and SEQ ID NO: 207), or anti-IL-2/IL-2-cytokine complex (Always-off IL-2 mut; ; SEQ ID NO: 208-209), as outlined in **TABLE 20**. Mice were bled via retro-orbital sinus at 30 minutes, 4, 24, 48, 72, 96, and 168 hours post-dosing. The blood was collected into serum separator tubes, and the isolated serum was frozen at -80°C until analysis. To determine serum levels of the cytokine complexes, 96-well high-binding ELISA plates were coated with 1 ug/mL rabbit anti-hu IL-2 capture antibody (clone ab9618, Abcam) in carbonate-bicarbonate buffer overnight at 4°C. Plates were washed three times and blocked for 1 hour with SuperBlock blocking buffer (Thermo Scientific). Serum samples from the various timepoints and treatment groups were diluted in SuperBlock, added to the plates, and incubated 1 hr. To detect cytokine complexes, plates were incubated with goat anti-mouse Fc-HRP (Jackson ImmunoResearch) at 1:5000 in SuperBlock for 1 hour. The plates

were then washed and developed with TMB substrate. Absorbance (OD) was measured using an EnVision 2105 microplate reader (PerkinElmer) at 450 nm. As shown in **FIG. 18**, at all timepoints examined the PD-1/IL-2 DBA-cytokine complex was detected at similar serum concentrations as the anti-IL-2/IL-2-cytokine complex. In contrast, the serum concentration of the non-regulated anti-HER2/IL-2-cytokine complex showed a greater decrease in serum concentration over time.

TABLE 20 – IgG PD-1/IL-2 DBA and control protein complexes

Protein Complexes	SEQ ID NO:	Sequence
2B07 IL-2 mut	SEQ ID NO: 205	APASSSTKKTQLQLEHLLLDLQMI L N G I N N Y K N P K L T R M L T A K F A M P K K A T E L K H L Q C L E E E L K P L E E V L N G A Q S K N F H L R P R D L I S N I N V I V L E L K G S E T T F M C E Y A D E T A T I V E F L N R W I T F A Q S I I S T L T G G G G S G G G G S G G G G S G G G S Q V Q L V Q S G A E V K K P G A S V K V S C K A S G D T F T R H Y V H W V R Q A P G Q G L E W M G I I N P S G G Y A S Y A Q K F Q G R V T M T R D T S T S T V Y M E L S S L R S E D T A V Y Y C A A G L F I W G Q G T L V T V S S A K T T A P S V Y P L A P V C G D T T G S S V T L G C L V K G Y F P E P V T L T W N S G S L S S G V H T F P A V L Q S D L Y T L S S S V T V T S S T W P S Q S I T C N V A H P A S S T K V D K K I E P R G P T I K P C P P C K C P A P N A A G G P S V F I F P P K I K D V L M I S L S P I V T C V V V D V S E D D P D V Q I S W F V N N V E V H T A Q T Q T H R E D Y N S T L R V V S A L P I Q H Q D W M S G K E F K C K V N N K D L G A P I E R T I S K P K G S V R A P Q V Y V L P P P E E E M T K K Q V T L T C M V T D F M P E D I Y V E W T N N G K T E L N Y K N T E P V L D S D G S Y F M Y S K L R V E K K N W V E R N S Y S C S V V H E G L H N H H T T K S F S R T P G K
	SEQ ID NO: 206	D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q S I G R W L A W Y Q Q K P G K A P K L L I Y S A S N L E T G V P S R F S G S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q Y E S F P V T F G P G T K V D I K R A D A A P T V S I F P P S S E Q L T S G G A S V V C F L N N F Y P K D I N V K W K I D G S E R Q N G V L N S W T D Q D S K D S T Y S M S S T L T L T K D E Y E R H N S Y T C E A T H K T S T S P I V K S F N R N E C
anti-HER2/IL-2-cytokine complex	SEQ ID NO: 64	D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V N T A V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S R S G T D F T L T I S S L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R A D A A P T V S I F P P S S E Q L T S G G A S V V C F L N N F Y P K D I N V K W K I D G S E R Q N G V L N S W T D Q D S K D S T Y S M S S T L T L T K D E Y E R H N S Y T C E A T H K T S T S P I V K S F N R N E C
	SEQ ID NO: 207	APASSSTKKTQLQLEHLLLDLQMI L N G I N N Y K N P K L T R M L T A K F A M P K K A T E L K H L Q C L E E E L K P L E E V L N G A Q S K N F H L R P R D L I S N I N V I V L E L K G S E T T F M C E Y A D E T A T I V E F L N R W I T F A Q S I I S T L T G G G G S G G G G S G G G G S G G G G S E V Q L V E S G G G L V Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q G T L V T V S S A K T T A P S V Y P L A P V C G D T T G S S V T L G C L V K G Y F P E P V T L T W N S G S L S S G V H T F P A V L Q S D L Y T L S S S V T V T S S T W P S Q S I T C N V A H P A S S T K V D K K I E P R G P T I K P C P P C K C P A P N A A G G P S V F I F P P K I K D V L M I S L S P I V T C V V V D V S E D D P D V Q I S W F V N N V E V H T A Q T Q T H R E D Y N S T L R V V S A L P I Q H Q D W M S G K E F K C K V N N K D L G A P I E R T I S K P K G S V R A P Q V Y V L P P P E E E M T K K Q V T L T C M V T D F M P E D I Y V E W T N N G K T E L N Y K N T E P V L D S D G S Y F M Y S K L R V E K K N W V E R N S Y S C S V V H E G L H N H H T T K S F S R T P G K
Always-off IL-2 mut	SEQ ID NO: 208	APASSSTKKTQLQLEHLLLDLQMI L N G I N N Y K N P K L T R M L T A K F A M P K K A T E L K H L Q C L E E E L K P L E E V L N G A Q S K N F H L R P R D L I S N I N V I V L E L K G S E T T F M C E Y A D E T A T I V E F L N R W I T F A Q S I I S T L T G G G G S G G G G S G G G G S G G G G S E V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S S Y T L A W V R Q A P G K G L E W V A A I D S S S Y T S P D T V R G R F T I S R D N A K N S L Y L Q M N S L R A E D T A V Y Y C A R D S N W D A L D Y W G Q G T L V T V S S A K T T A P S V Y P L A P V C G D T T G S S V T L G C L V K G Y F P E P V T L T W N S G S L S S G V H T F P A V L Q S D L Y T L S S S V T V T S S T W P S Q S I T C N V A H P A S S T K V D K K I E P R G P T I K P C P P C K C P A P N A A G G P S V F I F

Protein Complexes	SEQ ID NO:	Sequence
		PPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISWVFN NVEVHTAQTQTHREDYNST LRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKG SVRAPQVYVLPPE EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMYSKL RVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 209	DIQMTQSPSSLSASVGD RVSITCKASQNVGTNVGWYQQKPGKAPKALIYSASFRYS GVPSRFSGSGSGTDFLT ISSLQPEDFATYFCQQYYTYPTYFGGGTKLEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPK DINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

[0152] To examine the activity of PD-1/IL-2 DBA-cytokine complexes in peripheral tissues, wild-type C57BL/6 mice received a single 2.5 milligrams per kilogram intravenous dose of PD-1/IL-2 DBA-cytokine complex (2B07 IL-2 mut; SEQ ID NO: 205-206), anti-HER2/IL-2-cytokine complex (Always-on IL-2 mut; SEQ ID NO: 64 and SEQ ID NO: 207), anti-IL-2/IL-2-cytokine complex (Always-off IL-2 mut; SEQ ID NO: 208-209), as shown in **TABLE 20** or PBS. Prior to dosing, the presence of intact IL-2 within each IL-2 cytokine complex was confirmed by ELISA as a means of verifying their potential for biological activity. Blood and spleens were collected 5 days following treatment and analyzed by flow cytometry to quantify the number of CD8⁺ T cells and NK cells per spleen and per microliter of blood. The PD-1/IL-2 DBA-cytokine complex did not induce expansion of CD8 T cells or NK cells, whereas the HER2/IL-2-cytokine complex induced expansion of peripheral CD8⁺ T cells and NK cells (**FIG. 19A-D**).

EXAMPLE 18

PD-1/IL-2 DBA Cytokine Complex Modulation of Anti-Tumor Immunity in Syngeneic Tumor Models

[0153] This example describes PD-1/IL-2 DBA-cytokine complex modulation of anti-tumor immunity in a MC38 syngeneic mouse tumor model. A PD-1/IL-2 DBA-cytokine complex was assessed for the ability to drive anti-tumor immunity in vivo. 500,000 MC38 tumor cells were implanted subcutaneously in human PD-1 knock-in mice (GenOway). Tumors were measured twice weekly, and volumes calculated as (Length × Width × Width/2). Mice were randomized into treatment groups, and treatments were initiated when tumors reached a volume of ~100 mm³. Mice were treated intravenously with PD-1/IL-2 DBA-cytokine complex (2B07 IL-2 mut; SEQ ID NO: 210-212), PD-1/IL-2 DBA lacking IL-2 (2B07; SEQ ID NO: 212-213), or an isotype control (SEQ ID NO: 214-215), as shown in **TABLE 21** below, at the indicated doses of 5 or 0.5 milligrams per kilogram on days 7, 10, and 13 post tumor implantation. The PD-1/IL-2

DBA-cytokine complex showed increased tumor growth inhibition compared to either the PD-1/IL-2 DBA lacking IL-2 or the isotype control (**FIG. 20**).

TABLE 21 – IgG PD-1/IL-2 DBA and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
2B07 IL-2 mut	SEQ ID NO: 210	APASSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRMLTAKFAMPKKATELKHL QCLEEEELKPLEEVLNGAQSKNFHLRPRDLISNINNVIVLELKGSETTFMCEYADETATIV EFLNRWITFAQSIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKPGAS VKVSCASGDTFTRYVHWVRQAPGQGLEWMGIINPSGGYASYAQKFQGRVTM TRDTSTSTVYMESSLRSED TAVYYCAAGLFIWGQGT LTVSSAKTTAPSVYPLAPV CGDTTGSSVT LGCLVKGYFPEPVT LTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVT SSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPK IKDVLMI SLSPIVTCVVVDVSEDDPDVQISW FVNNVEVHTAQTQTHREDYNSTLRV VSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEE MTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMYSDLR VEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 211	QVQLVQSGAEVKKPGASVKVSCASGDTFTRYVHWVRQAPGQGLEWMGIINPS GGYASYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVYYCAAGLFIWGQGT LTV TVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVT LTWNSGSLSSGVHTF PAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCK CPAPNAAGGPSVFIFPPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISW FVNNVEV HTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPG KGSVRAPQVYVLPPEEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKN TEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 212	DIQMTQSPSSLSASVGDRTITCRASQSIGRYLAWYQQKPGKAPKLLIYSASNLETG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYN SFPVTFGPGTKVDIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDG SERQNGVLNSWTDQDSK DSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
PD-1/IL-2 DBA lacking IL-2	SEQ ID NO: 212	DIQMTQSPSSLSASVGDRTITCRASQSIGRYLAWYQQKPGKAPKLLIYSASNLETG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYN SFPVTFGPGTKVDIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDG SERQNGVLNSWTDQDSK DSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
	SEQ ID NO: 213	QVQLVQSGAEVKKPGASVKVSCASGDTFTRYVHWVRQAPGQGLEWMGIINPS GGYASYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVYYCAAGLFIWGQGT LTV TVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVT LTWNSGSLSSGVHTF PAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCK CPAPNAAGGPSVFIFPPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISW FVNNVEV HTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPG KGSVRAPQVYVLPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKN TEPVLDS DGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
isotype control	SEQ ID NO: 214	EVQLVESGGGLVQPGGSLRLS CAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTN GYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDY WGQGT LTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVT LTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISW F VNNVEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPI ERTISKPGSVRAPQVYVLPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKT

Protein Complex	SEQ ID NO:	Sequence
		ELNYKNTEPVLDSGDSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 215	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYS GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRADAAP TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

EXAMPLE 19

PD-1/IL-2 DBA Cytokine Complex Modulation of Anti-Tumor Immunity in Xenograft/Human Immune Cell Admixture Models

[0154] This example describes PD-1/IL-2 DBA-cytokine complex modulation of anti-tumor immunity in xenograft/human immune cell admixture models. To examine the ability of PD-1/IL-2 DBA-cytokine complexes to drive anti-tumor immunity in an *in vivo* setting, an admixture system is used. Total human PBMCs or a combination of human T cells and monocyte-derived dendritic cells (moDCs) are mixed with human tumor cells (e.g., HPAC, A375, H441) at a 1:4 ratio and co-implanted subcutaneously into the flanks of NSG mice. One day later, treatment with a PD-1/IL-2 DBA-cytokine complex of the present disclosure, or suitable non-regulated controls such as anti-PD-1, anti-HER2-IL-2, or anti-PD-1-IL-2, is initiated. Tumors are measured at least twice weekly and volumes calculated as (Length × Width × Height/2). PD-1/IL-2 DBA-cytokine complexes exhibit increased anti-tumor efficacy compared to anti-PD-1 and anti-HER2-IL-2 and decreased off-tumor activity compared to anti-PD-1-IL-2.

EXAMPLE 20

PD-L1/IFN- α DBA Cytokine Complex Induction of Myeloid Cell Maturation in the Presence of Plate-Bound PD-L1 or PD-L1-Expressing Tumor Cells

[0155] This example describes PD-L1/IFN- α DBA-cytokine complex induction of myeloid cell maturation in the presence of plate-bound PD-L1 or PD-L1-expressing tumor cells. CD14⁺ monocytes are purified from fresh human PBMCs by immunomagnetic negative selection (STEMCELL). Monocyte-derived dendritic cells (moDCs) are generated by culturing purified monocytes with hGM-CSF and hIL-4 in RPMI-1640 medium containing 10% FBS for 5 days. To examine the conditional activity of PD-L1/IFN- α DBA-cytokine complex, monocytes or moDCs are added to plates coated with either PD-L1 or HER-2 along with titrating concentrations of a PD-L1/IFN- α DBA-cytokine complex of the present disclosure. In some

experiments, human monocytes or moDCs are co-cultured with tumor cell lines expressing varying levels of PD-L1 and titrating concentrations of PD-L1/IFN- α DBA-cytokine complex. Cultures are incubated overnight at 37 °C, and expression of CD80, CD83, CD86, and HLA-DR is assessed by flow cytometry as a measurement of myeloid cell activation. PD-L1/IFN- α DBA-cytokine complex is expected to induce monocyte and moDC activation solely in the presence of PD-L1.

EXAMPLE 21

PD-L1/IFN- α DBA Cytokine Complex Induction of T cell Activation in a Mixed Lymphocyte Reaction

[0156] This example describes PD-L1/IFN- α DBA-cytokine complex induction of T cell activation in a mixed lymphocyte reaction. To assess the direct and indirect effects of PD-L1/IFN- α DBA-cytokine complex on T cell function, CD14⁺ monocytes are isolated from human PBMCs using immunomagnetic negative selection (STEMCELL) and cultured for 5 days in the presence of hGM-CSF and hIL-4 to induce moDCs. CD8⁺ T cells are purified from human PBMCs of a different healthy donor and labeled with cell proliferation dye. The two cell types are combined in plates coated with PD-L1 or HER2 along with titrating concentrations of a PD-L1/IFN- α DBA-cytokine complex of the present disclosure. In other experiments, the two cell types are cultured with titrating concentrations of PD-L1/IFN- α DBA-cytokine complex and tumor cell lines expressing varying levels of PD-L1. In other experiments, the cells may be of mouse origin. Cultures are incubated for 5 days, and T cell dye dilution is assessed by flow cytometry as a measurement of proliferation. The concentration of cytokines (e.g., IFN- γ) in culture supernatants is assessed by ELISA. The PD-L1/IFN- α DBA-cytokine complex increases T cell activation and proliferation solely in the presence of PD-L1.

EXAMPLE 22

***In Vivo* PD-L1/IFN- α DBA Cytokine Complex Signaling in Peripheral Tissues**

[0157] This example describes *in vivo* PD-L1/IFN- α DBA-cytokine complex signaling in peripheral tissues. To examine PD-L1/IFN- α DBA-cytokine complex activity in non-tumor tissue, wild-type C57BL/6 mice are injected intravenously (i.v.) with 100 ug of either a PD-L1/IFN- α DBA-cytokine complex of the present disclosure or a nonregulated immunocytokine of a comparable structure consisting of anti-PD-L1 and IFN- α (PD-L1-IFN α immunocytokine). Animals are weighed daily to monitor IFN- α induced toxicity. Serum is collected at 6 and 24 hours post dosing, and MCP-1, IL-6, IL-10, TNF- α , and IFN- γ levels are quantified by ELISA. In some groups, RNA is isolated from the spleen and liver 6 and 24 hours post dosing. Induction of IFN-stimulated genes including ISG15, IRF7, and MX2 is assessed by qPCR. Mice that

received unregulated anti-PD-L1-IFN- α immunocytokine experience weight loss, increased serum cytokine levels, and IFN target gene induction, whereas those dosed with the PD-L1/IFN- α DBA-cytokine complex display minimal evidence of peripheral IFN- α signaling.

EXAMPLE 23

PD-L1-IFN- α DBA-Cytokine Complex Modulation of Anti-Tumor Immunity in Syngeneic Tumor Models

[0158] This example describes PD-L1/IFN- α DBA-cytokine complex modulation of anti-tumor immunity in syngeneic tumor models. PD-L1/IFN- α DBA cytokine complex proteins are assessed for their ability to drive anti-tumor immunity *in vivo*. Wild-type or human PD-L1-expressing syngeneic mouse tumor cells (e.g., MC38, CT26, 4T1, or A20) are implanted subcutaneously into wild-type or human PD-L1 knock-in mice (Genoway). Tumors are measured at least twice weekly and volumes are calculated as (Length $\times$ Width $\times$ Height/2). Mice are randomized into different groups and therapy is initiated when tumors reached a volume of $\sim 100 \text{ mm}^3$. Mice are treated i.v. or intratumorally with a PD-L1/IFN- α DBA-cytokine complex of the present disclosure or suitable nonregulated controls such as anti-PD-L1, anti-HER2-IFN- α immunocytokine, or anti-PD-L1-IFN- α immunocytokine. In some experiments, mice are sacrificed 5 days post treatment, and tumors are harvested and enzymatically dissociated for immunophenotyping. The frequency and phenotype of tumor-infiltrating immune cell subsets, including CD4 $^{+}$ and CD8 $^{+}$ T cells, Treg cells, NK cells, and DCs, is determined by flow cytometry. The PD-L1/IFN- α DBA-cytokine complex inhibits tumor growth to an equal or greater extent than anti-HER2-IFN- α , but with less off-tumor activity. The PD-L1/IFN- α DBA-cytokine complex increases an anti-tumor immune response as indicated by the amount and phenotype of immune infiltrates to an equal or greater extent than anti-HER2-IFN- α immunocytokine, but with less off-tumor activity.

EXAMPLE 24

PD-L1/IFN- α DBA Modulation of Anti-Tumor Immunity in Xenograft/Human Immune Cell Admixture Models

[0159] This example describes PD-L1/IFN- α DBA-cytokine complex modulation of anti-tumor immunity in xenograft/human immune cell admixture models. To examine the ability of PD-L1/IFN- α DBA-cytokine complexes to drive anti-tumor immunity in an *in vivo* setting, an admixture system is used. Total human PBMCs or a combination of human T cells and moDCs are mixed with human tumor cells (e.g., HPAC, A375, H441) at a 1:4 ratio and co-implanted subcutaneously into the flanks of NSG mice. One day later, i.v. treatment with a PD-L1/IFN- α DBA-cytokine complex of the present disclosure or suitable non-regulated controls such as anti-

PD-L1, anti-HER2-IFN- α immunocytokine, or anti-PD-L1-IFN- α immunocytokine is initiated. Tumors are measured at least twice weekly and volumes are calculated as (Length $\times$ Width $\times$ Height/2). The PD-L1/IFN- α DBA-cytokine complex inhibits tumor growth to an equal or greater extent than anti-HER2-IFN- α , but with less off-tumor activity.

EXAMPLE 25

In Vitro and In Vivo Characterization of Protein Complexes

[0160] This example describes the evaluation of DBA-cytokine complexes for *in vitro* and *in vivo* stability. A protein complex of the present disclosure is recombinantly expressed or chemically synthesized. The protein complex includes a sensor domain linked to a therapeutic domain. The linker is a peptide linker. The sensor domain is capable of binding to the therapeutic domain and a marker. In the absence of the marker, the sensor domain binds the therapeutic domain rendering the therapeutic domain unable to bind to its target and unable to exert therapeutic activity. In the presence of the marker, the sensor domain binds the marker rendering the therapeutic domain free to bind to its target and able to exert therapeutic activity.

[0161] *In vitro*, the protein complexes are tested for stability and functionality at baseline or after incubation in conditions of stress, such as elevated temperature, pH changes, oxidative buffers, or serum/plasma, using methods of biophysical characterization to measure fragmentation, unfolding, or aggregation, and/or using methods to test for changes in functional activity. *In vivo*, the pharmacokinetic properties of the proteins are measured following dosing in a mammal, such as a mouse, rat, or non-human primate, and properties of distribution, clearance and degradation are measured. These measurements are used to engineer or select the optimal therapeutic form of the DBA-protein complex.

EXAMPLE 26

Regulated IL-2 Receptor Signaling by a PD-1/IL-2 Dual Binding Antibody (DBA) Cytokine Complex

[0162] This example describes PD-1 regulated IL-2 activity in a HEK-Blue™ IL-2 reporter cell by PD-1/IL-2 DBA-cytokine complexes. The DBA-cytokine complexes and control antibody-cytokine complexes were produced in three formats shown in FIGS. 14A-C by expression in mammalian cells using standard protocols. The wells of a 384-well ELISA plate were coated with constant concentration of PD-1-Fc or an IgG1 control protein captured with an anti-Fc antibody (Jackson ImmunoResearch, Prod. # 109-005-098). The cytokine complexes were serially diluted 1:4 for 8 points in growth media from a starting concentration of 6 nM and incubated briefly before addition of the HEK-Blue™ IL-2 reporter cells.

[0163] Results with a protein complexes comprising the structure shown in **FIG. 14A** are shown in **FIG. 15A-D**. As depicted in **FIG. 14A**, this symmetric format is comprised of one IL-2 linked to each antibody variable domain. The IL-2 activity of the PD-1/IL-2 DBA-IL-2 complex AF4379 comprising SEQ ID NO: 174-175 had an EC50 of 31 pM in the PD-1 coated wells versus 62 pM in the IgG1 coated wells, as shown in **FIG. 15A**, demonstrating PD-1 dependence. The IL-2 activity of antibody-cytokine complexes AF4377 comprising SEQ ID NO: 64 and 176 (anti-Her2 antibody) and AF4378 comprising SEQ ID NO: 177-178 (anti-IL-2 antibody) was unchanged in the presence of PD-1 (as shown in **FIG. 15B** and **FIG. 15C**, respectively), while the IL-2 activity of the anti-PD-1 antibody AF4376 comprising SEQ ID NO: 179-180 is reduced in the presence of PD-1, as shown in **FIG. 15D**. Sequences of the protein complexes are summarized in **TABLE 22** below.

TABLE 22 – IgG PD-1/IL-2 DBA with heavy chain IL-2 therapeutic domains, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4379	SEQ ID NO: 174	APTSSSTKKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFEFYM PKKATELKHLQCLERELKPLEEVNLNAQSKNFHLRPRDLISNINVIV LELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGG GGSGGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSKASGDTFTR YYVHWVRQAPGQGLEWMGIINPSGGYASYAQKFQGRVTMTRDTS TSTVYMELSSLRSEDTAVYYCAAGLFIWGQGLTVTVSSAKTTAPSV YPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG PTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDV SEDDPDVQISWFWNNVEVHTAQTQTHREDYNSTLRVVSALPIQH DWMGSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSD GSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG K
	SEQ ID NO: 175	DIQMTQSPSSLSASVGDRVTITCRASQSIGRYLAWYQQKPGKAPKL LIYSASNLETGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNSF PVTFGPGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYP KDINVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTTLTKDEY ERHNSYTCEATHKTSTSPIVKSFNRECE
AF4377	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK LLIYSASFLYSGVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQHYT TPPTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTTLTKDE YERHNSYTCEATHKTSTSPIVKSFNRECE
	SEQ ID NO: 176	APTSSSTKKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFEFYM PKKATELKHLQCLERELKPLEEVNLNAQSKNFHLRPRDLISNINVIV LELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGG GGSGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKN TAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSS

Protein Complex	SEQ ID NO:	Sequence
		AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSL SSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIV TCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVY VLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNT EPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTT KSFSRTPGK
AF4378	SEQ ID NO: 177	APTSSSTKKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFEFYM PKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIV LELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGG GGSGGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYT LAWVRQAPGKGLEWVAIDSSSYTYSPDTRGRFTISRDNKNSL YLQMNSLRAEDTAVYYCARDSDALDYWGQGTLLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGV HTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVV VDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPI QHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLP PEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNT EPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR TPGK
	SEQ ID NO: 178	DIQMTQSPSSLSASVGDRVSITCKASQNVGTNVGWYQQKPGKAPK ALIYSASFYSGVPSRFGSGSGTDFTLTISSLQPEDFATYFCQQYYT YPYTFGGGTKEIKRADAAPTVISFPPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSRQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKSFNNEC
AF4376	SEQ ID NO: 179	APTSSSTKKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFEFYM PKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIV LELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGG GGSGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLDCKASGITFSNS GMHWVRQAPGKGLEWVAWIWYDGSKRYYADSVKGRFTISRDN KNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLLTVSSAKTTAP SVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP RGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVV VDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQ HQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLP PEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNT EPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR TPGK
	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRL IYDASNRTGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQSSNW PRTFGQGTKEIKRADAAPTVISFPPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSRQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKSFNNEC

[0164] Results with protein complexes comprising the structures depicted in **FIG. 14B**, are shown in **FIGS. 16A-F**. This format is composed of an asymmetric complex comprised of two

antibody domains with a single IL-2 linked to one of the domains. The IL-2 activity of the PD-1/IL-2 DBA-IL-2 complexes AF4386 (comprising SEQ ID NO: 212 and 181-182, results shown in **FIG. 16A**), AF4387 (comprising SEQ ID NO: 183-185, results shown in **FIG. 16B**) and AF4389 (comprising SEQ ID NO: 186-188, results shown in **FIG. 16C**) had an EC₅₀ of 50 pM, 57 pM and 118 pM respectively in the PD-1 coated wells and 1.79 nM, 419 pM and 1.67 nM respectively in the IgG1 coated wells, demonstrating PD-1 dependence. The IL-2 activity of the anti-PD1 control protein AF4380 (comprising SEQ ID NO: 180, 189-190, results shown in **FIG. 16D**), the anti-Her2 control protein AF4383 (comprising SEQ ID NO: 64, 191-192, results shown in **FIG. 16E**), and the anti-IL-2 control protein AF4384 (comprising SEQ ID NO: 178, 193-194, results shown in **FIG. 16F**) were unchanged. Sequences of the protein complexes are summarized in **TABLE 23** below.

TABLE 23 – IgG PD-1/IL-2 PDA with single IL-2, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4386	SEQ ID NO: 181	APTSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTFEFYMPKKATELKHLQ CLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSQVQLVQSGAEVKKPGASV KVSCASGDTFTRYVHWVRQAPGQGLEWMGIINPSGGYASYAQKFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCAAGLFIWGQGTTLTVSSAKTTAPSVYPLAPVC GDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSS TWPSQSITCNVAHPASSTKVDKKEIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIK DVLMLISLPIVTCVVDVSEDDPDVQISWVFNVEVHTAQTQTHREDYNSTLRVV SALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMT KKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 182	QVQLVQSGAEVKKPGASVKVSCASGDTFTRYVHWVRQAPGQGLEWMGIINPS GGYASYAQKFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCAAGLFIWGQGTTLV TVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTF PAVLQSDLYTLSSSVTVTSS TWPSQSITCNVAHPASSTKVDKKEIEPRGPTIKPCPPCK CPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVDVSEDDPDVQISWVFNVEV HTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISK KGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTE EPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGG SGGGSHHHHHH
	SEQ ID NO: 212	DIQMTQSPSSLSASVGDRVTITCRASQSIGRYLAWYQQKPGKAPKLLIYSASNLETG VPSRFGSGSGTDFTLTISSLQPEDFATYYCQQYNSFPVTFGPGTKVDIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDIVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKEDEYERHNSYTCEATHKSTSTSPIVKSFNRECE
AF4387	SEQ ID NO: 183	APTSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTDMLTFEFYMPKKATELKHLQ CLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSQVQLVQSGAEVKKPGASV KVSCASGYTFTDYMHVVRQAPGQGLEWMGIINPRAGYTSYALKFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCTSGWDVWGQGTTLTVSSAKTTAPSVYPLAPV CGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVT

Protein Complex	SEQ ID NO:	Sequence
		SSTWPSQSITCNVAHPASSTKVDKKEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPK IKDVLMLISLPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRV VSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLR VEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 184	QVQLVQSGAEVKKPGASVKVSCASGYTFTDYYMHVWRQAPGQGLEWMGIINP RAGYTSYALKFQGRVTMTRDTSTSTVYMESSLRSEDTAVYYCTSGWDVWGQGT LTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKEPRGPTIKPCPPC KCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWVFNNEV HTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISK KGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKN TEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGG SGGGSHHHHHH
	SEQ ID NO: 185	DIQMTQSPSSLSASVGDRVTITCRASQSISTWLAWYQQKPGKAPKLLIYAASSLDSG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSPVTFGQGTKVEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNFFPKDINVKWKIDGSERQNGVLNSWTDQDSKDS TYSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNRECE
AF4389	SEQ ID NO: 186	APTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTDMLTFEFYMPKKATELKH LQCLERELKPLEEVLNLAQSKNFHLRPRDLISNINIVLELKGSETTFMCEYADETAT IVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSQVQLVQSGAEVKKPGASV KVSCASGHTFTRYMHVWRQAPGQGLEWMGIINPSGGYATYAQKFQGRVTMT RDTSTSTVYMESSLRSEDTAVYYCASGLFIWGQGTLTVTSSAKTTAPSVYPLAPV CGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTV TSS TWPSQSITCNVAHPASSTKVDKKEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPK IKDVLMLISLPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRV VSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEM T KKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 187	QVQLVQSGAEVKKPGASVKVSCASGHTFTRYMHVWRQAPGQGLEWMGIINP SGGYATYAQKFQGRVTMTRDTSTSTVYMESSLRSEDTAVYYCASGLFIWGQGT LTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKEPRGPTIKPCPPC KCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWVFNNEV HTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISK KGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKN TEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGG SGGGSHHHHHH
	SEQ ID NO: 188	DIQMTQSPSSLSASVGDRVTITCRASQSINSLAWYQQKPGKAPKLLIYATSTLES G VPSRFGSGSGTDFTLTISLQPEDFATYYCQQYRFPVTFGQGTKVEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNFFPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNRECE
AF4380	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRAITGIPARFSGSGSGTDFTLTISLQPEDFAVYYCQQSSNW PRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNFFPK DINVKWKIDGSERQNGVLNSWTDQDSKDSSTYSMSSTLTLTKEDEY ERHNSYTCEATHKTSTSPIVKSFNRECE

Protein Complex	SEQ ID NO:	Sequence
	SEQ ID NO: 189	APTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTDMLTFFFYMPKKATELKHLQ CLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSL RLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGRFTISR DNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGLTVTVSSAKTTAPSVYPLAPV CGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVT SSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKCPPCKCPAPNAAGGPSVFIFPPK IKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRV VSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLR VEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 190	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGRFTISR DNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
AF4383	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLLYSGVPSRFSGSRSGTDFLTITSLQPEDFATYYCQQHYYTTPPTFGQGTKVEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC
	SEQ ID NO: 191	APTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTDMLTFFFYMPKKATELKHLQ CLERELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSGVQLVESGGGLVQPGGSL RLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADT SKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRVEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 192	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADT SKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
AF4384	SEQ ID NO: 178	DIQMTQSPSSLSASVGDRVSITCKASQNVGTNVGWYQQKPGKAPKALIIYSASFRRYS GVPSRFSGSGSGTDFLTITSLQPEDFATYFCQQYYTYPTFGGGTKLEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC

Protein Complex	SEQ ID NO:	Sequence
	SEQ ID NO: 193	APTSSSTKKTQLQLEHLLDLQMI L N G I N N Y K N P K L T D M L T F E F Y M P K K A T E L K H L Q C L E R E L K P L E E V L N L A Q S K N F H L R P R D L I S N I N V I V L E L K G S E T T F M C E Y A D E T A T I V E F L N R W I T F C Q S I I S T L T G G G G S G G G G S G G G G S G G G G S E V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S S Y T L A W V R Q A P G K G L E W V A A I D S S S Y T S P D T V R G R F T I S R D N A K N S L Y L Q M N S L R A E D T A V Y Y C A R D S N W D A L D Y W G Q G T L V T V S S A K T T A P S V Y P L A P V C G D T T G S S V T L G C L V K G Y F P E P V T L T W N S G S L S S G V H T F P A V L Q S D L Y T L S S S V T V T S S T W P S Q S I T C N V A H P A S S T K V D K K I E P R G P T I K P C P P C K P A P N A A G G P S V F I F P P K I K D V L M I S L S P I V T C V V V D V S E D D P D V Q I S W F V N N V E V H T A Q T Q T H R E D Y N S T L R V V S A L P I Q H Q D W M S G K E F K C K V N N K D L G A P I E R T I S K P K G S V R A P Q V Y V L P P P E E E M T K K Q V T L T C M V T D F M P E D I Y V E W T N N G K T E L N Y K N T E P V L D S D G S Y F M Y S D L R V E K K N W V E R N S Y S C S V V H E G L H N H H T T E S F S R T P G K
	SEQ ID NO: 194	E V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S S Y T L A W V R Q A P G K G L E W V A A I D S S S Y T S P D T V R G R F T I S R D N A K N S L Y L Q M N S L R A E D T A V Y Y C A R D S N W D A L D Y W G Q G T L V T V S S A K T T A P S V Y P L A P V C G D T T G S S V T L G C L V K G Y F P E P V T L T W N S G S L S S G V H T F P A V L Q S D L Y T L S S S V T V T S S T W P S Q S I T C N V A H P A S S T K V D K K I E P R G P T I K P C P P C K C P A P N A A G G P S V F I F P P K I K D V L M I S L S P I V T C V V V D V S E D D P D V Q I S W F V N N V E V H T A Q T Q T H R E D Y N S T L R V V S A L P I Q H Q D W M S G K E F K C K V N N K D L G A P I E R T I S K P K G S V R A P Q V Y V L P P P E K E M T K K Q V S L T C L V K D F M P E D I Y V E W T N N G K T E L N Y K N T E P V L K S D G S Y F M Y S K L T V E K K N W V E R N S Y S C S V V H E G L H N H H T T K S F S R T P G G G G S G G G S H H H H H H

[0165] Results with protein complexes comprising the structures depicted in **FIG. 14C** are shown in **FIGS. 17A-H**. As depicted in **FIG. 14C**, these complexes are asymmetric and comprised of two identical monospecific Fab arms with a single IL-2 attached to one Fc domain by flexible linker and a single scFv attached to the other Fc domain by a flexible linker. The active PD-1/IL-2 DBA complexes, AF4403 comprising SEQ ID NO: 180, 195, 199 and AF4404 comprising SEQ ID NO: 180, 196, 199, are composed of anti-PD-1 domains in the Fab arms and a PD-1/IL-2 DBA scFv on the Fc arm. The control antibody-cytokine complexes are composed of a) antibody-cytokine complexes with an irrelevant antibody on the Fab arms with the DBA scFv on the Fc (AF4395 comprising SEQ ID NO: 64, 197, 202 and AF4396 comprising SEQ ID NO: 64, 198, 202), b) antibody-cytokine complexes with a non-DBA scFv on the Fc arm (AF4400 comprising SEQ ID NO: 180, 199-200 and AF4401 comprising SEQ ID NO: 180, 199, 201), and c) antibody-cytokine complexes with non-DBA antibodies in both the Fab and scFv domains (AF4392 comprising SEQ ID NO: 64, 202-203 and AF4393 comprising SEQ ID NO: 64, 202, 204). As shown in **FIGS. 17B** and **17D**, the IL-2 activity of the DBA-cytokine complexes AF4403 and AF4404 had an EC₅₀ of 31 pM and 26 pM respectively in the PD-1 coated wells and 62 pM and 64 pM respectively in the control wells, demonstrating PD-1 dependence of the IL-2 activity. None of the control proteins AF4395, AF4396, AF4400, AF4401, AF4392 and AF4393 described above showed a lower EC₅₀ on PD-1 coated wells

than on wells coated with the IgG1 protein, as shown in **FIGS. 17A, 17C and 17E-H**. Sequences of the protein complexes are summarized in **TABLE 24** below.

TABLE 24 – IgG PD-1 with C-terminal scFv and IL-2, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4403	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLI IYDASNRAITGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQSSNW PRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNFP KDINVKWKIDGSEKQNGVLNSWTDQDSKDSSTYSMSSTLTTLTKDEY ERHNSYTCEATHKTSTSPIVKSFRNEC
	SEQ ID NO: 195	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWDGSKRYYADSVKGRFTISRDNKNTLFLQMNSLRAE DTAVYYCATNDDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDITG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSS VTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLV KDFMPEDIYVEWTNNGKTELNYKNTEPVLSKDSGSYFMYSKLTVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGDTFTRYVHW VRQAPGQGLEWMGIINPSGGYASYAQKFQGRVTMTTRDTSTSTVY MELSSLRSEDTAVYYCAAGLFIWGQGLTVTVSSASGGGGSGGGGS GGGGSHASDIQMTQSPSSLSASVGDRTITCRASQSIGRYLAWYQQ KPGKAPKLLIYSASNLETGVPSRFSGSGSGTDFTLTISSELPEDFATY YCQQYNSTFPVTFPGGTKVDIKGGGSGGGSHHHHHH
	SEQ ID NO: 199	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWDGSKRYYADSVKGRFTISRDNKNTLFLQMNSLRAE DTAVYYCATNDDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDITG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSS VTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGSGGGGSGG GGSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFE FYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADETATIFEFLNRWITFCQSIISTLT
AF4404	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLI IYDASNRAITGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQSSNW PRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNFP KDINVKWKIDGSEKQNGVLNSWTDQDSKDSSTYSMSSTLTTLTKDEY ERHNSYTCEATHKTSTSPIVKSFRNEC
	SEQ ID NO: 196	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWDGSKRYYADSVKGRFTISRDNKNTLFLQMNSLRAE DTAVYYCATNDDYWGQGLTVTVSSAKTTAPSVYPLAPVCGDITG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSS VTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWV

Protein Complex	SEQ ID NO:	Sequence
		NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLV KDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLTVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSGGGGSGG GGSGGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYMH WVRQAPGQGLEWMGIINPRAGYTSYALKFQGRVTMTRDTSTSTV YMELSSLRSEDТАVYYCTSGWDVWGQGLTVTVSSASGGGGSGGG GGSGGGGSHASDIQMTQSPSSLSASVGDRVITICRASQSISTWLAWY QQKPGKAPKLLIYAASSLDGVPSTRFSGSGSGTDFTLTISLQPEDFA TYYCQQSYSPVTFGQGTKVEIKGGGSGGGGSHHHHHH
	SEQ ID NO: 199	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAE DTAVYYCATNDDYWGGQGLTVTVSSAKTTAPSVYPLAPVCGD TTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMI SLPIVTCVVVDVSEDDPDVQISWFV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGSGGGGSGG GGSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTDMLTFE FYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
AF4395	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVITICRASQDVNTAVAWYQQKPGKAPK LLIYSASFLYSGVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQHYT TPPTFGQGTKVEIKRADAAPT VSIFFPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKSFN RNEC
	SEQ ID NO: 197	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLTVTVSSAKTTAPSVYPLAPV CGD TTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMI SLPIVTCVVVDVSEDDPD VQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQ VSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMY SKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSG GGSGGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGDTFT RYYVHWVRQAPGQGLEWMGIINPSGGYASYAQKFQGRVTMTRDT STSTVYMELSSLRSEDТАVYYCAAGLFIWGQGLTVTVSSASGGGG GGGGSGGGGSHASDIQMTQSPSSLSASVGDRVITICRASQSIGRYL AWYQQKPGKAPKLLIYSASNLETGVPSRFSGSGSGTDFTLTISLQ EDFATYYCQQYNSFPVTFGP GTKVDIKGGGSGGGGSHHHHHH
	SEQ ID NO: 202	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLTVTVSSAKTTAPSVYPLAPV CGD TTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMI SLPIVTCVVVDVSEDDPD

Protein Complex	SEQ ID NO:	Sequence
		VQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGDSYFM YSDLRVEKKNWVERNNSYSCSVVHEGLHNHHTTESFSRTPGGGGGS GGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKL TDMLTFEFYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRP RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIST LT
AF4396	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK LLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYT TPPTFGQGTKVEIKRADAAPTVISFPPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSRQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDE YERHNSYTCEATHKTSTSPIVKSFNNEC
	SEQ ID NO: 198	EVQLVESGGGLVQPGGSLRLSCAASGFFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLVTVSSAKTTAPSVYPLAPV CGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPD VQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQ VSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGDSYFMY SKLTVEKKNWVERNNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSG GGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFT DYMHVWRQAPGQGLEWMGIINPRAGYTSYALKFQGRVTMTRD TSTSTVYMELSSLRSEDTAVYYCTSGWDVWGQGLVTVSSASGGG GSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQSIST WLAWYQQKPGKAPKLLIYAASSLDSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQSYSPVTFGQGTKVEIKGGGSGGGGSHHHHHH
	SEQ ID NO: 202	EVQLVESGGGLVQPGGSLRLSCAASGFFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLVTVSSAKTTAPSVYPLAPV CGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPD VQISWVFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGDSYFM YSDLRVEKKNWVERNNSYSCSVVHEGLHNHHTTESFSRTPGGGGGS GGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKL TDMLTFEFYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRP RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIST LT
AF4400	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRAIGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSSNW PRTFGQGTKVEIKRADAAPTVISFPPSSEQLTSGGASVVCFLNNFY KDINVKWKIDGSRQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDEY ERHNSYTCEATHKTSTSPIVKSFNNEC
	SEQ ID NO: 199	QVQLVESGGGVVQPGRSLRLDCKASGITFSNMGHWVRQAPGKG LEWVAVIWDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAE

Protein Complex	SEQ ID NO:	Sequence
		DTAVYYCATNDDYWGGQGLTVTVSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWFV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGSGGGGSGG GGSAPTSSSTKKTKLQLEHLLLDLQMLNGINNYKNPKLTDMLTFE FYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
	SEQ ID NO: 200	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAE DTAVYYCATNDDYWGGQGLTVTVSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWFV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLV KDFMPEDIYVEWTNNGKTELNYKNTEPVLSKSDGSYFMYSKLTVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSGGGGSGG GGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWV RQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQ MNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASGGG GSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRTITCRASQDVNT AVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISSL QPEDFATYYCQGHYTTPTFGQGTKVEIKGGGSGGGGSHHHHHH
AF4401	SEQ ID NO: 180	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLI YDASNRAITGIPARFSGSGGTDFTLTISSLEPEDFAVYYCQSSNW PRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNFPY KDINVKWKIDGSERQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEY ERHNSYTCEATHKTSTSPIVKSFNRECE
	SEQ ID NO: 199	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAE DTAVYYCATNDDYWGGQGLTVTVSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWFV NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSDLRVEK KNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGSGGGGSGG GGSAPTSSSTKKTKLQLEHLLLDLQMLNGINNYKNPKLTDMLTFE FYMPKKATELKHLQCLERELKPLEEVLNLAQSKNFHLRPRDLISNI NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
	SEQ ID NO: 201	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKG LEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAE DTAVYYCATNDDYWGGQGLTVTVSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSS VTVTSSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAP

Protein Complex	SEQ ID NO:	Sequence
		NAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFN NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKV NNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLV KDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLTVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSGGGGSGG GGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTLAWV RQAPGKGLEWVAAIDSSSYTSPDTRGRFTISRDNKNSLYLQM NSLRAEDTAVYYCARDSDWDALDYWGQGTLLTVSSASGGGGSG GGSGGGGSHASDIQMTQSPSSLSASVGDRVSITCKASQNVGTNVG WYQQKPGKAPKALIIYSASFYSYSGVPSRFSGSGSGTDFTLTISLQPE DFATYFCQQYYTYPTYTFGGGKLEIKGGGSGGGSHHHHHH
AF4392	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK LLIYSASFYSYSGVPSRFSGSRSGTDFTLTISLQPEDFATYFCQQHYT TPPTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY PKDINVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTCKDE YERHNSYTCEATHKTSTSPIVKSFNRNEC
	SEQ ID NO: 202	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGTLLTVSSAKTTAPSVYPLAPV CGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSYFM YSDLRVEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGS GGGGSGGGGSAPTSSSTKKTLQLLEHLLLDLQMLNGINNYKNPKL TDMLTFFEFYMPKKA TELKHLQCLERELKPLEEVLNLAQSKNFHLRP RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIST LT
	SEQ ID NO: 203	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGTLLTVSSAKTTAPSVYPLAPV CGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQ VSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMY SKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSG GGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKD TYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSK NTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVS SASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRA SQDVNTAVAWYQQKPGKAPKLLIYSASFYSYSGVPSRFSGSRSGTDF TLTISLQPEDFATYFCQQHYTTPPTFGQGTKVEIKGGGSGGGSHH HHHH
AF4393	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK LLIYSASFYSYSGVPSRFSGSRSGTDFTLTISLQPEDFATYFCQQHYT TPPTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY

Protein Complex	SEQ ID NO:	Sequence
		PKDINVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
	SEQ ID NO: 202	EVQLVESGGGLVQPGGSLRLSCAASGFTNIKDTYIHWRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLVTVSSAKTTAPSVYPLAPV CGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPD VQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFM YSDLRVEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGGGGGS GGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKL TDMLTTFEYMPKKATELKHLLQCLERELKPLEEVLNLAQSKNFHLRP RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIST LT
	SEQ ID NO: 204	EVQLVESGGGLVQPGGSLRLSCAASGFTNIKDTYIHWRQAPGKGL EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLVTVSSAKTTAPSVYPLAPV CGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP PCKCPAPNAAGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSEDDPD VQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSG KEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQ VSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMY SKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGGGGGSG GGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSS YTLAWVRQAPGKGLEWVAIDSSSYTSPDTRGRFTISRDNANKN SLYLQMNSLRAEDTAVYYCARDSDNDALDYWGQGLVTVSSASG GGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGRVSIITCKASQNV GTNVGWYQQKPGKAPKALISASFRYSRVPSRFSGSGSGTDFTLTI SSLQPEDFATYFCQQYYTYPTFTGGGTKLEIKGGGSGGGSHHHHH H

EXAMPLE 27**Improved Regulation by Engineering DBA Affinity using Standard Methods**

[0166] This example describes the use of standard techniques to modify DBA affinity and improve the range of sensor-dependent activation of a DBA-cytokine construct. A series of variants of the DBA PDL1-IFN R01 A05 (EXAMPLE 1) were prepared as described in EXAMPLE 4, assembled into DBA-cytokine-complexes and assayed as described in EXAMPLE 9. Results with six exemplary variant DBA-cytokine complexes are shown in **FIG. 21A-F**. Each plot includes data for IFNAR2 binding in the presence (triangles) and absence (squares) of PD-L1. Binding to a control IFN α antibody (circles) is used to confirm the presence of intact DBA-complex and provide a relative estimate of the amount of DBA-complex

captured in the wells. AF2719 and the five variant DBA-cytokine complexes show negligible IFNAR2 binding in the absence of PD-L1 and different levels of IFNAR2 binding in the presence of PD-L1. AF3099 (SEQ ID NO: 293) shows negligible IFNAR2 binding at all concentrations of PD-L1, while the IFNAR2 binding signal with AF3092 (SEQ ID NO: 292) is similar to the anti-IFN α antibody binding. AF2719 (SEQ ID NO: 41), AF3101 (SEQ ID NO: 289), AF3093 (SEQ ID NO: 290) and AF3094 (SEQ ID NO: 291) show intermediate levels of IFNAR binding relative to anti-IFN α binding. Together, these results demonstrate that standard methods of antibody engineering may be used to improve the regulation of the therapeutic activity of a DBA-cytokine complex. Protein complex sequences are provided in **TABLE 25** below.

TABLE 25 – DBA-cytokine protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF3099	SEQ ID NO: 293	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSGYIYH WVRQAPGQGLEWMGWMDNSGGTGYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGSGGGGSGGGGSHASDI QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKVEIKGKPIPNPLLGL DST
AF3092	SEQ ID NO: 292	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIH WVRQAPGQGLEWMGWMDPNSSGGTGYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGSGGGGSGGGGSHASDI QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKVEIKGKPIPNPLLGL DST
AF2719	SEQ ID NO: 41	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYV HWVRQAPGQGLEWMGWMDPNSSGGTGYAHQFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGSGGGGSGGGGSHAS DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKVEIKGKPIPNPLL GLDST
AF3101	SEQ ID NO: 289	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIH

Protein Complex	SEQ ID NO:	Sequence
		WVRQAPGQGLEWMGWMDGNSGGTGYAQKFQGRVTMTRDTSTSTVYMELSSL RSED TAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGGSGGGGSGGGGSHASDI QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPYTFGQGTKVEIKGKPIPNLLGL DST
AF3093	SEQ ID NO: 290	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIH WVRQAPGQGLEWMGWMDNSNGYTGYAQKFQGRVTMTRDTSTSTVYMELSSL RSED TAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGGSGGGGSGGGGSHASDI QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPYTFGQGTKVEIKGKPIPNLLGL DST
AF3094	SEQ ID NO: 291	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTET PLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVRAEIMRSFSLSTNLQESLSRKEG GGGSGGGGSGGGGSGGGGSGQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYIH WVRQAPGQGLEWMGWMDPNSGYTGYAHQFQGRVTMTRDTSTSTVYMELSSL RSED TAVYYCAKEVFSGWYDYWGQGLTVTVSSASGGGGSGGGGSGGGGSHASDI QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPYTFGQGTKVEIKGKPIPNLLGL DST

EXAMPLE 28

Regulated Interferon Receptor Binding by PD-L1/IFN α Dual Binding Antibodies

[0167] This example describes regulated interferon receptor binding by PD-L1/IFN α DBA-cytokine complexes. DBA-cytokine complexes AF2659 (SEQ ID NO: 276-277), AF2666 (SEQ ID NO: 96 and 277), AF2645 (SEQ ID NO: 95 and 112), AF2615 (SEQ ID NO: 279-280) and AF2616 (SEQ ID NO: 281-282) were chosen for analysis. The DBAs used to assemble these complexes were derived from three parental PD-L1/IFN α DBAs described in EXAMPLE 1: PDL1-IFN-R01-A05 (AF2659 and AF2666), PDL1-IFN-R01-C08 (AF2645) and PDL1-IFN-R01-B12 (AF2615 and AF2616) using standard antibody engineering techniques as described in EXAMPLE 4. Three control antibody-cytokine constructs were assembled from monospecific antibodies: AF2696 (anti-PDL1, SEQ ID NO: 283-284), AF2697 (anti-Her2, SEQ ID NO: 214 and 286) and AF2698 (anti-IFN α , SEQ ID NO: 287-288). Protein complex sequences are provided in **TABLE 26** below. The eight antibody-cytokine complexes were produced as symmetric IgG molecules with IFN α appended to the N-terminus of the heavy chain through a flexible linker (AF2659, AF2666 and AF2645, shown schematically in FIGURE 9e) or the N-terminus of the light chain through a flexible linker (AF2615, AF2616, AF2696, AF2697 and

AF2698, shown schematically in FIGURE 9d). The proteins were expressed in mammalian cells and purified using standard protocols. An ELISA assay was performed with a constant amount of the antibody-cytokine construct coated on each well probed with biotinylated interferon receptor (IFNAR2) in the presence of varying amounts of PD-L1-Fc or Her2-Fc. 384-well ELISA plates were coated with anti-Fc antibody at 10 micrograms/ml overnight at 4°C and washed twice with SuperBlock. Twenty microliters of a 66.7 nM antibody-cytokine complex was added to each well, incubated for one hour and washed three times in PBS. Biotinylated IFNAR2 protein was added to each well at a final concentration of 5 nM with PD-L1-Fc protein or HER2-Fc protein at a final concentration of 0.64 nM, 3.2 nM, 16 nM, 80 nM, or 400 nM. The plates were incubated for an hour, washed and biotinylated IFNAR2 detection was performed using streptavidin-HRP and standard ELISA protocols. As shown in **FIG. 22A-H**, DBA-cytokine complexes AF2659, AF2666, AF2645, AF2615 and AF2616 show a dose-dependent induction of IFNAR2 binding in the presence of PD-L1 protein but were not affected by the same dose range of Her2 protein, demonstrating PD-L1 dependent INF activity in five DBA constructs derived from three different parental PD-L1/IFNA dual-binding antibodies. IFNAR2 binding to the three control antibody complexes AF2696, AF2697 and AF2698 was not significantly affected by PD-L1 concentration. Protein complexes of the present invention can be produced from multiple dual-binding antibodies using standard antibody engineering methods.

TABLE 26 – DBA-cytokine protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF2659	SEQ ID NO: 276	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEVPGVG VPGAGVPGVGVPGGGVPGVGVPGGGVPGAGVPGGGVPGVGVPGAGVPGVGV PGGGQVQLVQSGAEVKKPGASVKVSCASGYTFSNYYIHWVRQAPGQGLEWMG WMDSNSGYTGQAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCAKEVFSG WYDYWGQGTLVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIVVEW TNNGKTELNYKNTEPVLDSGYSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNNH TTKSFSRTPGK
	SEQ ID NO: 277	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGGQTKVEIKRADAAPT SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWKIDGSEKQNGVLNSWTDQDSKDS TYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Protein Complex	SEQ ID NO:	Sequence
AF2666	SEQ ID NO: 96	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEVPGVG VPGAGVPGVGVPGGGVPGVGVPGGGVPGAGVPGGGVPGVGVPGAGVPGVGV PGGGQVQLVQSGAEVKKPGASVKVSKASGYTFSNYYIHWVRQAPGQGLEWMG WMDSNSGYTGYAQQFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKEVFSG WYDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNVNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEW TNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNNH TTKSFSRTPGK
	SEQ ID NO: 277	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKVEIKRADAAPTV SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWKIDGSEKQNGVLNSWTDQDSKDS TYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF2645	SEQ ID NO: 95	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEVPGVG VPGAGVPGVGVPGGGVPGVGVPGGGVPGAGVPGGGVPGVGVPGAGVPGVGV PGGGQVQLVQSGAEVKKPGASVKVSKASGGTFSSYAIWVRQAPGQGLEWMG IIDPSVTYTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSLEPTIFGV EVAFDIWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNVNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEW TNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNNH TTKSFSRTPGK
	SEQ ID NO: 112	DIQMTQSPSSLSASVGDRVTITCRASQSISSNRLAWYQQKPGKAPKLLIYKASSLESG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSNSTPFTFGQGTKVEIKRADAAPTV SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWKIDGSEKQNGVLNSWTDQDSKDS TYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF2615	SEQ ID NO: 279	QVQLVQSGAEVKKPGASVKVSKASGNFTDYYMHWVRQAPGQGLEWMGMW NPNSGNTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSLEPTIFGV EVAFDIWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNVNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEW TNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNNH TTKSFSRTPGK
	SEQ ID NO: 280	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQK

Protein Complex	SEQ ID NO:	Sequence
		PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPTF GQGTRLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER QNGVLNSWTDQDSKDYSTYSMSSTLTLTKEYERHNSYTCEATHKTSTSPIVKSFN NEC
AF2616	SEQ ID NO: 281	QVQLVQSGAEVKKPGASVKVCKASGGTFSSYAISWVRQAPGQGLEWMGIIDPS VTYTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDAVYYCARSIFPTIFGVEVAF DIWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG PTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQIS WVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLG APIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNN GKTELNYKNTEPVLDSGSGYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTK SFSRTPGK
	SEQ ID NO: 282	CDLPQTHSLGSRRTLMLLAQMRRLSFLSCLKDRHDFGFPQEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQQLNDLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEGGGGS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQSISNRLAWYQQK PGKAPKLLIYKASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSTPITFG QGTKEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ NGVLNSWTDQDSKDYSTYSMSSTLTLTKEYERHNSYTCEATHKTSTSPIVKSFN NEC
AF2696	SEQ ID NO: 283	QVQLVQSGAEVKKPGASVKVCKASGYTFSGYMHVVRQAPGQGLEWMGMW DPNSGYTGYAHQFQGRVTMTRDTSTSTVYMELSSLRSEDAVYYCAKEVFSGWYD YWGGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGP TIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISW FVNNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAP IERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKT ELNYKNTEPVLDSGSGYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR TPGK
	SEQ ID NO: 284	CDLPQTHSLGSRRTLMLLAQMRRLSFLSCLKDRHDFGFPQEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQQLNDLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEGGGGS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQTISYLNWYQQKP GKAPKLLIYAASLESVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQGYSTPITFG PGTKVDIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ NGVLNSWTDQDSKDYSTYSMSSTLTLTKEYERHNSYTCEATHKTSTSPIVKSFN NEC
AF2697	SEQ ID NO: 214	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTN GYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDY WGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISW VNNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPI ERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKT ELNYKNTEPVLDSGSGYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR TPGK

Protein Complex	SEQ ID NO:	Sequence
	SEQ ID NO: 286	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQ KPGKAPKLLIYSASFLYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPT FGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE RQNGVLNSWTDQDSKDYMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC
AF2698	SEQ ID NO: 287	EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYD ITNYNQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWISDFFDYWGQGT LTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKIEPRGPTIKPCPPC KCPAPNAAGGPSVFIFPPKIKDVLMSLSPITCVVVDVSEDDPDVQISWVFNNEV HTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISK KGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN TEPVLDSGSGYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 288	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMH WYQQKPGKAPKVLISYASNLESGVPSRFSGSGTDFTLTISLQPEDFATYYCQHSW GIPRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI DGSERQNGVLNSWTDQDSKDYMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNNEC

EXAMPLE 29

Selection of IL-15 and PD-L1 Specific Dual Binding Antibodies

[0168] This example describes isolation of sensor domains of the present disclosure, specifically, selection of IL-15 and PD-L1 specific dual binding antibodies (DBAs). Anti-PD-L1 and anti-IL-15 DBAs were isolated from the IFN α Tumbler antibody phage display library described in EXAMPLE 1. The selection was similar to the protocol described in EXAMPLE 1, alternating between PD-L1 selection and IL-15 selection.

[0169] The final selection was plated as single colonies and 380 colonies were picked for Sanger sequencing. Thirty-eight unique clones were screened for PD-L1 and IL-15 binding. The scFv DNA sequence for each clone was synthesized as a gBlock (Integrated DNA Technologies, Inc.) with a T7 promoter, a translation initiation site, a Myc tag, the scFv sequence, a V5 tag and a T7 terminator. Proteins were expressed using the PUREfrex2.1 cell-free transcription/translation system as described in previous examples. The scFv samples were subjected to ELISA analysis to detect PDL1 and IL15 binding. In these experiments, wells of a 384-well plate were coated with an anti-V5 antibody (Sv5-Pk1, BioRad) at 1ug/ml overnight at

4 degrees. After washing, wells were blocked with SuperBlock (ThermoFisher, 37515) followed by addition of saturating levels of scFvs in SuperBlock. After washing, antigens were added and plates incubated for one hour (PDL1-hFc-Avi, Acro Biosystems, PDL-H82F2); AF33 (SEQ ID NO: 298-299), biotinylated using standard methods; controls of PD1-hFc-Avi (Acro Biosystems, PD1-H82F1); AF35 (SEQ ID 63-64), biotinylated using standard methods). Biotinylated antigens were detected using streptavidin HRP using standard methods. Varying amounts of labeled test antigen were added to show binding and to estimate relative affinities of the different scFvs. **FIGS. 23A-D** show the ELISA binding data for four exemplary dual-binding scFvs AF635 (SEQ ID NO: 216), AF636 (SEQ ID NO: 217), AF666 (SEQ ID NO: 218) and AF614 (SEQ ID NO: 219). All four antibodies show binding to both PD-L1 and IL-15, with binding to PD-L1 detectable at a lower concentration of the antigen. Protein complex sequences are summarized in **TABLE 27** below.

TABLE 27 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF33	SEQ ID NO: 298	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTN GYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDY WGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWF VNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPI ERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKT ELNYKNTEPVLDSGYSFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR TPGKGGGSGGGSHHHHHH
	SEQ ID NO: 299	ITCPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHW TPSLKCIRDPAVLHQRPAAPSGSGGGGSGGGGSGGGGSLQNWVNVISDLKKIEDLI QSMHIDATLYTESDVHPSCVKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSL SSNGNVTESGCKECELEEKNIKEFLQSFVHIVQMFINTSGGGSGGGGSGGGGSGG GGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSA SFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRA DAAPTVSIFPPSSEQLTSGGASVVCFLNFPKDIVKWKIDGSRQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC
AF35	SEQ ID NO: 63	CDLPQTHSLGSRRTLMLLAQMRRLSFLSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNDEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYY CSRWGGDGFYAMDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLV KGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAH PASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMLISLPIVTCV VVDVSEDDPDVQISWFWNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMS GKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTD

Protein Complex	SEQ ID NO:	Sequence
		FMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFMYSKLRVEKKNWVERNSYSCS VVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVITICRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYS GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRADAAP TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF635	SEQ ID NO: 216	MSTSTEQKLISEEDLQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHVWRQAP GQGLEWMGIINPSGGSTRYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYC ARSLFPTIFGVEVAFDIWGQGTLLTVSSASGGGGSGGGGSGGGGSHASDIQMTQ SPSSLSASVGDRVITICRASQSIRTYLNWYQQKPGKAPKLLIYSASNLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQANSFPFTFGPGTKVDIKGKPIPNLLGLDST
AF636	SEQ ID NO: 217	MSTSTEQKLISEEDLQVQLVQSGAEVKKPGASVKVSCKASGYSFTSYLHWVRQAP GQGLEWMGRISPRSGGTNAQNFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYY CVRSFPTIFGVEVAFDIWGQGTLLTVSSASGGGGSGGGGSGGGGSHASDIQMT QSPSSLSASVGDRVITICRASQSISSWLAWYQQKPGKAPKLLIYASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYCQQGYQYPYTFGQGTKLEIKGKPIPNLLGLDST
AF666	SEQ ID NO: 218	MSTSTEQKLISEEDLQVQLVQSGAEVKKPGASVKVSCKASGYTFTSTYYIHVWRQAP GQGLEWMGWMNPNSGNTGYAQTFQGRVTMTTRDTSTSTVYMELSSLRSEDTAV YYCARSLFPTIFGVEVAFDIWGQGTLLTVSSASGGGGSGGGGSGGGGSHASDIQM TQSPSSLSASVGDRVITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPRTFGQGTKVEIKGKPIPNLLGLDS T
AF614	SEQ ID NO: 219	MSTSTEQKLISEEDLQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYIMHWVRQA PGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTA VYYCARSLFPTIFGVEVAFDIWGQGTLLTVSSASGGGGSGGGGSGGGGSHASDIQ MTQSPSSLSASVGDRVITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPRTFGQGTKLEIKGKPIPNLLGLD ST

EXAMPLE 30

Regulated IL-2 Receptor Signaling by a PD-L1/IL-15 Dual Binding Antibody (DBA)

Cytokine Complex

[0170] This example describes regulated IL-15 activity in a reporter cell line by PD-L1/IL-15 DBA-cytokine complexes. HEK-Blue™ IL-2 reporter cells (Invivogen Catalog # hkb-il2) were grown according to the vendors instructions. The cells express IL-2 receptor and respond to IL-2 or IL-15 signaling by induction of an enzyme that can be read with a colorimetric assay. The exemplary dual-binding scFv sequences AF635 (SEQ ID NO: 216), AF636 (SEQ ID NO: 217), AF666 (SEQ ID NO: 218) and AF614 (SEQ ID NO: 219) described in EXAMPLE 29 and **TABLE 28**, were used to assemble scFv DBA-cytokine complexes AF4455 (SEQ ID NO: 220), AF4456 (SEQ ID NO: 221), AF4457 (SQ ID NO: 222), and AF4440 (SEQ ID NO: 223) respectively. Two monospecific anti-IL-15 scFv sequences were assembled into cytokine-scFv complexes AF4478 (SEQ ID NO: 224) and AF4479 (SEQ ID NO: 225) to serve as negative

controls. Protein complex sequences are provided in **TABLE 28** below. The proteins were expressed using a PUREfrex2.1 cell-free transcription/translation system. 384-well ELISA plates (Corning 3700) were coated with 25 microliters per well of 1 microgram per ml anti-V5 antibody (SV5-pk1) in 100 mM bicarbonate solution pH 9.0 overnight at 4°C. The plates were washed three times with 100 microliters PBS + Tween and once with 50ul/well of SuperBlock. The PUREfrex reactions for each sample were diluted 1:2,160 in Superblock, added to the anti-V5-coated plates at 20 µl/well and incubated for 1 hour at room temperature to capture a uniform quantity of the scFv protein on the plate. Each plate was then washed three times with PBS with 0.05% Tween 20 (PBST). PDL-1 protein (Acro Biosystems Product # PD1-H5358) or Fc protein (Acro Biosystems Product # FCC-H5214) was diluted in growth media (DMEM complete) to 2-fold higher than the final concentration and 12.5 microliters added per well. After a 15 minute incubation 12.5 microliters of HEK-Blue™ IL-2 reporter cells (12,500 cells) were added to each well and incubated overnight. Five microliters from each well was transferred to a new plate containing 45 microliters of QuantiBlue solution (Invivogen Product # rep-qbs). After 30 to 60 minutes the absorbance at 630 nm was determined using a Perkin-Elmer Envision.

TABLE 28 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4455	SEQ ID NO: 220	MSTSTITCPPPMMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPPSSGGSGGGGSGGGGSLQNWWNVISDL KKIEDLIQSMHIDATLYTESDVHPSCCKVTAMKCFLELQVISLES GDASIHDTVENLIIL ANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGG GSGSGSGSGSQVLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGL EWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARSLF PTIFGVEVAFDIWGQGT LVTVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLS ASVGDRVTITCRASQSIRTYLNWYQQKPGKAPKLLIYSANLQSGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQANSFPFTFGPGTKVDIKAAAGSGSEQKLISEEDLGKPI PNPLLGLDSTNA
AF4456	SEQ ID NO: 221	MSTSTITCPPPMMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPPSSGGSGGGGSGGGGSLQNWWNVISDL KKIEDLIQSMHIDATLYTESDVHPSCCKVTAMKCFLELQVISLES GDASIHDTVENLIIL ANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGG GSGSGSGSGSQVLVQSGAEVKKPGASVKVSCKASGYSFTSYLLHWVRQAPGQGL EWMGRISPRSGGTKNAQNFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCVRSL FPTIFGVEVAFDIWGQGT LVTVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSL SASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQQGYQYPYTFGQGTKEIKAAAGSGSEQKLISEEDLGK PIPPLLGLDSTNA
AF4457	SEQ ID NO: 222	MSTSTITCPPPMMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPPSSGGSGGGGSGGGGSLQNWWNVISDL KKIEDLIQSMHIDATLYTESDVHPSCCKVTAMKCFLELQVISLES GDASIHDTVENLIIL

Protein Complex	SEQ ID NO:	Sequence
		ANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGSGSGSGSGSQVQLVQSGAEVKKPGASVKVSKASGYTFSTYYIHWVRQAPGQGLEWMGWMNPNSGNTGYAQTFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARS LFPTIFGVEVAFDIWGQGT LVT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQGYSTPRTFGQGTKVEIKAAAGSGSEQKLISEEDLGK PIPNPLLGLDSTNA
AF4440	SEQ ID NO: 223	MSTSTITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALVHQR PAPPSSGGSGGGGSGGGGSGGGGSLQNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGSGSGSGSGSQVQLVQSGAEVKKPGASVKVSKASGYTFTNYYMHVVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARSLFPTIFGVEVAFDIWGQGT LVT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQSYSTPRTFGQGTKLEIKAAAGSGSEQKLISEEDLGK PIPNPLLGLDSTNA
AF4478	SEQ ID NO: 224	MSTSTITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALVHQR PAPPSSGGSGGGGSGGGGSGGGGSLQNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGSGSGSGSGSQVQLVQSGAEVKKPGASVKVSKASGYTFTGYIHWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARSLFPTIFGVEVAFDIWGQGT LVT VSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQSYSTPRTFGQGTKVEIKAAAGSGSEQKLISEEDLGK PIPNPLLGLDSTNA
AF4479	SEQ ID NO: 225	MSTSTITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD PALVHQR PAPPSSGGSGGGGSGGGGSGGGGSLQNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSGGSGSGSGSGSGSGSGSGSQVQLVQSGAEVKKPGSSVKVSKASGYSFTDYYVHWVRQAPGQGLEWVGGINPKRGDTVFAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCARGGLGVFGVVDVWGQGT TVT VSSASGGGGSGGGGSGGGGSHASDIVMTQSPLSLPVT PGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYAATTLQSGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCMQALQTP LTFGGG TKLEIKAAAGSGSEQKLISEEDLGK PIPNPLLGLDST

[0171] The results are shown in **FIGS. 24A-F**. IL-15 activity increased in a dose dependent manner with the addition of PD-L1 (circles) but not with the addition of Fc protein (squares) for DBA-cytokine complexes AF4455 (SEQ ID NO: 220), AF4456 (SEQ ID NO: 221), AF4457 (SEQ ID NO: 222) and AF4440 (SEQ ID NO: 223). IL-15 activity from the monospecific IL-15 scFv cytokine complexes AF4478 (SEQ ID NO: 224) and AF4479 (SEQ ID NO: 225) did not change with the addition of PD-L1 or Fc protein.

[0172] The exemplary dual-binding antibody sequences from AF614 (SEQ ID NO: 219) and AF666 (SEQ ID NO: 218) were assembled into asymmetric IgG molecules with IL-15 appended to the N-terminus of one heavy chain through a flexible linker (as shown schematically in FIGURE 9b) to create AF4591 (SEQ ID NO: 226-228) and AF4592 (SEQ ID NO: 229-231) respectively. Two controls were assembled in the same format from an anti-IL-15 antibody (AF4659, SEQ ID NO: 232-234) and a PDL1-IFN dual-binding antibody (AF4660, SEQ ID NO: 235-237). Protein complex sequences are summarized in **TABLE 29**. The proteins were expressed in mammalian cells and purified using standard protocols. The four antibody-cytokine complexes were assayed for IL-15 activity using HEK-Blue™ IL-2 reporter cells in an assay similar to that described above, with the exception that all of the proteins were in solution in the growth media. The purified antibody-cytokine complexes were diluted to a final concentration of 100 pM and assayed in varying concentrations of PD-L1 or a control IgG1 antibody.

TABLE 29 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4591	SEQ ID NO: 226	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPSGGGSGGGSGGGSGGGGSLQNW VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCVKVTAMKCFLELQVISLESG DASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQ MFINTSGGGSGGGSGGGSGGGSGGGSGQVQLVQSGAEVKKPGASVKVS CKASGYFTNYYMHWVRQAPGQGLEWMGMNPNSGNTGYAQKFQ GRVTMTRDTSTSTVYMESSLRSED TAVYYCARSLFPTIFGVEVAFDIWGQ GTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVD KKIEPRGPTIKCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVV DVSEDDPDVQISWVFNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQD WMSGKEFKCKVNNKDLGAPIERTISKPGSVRAPQVYVLPPEEEMTKK QVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSDL RVEKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 227	QVQLVQSGAEVKKPGASVKVSCKASGYFTNYYMHWVRQAPGQGLEW MGWMNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMESSLRSED TAVY YCARSLFPTIFGVEVAFDIWGQGTTLTVSSAKTTAPSVYPLAPVCGDTTG SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTS TWPSQSITCNVAHPASSTKVDKKIEPRGPTIKCPPCKCPAPNAAGGPSVF IFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNVEVHTAQTQTH REDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPGS VRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNY KNTEPVLDSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSF SRTPGK
	SEQ ID NO: 228	DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQQKPKGAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSYSTPRTFGQGTK LEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR

Protein Complex	SEQ ID NO:	Sequence
		QNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC
AF4592	SEQ ID NO: 229	ITCPPPMSVEHADIWVKSYSLYRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPSGGSGGGGSGGGSGGGGSLQNW VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLESG DASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQ MFINTSGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKPGASVKVS CKASGYTFSTYYIHWVRQAPGQGLEWMGWMNPNSGNTGYAQTFQGR VTMTRDTSTSTVYMELSSLRSED TAVYYCARSLFPTIFGVEVAFDIWGQGT LTVVSSAKTTAPSVYPLAPVCGD TTGSSVT LGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI EPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDV SEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQV TLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRV EKKNWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 230	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYYIHWVRQAPGQGLEWM GWMNPNSGNTGYAQTFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYC ARSLFPTIFGVEVAFDIWGQGT LTVVSSAKTTAPSVYPLAPVCGD TTGSSV TLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSST WPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFI FPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTH REDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGS VRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNY KNTEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSF SRTPGK
	SEQ ID NO: 231	DIQMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPRTFGQGT KVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE RQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSP IVKSFNRNEC
AF4659	SEQ ID NO: 232	ITCPPPMSVEHADIWVKSYSLYRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPALVHQRPAAPSGGSGGGGSGGGSGGGGSLQNW VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLESG DASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQ MFINTSGGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKPGASVKVS CKASGDTFSSYAISWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGR VTMTRDTSTSTVYMELSSLRSED TAVYYCATGITMIGYWGQGT LTVVSSA KTTAPSVYPLAPVCGD TTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTI KPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPD VQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFK CKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVT DFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRVEKKNWV ERNYSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 233	QVQLVQSGAEVKKPGASVKVSCKASGDTFSSYAISWVRQAPGQGLEWM GWMNPNSGNTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYC

Protein Complex	SEQ ID NO:	Sequence
		ATGITMIGYWGQGTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVK GYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTL RVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVY VLPPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTEPVLK SDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
	SEQ ID NO: 234	DIQMTQSPSSLSASVGDRVITTCQASQDISSYLNWYQQKPGKAPKLLIYAA STLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGQGTK VEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR QNGVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC
AF4660	SEQ ID NO: 235	ITCPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATN VAHWTTPSLKCIRDPAVHQRPAAPSGGGSGGGSGGGSGGGGSLQNW VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLESG DASIHDTVENLILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQ MFINTSGGGSGGGSGGGSGGGSGGGSGQVQLVQSGAEVKKPGASVKVS CKASGGTFSSYAISWVRQAPGQGLEWMGIIDPSMTYTRYAQKFQGRVT MTRDTSTSTVYMELSSLRSEDTAVYYCARSLFPTIFGLEVAFDIWGQGTLV TVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSL SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP RGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSE DDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQQDWMS GKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLT CMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSYFMYSDLRVEKK NWVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 236	QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYAISWVRQAPGQGLEWM GIIDPSMTYTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR SLFPTIFGLEVAFDIWGQGTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLG CLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPS QSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPK IKDVLMSLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDY NSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAP QVYVLPPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTELNYKNTE PVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTP GK
	SEQ ID NO: 237	DIQMTQSPSSLSASVGDRVITTCQASQSIENRLAWYQQKPGKAPKLLIYKA SSLESGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPITFGQGTK VEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR QNGVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC

[0173] The results are shown in **FIGS. 25A-D**. IL-15 activity increased in a dose dependent manner with the addition of PD-L1 but not with the addition of Fc protein for DBA-cytokine complexes AF4591 (SEQ ID NO: 226-228) and AF4592 (SEQ ID NO: 229-231). IL-15 activity

from the monospecific IL-15 scFv cytokine complexes AF4659 (SEQ ID NO: 232-234) and AF4660 (SEQ ID NO: 235-237) did not change with the addition of PD-L1 or Fc protein.

[0174] Protein complexes of the present invention based on four different PD-L1/IL-15 dual-binding antibodies produced in two different formats showed PD-L1-dependent IL-15 activity.

EXAMPLE 31

Selection and Binding of IFN and CEA Specific Dual Binding Antibodies

[0175] This example describes isolation of sensor domains of the present disclosure, specifically, selection of IFN α and CEA specific dual binding antibodies (DBAs). Anti-CEA and anti-IFN α DBAs were isolated from a Tumbler antibody phage display library similar to the library described in EXAMPLE 1. The antibody phage display library was constructed to incorporate the heavy chain CDR1, heavy chain CDR2, and light chain diversity of the Superhuman 2.0 antibody library combined with various heavy chain (“HC”) CDR3 sequences from anti-IFN α antibodies (TABLE 18). The selection was similar to the protocol described in EXAMPLE 1, using one round of IFN α selection (IFN α 2b, GenScript, Z03002, biotinylated using standard protocols) and one round of CEA selection (CEA-hFc, Sino Biologicals, 11077-H02H).

TABLE 18 – HC-CDR3 of IFN α binders

SEQ ID NO	Sequence	Description
SEQ ID NO: 238	CASGGSYSPWYFDLW	HC-CDR3 of IFN α binder
SEQ ID NO: 239	CASLAAAGPYYYYGMDVW	HC-CDR3 of IFN α binder
SEQ ID NO: 240	CVSSVGAGAYYYQGLDVW	HC-CDR3 of IFN α binder
SEQ ID NO: 241	CARDHDYLTSGFYW	HC-CDR3 of IFN α binder
SEQ ID NO: 242	CAFSSPTYYYYGMDVW	HC-CDR3 of IFN α binder
SEQ ID NO: 243	CARVNYDFWSGQSLRFPDW	HC-CDR3 of IFN α binder
SEQ ID NO: 244	CATIKGLGAYYYYGMDVW	HC-CDR3 of IFN α binder
SEQ ID NO: 245	CASDHGWLDAFDIW	HC-CDR3 of IFN α binder
SEQ ID NO: 246	CARDWYGDFDYW	HC-CDR3 of IFN α binder
SEQ ID NO: 247	CARGILSDYGDHAFDYW	HC-CDR3 of IFN α binder
SEQ ID NO: 248	CARVDSSSSLHFDYW	HC-CDR3 of IFN α binder
SEQ ID NO: 249	CARTSGYDLLFDYW	HC-CDR3 of IFN α binder
SEQ ID NO: 250	CARVGGWGIYYYGMDVW	HC-CDR3 of IFN α binder
SEQ ID NO: 251	CARDPSYSTGYDYW	HC-CDR3 of IFN α binder
SEQ ID NO: 252	CARGSRADYW	HC-CDR3 of IFN α binder

[0176] Following two rounds of selection in phage, the resulting library of DBAs was subcloned into a yeast surface display vector and transformed into yeast for further screening using standard protocols. The yeast library was sorted four times for binding to CEA and IFN α . In each round of sorting, the library was labeled with either CEA-Fc-biotin or IFN α -biotin, then with Streptavidin-PE (Abcam #ab239759), and sorted based on PE fluorescence on a Sony

MA900 cell sorter. The four sorts were carried out with labelling at 100 nM CEA-Fc-biotin, 1000 nM IFN α -biotin, 10 nM CEA-Fc-biotin, and 20 nM CEA-Fc-biotin. Plasmids were rescued from the yeast after the final sort using a Zymoprep Yeast Plasmid Miniprep II kit (Zymo research D2004) and transformed into DH5a *E. coli* for cloning. Ninety-six colonies were picked for Sanger sequencing, from which thirty-four unique clones were identified and screened for IFN α and CEA binding. The scFv DNA sequence for each clone, including c-myc and V5 tags, was amplified by PCR using a forward primer containing a T7 promoter and a translation initiation site, and a reverse primer containing a T7 terminator. Proteins were expressed using the PUREfrex2.1 cell-free transcription/translation system as described in previous examples. The scFv samples were subjected to ELISA analysis to detect CEA and IFN α binding. In these experiments, wells of a 384-well plate are coated with an anti-V5 antibody (Sv5-Pk1, BioRad) at 1 μ g/ml overnight at 4 degrees. After washing, wells are blocked with SuperBlock (ThermoFisher, 37515) followed by addition of saturating levels of scFvs in SuperBlock. After washing, antigens are added and plates incubated for one hour. Biotinylated IFN α is detected using streptavidin HRP and CEA-Fc is detected using anti-hFc-HRP, and developed using standard methods. Varying amounts of labelled test antigen were added to show binding and to estimate relative affinities of the different scFvs. **FIG. 26** shows the ELISA binding data for five exemplary dual-binding scFvs binding to CEA. Because the binding affinity for IFN α was too low to detect by ELISA, the binding to IFN α was measured by Biolayer Interferometry (OctetRED96e) as described in Example 5. Results are tabulated in **TABLE 19**. All five show binding to both CEA and IFN, with binding to CEA detectable at a lower concentration of the antigen.

TABLE 19 – Anti-IFN α Binding Results

CloneID	IFN α binding (@5uM)	ELISA	SEQUENCES	HC-CDR3
8b2_A09	+	-	(SEQ ID NO: 253) MSTSTEVQLLESGGGLVQPGGSLRLSCAAS GFTFSSYAMHWVRQAPGKGLEWVSAIGA GGGTYYADSVKGRFTISRDDSKNTLYLQM NSLKTEDTAVYYCVSSVGAGAYYYQGLDV WGQGTLLVTVSSASGGGGSGGGSGGGG SHASDIQMTQSPSSLSASVGDRTITCRAS QDIFTYLNWYQQRPGKAPKLLIYDASRLQT GVPSRFGSGSGTDFTLTISLQPEDFATYY CQQSYSIPYTFGQGTKLEIKRAAAGSGSEQ KLISEEDLGKIPNPPLLGLDST	SEQ ID NO: 240

8b2_B10	+	-	(SEQ ID NO: 254) MSTSTEVQLLESGAEVKKPGGSLR LSCAASGFTVSSNYMSWVRQAPG KGLEWVSAISGSGGSTYYADSVKGR RFTISRDNSKNTLYLQMNSLRAED TAVYYCVSSVGAGAYYYQGLDV WGQGTLLTVSSASGGGGSGGGGS GGGGSHASDIQMTQSPSSLSASVG DRVITTCRASQGVGNFLAWYQQKP GKAPKLLIYGASTLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQ SYSTPFTFGGGTKLEIKRAAAGSGS EQKLISEEDLGKPIPNPLLGLDST	SEQ ID NO: 240
8b2_C02	+	-	-	
8b2_C03	+	-	-	
8b2_C08	+	-	(SEQ ID NO: 256) MSTSTEVQLLESGAEVKKPGGSLR LSCAASGFTFSSYAMSWVRQAPGK GLEWVSAISGSGGSTYYADSVKGR FTISRDNSKNTLYLQMNSLRAEDT AVYYCARVDSSSSLHFDYWQGT LTVSSASGGGGSGGGGSGGGGSH ASDIQMTQSPSSLSASVGDRVITTC RASQRIGTYLNWYQQKPGKAPKLL IYAASNLSQGVPSRFSGSGSGTDF LTISSLQPEDFATYYCLQTFNTPTF GPGTKVDIKRAAAGSGSEQKLISEE DLGKPIPNPLLGLDST	SEQ ID NO: 248
AF317	(KD < 10nM)	+++	(SEQ ID NO: 257) MSTSTEKLISEEDLQVQLVQSGAE VKKPGASVKVSCKASGYSFTSYDI NWVRQAPGQGLEWIGMINPSSGFT	SEQ ID NO: 244

			SAAQTFQGRVTMTRDTSTSTVYME LSSLRSED TAVYYCATIKGLGAYY YYGMDVWGQGTTVTVSSASGGGG SGGGSGGGGSHASDIQMTQSPSS LSASVGDRVTITCRASQSIDRYLNW YQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATY YCQQSYSPPLTFGGGKVEIKGSL NDIFEAQKIEWHEGKPIPNPLLGLD ST	
AF372	-	-	(SEQ ID NO: 258) MSTSTEQKLISEEDLEVQLVESGGG LVQPGGSLRLSCAASGFNIKDTYIH WVRQAPGKGLEWVARIYPTNGYT RYADSVKGRFTISADTSKNTAYLQ MNSLRAEDTAVYYCSRWGGDGFY AMDYWGQGTLLTVSSASGGGGSG GGGSGGGGSHASDIQMTQSPSSLS ASVGDRVTITCRASQDVNTAVAW YQQKPGKAPKLLIYSASFLYSGVPS RFSGSRSGTDFTLTISSLQPEDFATY YCQQHYTTPPTFGQGKVEIKGSG LNDIFEAQKIEWHEGKPIPNPLLGL DST	-

EXAMPLE 32

Regulated IFNAR2 (IFN α Receptor 2) Binding by a CEA-IFN α Dual Binding Antibody (DBA) Cytokine Complex

This example describes regulated binding of IFN to the receptor IFNAR2 by CEA/IFN DBA-cytokine complexes in the form shown in Figure 8. DBA-cytokine complexes of SEQ ID NO: 259, SEQ ID NO: 260 and SEQ ID NO: 261 were chosen for analysis with a negative control with a similar structure based on an IFN α monospecific binding scFv (SEQ ID NO: 300) and two non-IFN α binding scFvs (one with SEQ ID NO: 301 and one with SEQ ID NO: 302). DBA-

cytokine complex and control protein complex sequences are summarized in **TABLE 30**. To test the ability of Carcino Embryonic Antigen (CEA) to regulate the binding of IFNAR2, V5-tagged constructs were generated consisting of a CEA-IFN- α DBA scFv linked to IFN- α . scFvs were synthesized using the PUREfrex 2.1 in vitro translation system and added to a 384 well plate at a single dilution. Titrating concentrations of either CEA-Fc (SINO Biological) or PDL1-Fc (ACROBiosystems) were added, and the plate was incubated for 30 minutes at room temperature. Eu-labeled IFNAR2 (ACROBiosystems) and Alexa Fluor 647-labeled anti-V5 antibody (Perkin Elmer) were added to all wells and incubated for 24 hours at room temperature. The HTRF signal was then read on an Envision 2105 microplate reader (Perkin Elmer). IFNAR2 was able to bind IFN- α on the DBA-scFv complex in the presence of increasing concentrations of CEA-Fc. No increase in IFNAR2 binding was seen in the presence of the PD-L1-Fc control protein, which does not bind the DBA-scFv protein complex. Results shown in **FIGS. 27A-F** demonstrate IFNAR2 binding increased in a dose dependent manner with the addition of CEA but not with the addition of control protein PDL1 for DBA-cytokine complexes of SEQ ID NO: 259 (**FIG. 27A**), SEQ ID NO: 260 (**FIG. 27B**) and SEQ ID NO: 261 (**FIG. 27C**). IFNAR2 binding from the monospecific IFN scFv cytokine complexes did not change with the addition of CEA or PD-L1.

TABLE 30 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
DBA-cytokine complex	SEQ ID NO: 259	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTETPLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVR AEIMRSFSLSTNLQESLRSKEGGSGSGSGSGSGSGS GGSGSEVQLLES GGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQA PGKGLEWVSAIGAGGGTYADSVKGRFTISRDDSKNTLYLQMNSL KTEDTAVYYCVSSVGAGAYYYQGLDVWGQGLTVTVSSASGGGGS GGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQDIFTYL NWYQQRPGKAPKLLIYDASRLQTGVPSRFSGSGSGTDFTLTISLQP EDFATYYCQQSYSIPYTFGQGTKLEIKRAAAGSGSEQKLISEEDLGK PIPNPLLGLDST
DBA-cytokine complex	SEQ ID NO: 260	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTETPLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVR AEIMRSFSLSTNLQESLRSKEGGSGSGSGSGSGSGS GGSGSEVQLLES GA EVKKPGGSLRLSCAASGFTVSSNYMSWVRQA PGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCVSSVGAGAYYYQGLDVWGQGLTVTVSSASGGGGS GGGGSGGGGSHASDIQMTQSPSSLSASVGDRVTITCRASQGVGNFL AWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISLQP EDFATYYCQQSYSTPFTFGGGTKLEIKRAAAGSGSEQKLISEEDLGK PIPNPLLGLDST

Protein Complex	SEQ ID NO:	Sequence
DBA-cytokine complex	SEQ ID NO: 261	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTETPLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVRAEIMRSFSLSTNLQESLSRKEGGSGSGSGSGSGSGS GGSGSEVQLLES GA EVKKPGGSLRLSCAASGFTFSSYAMSWVRQA PGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARVDSSSLHFDYWGGQGLTVTVSSASGGGGSGGG GGSGGGGSHASDIQMTQSPSSLSASVGDRTITCRASQRIGTYLNWY QQKPGKAPKLLIYAASNLSGVPSPRFSGSGSGTDFTLTISLQPEDF ATYYCLQTFNTPFTFGPGTKVDIKRAAAGSGSEQKLISEEDLGKPIP NPLLGLDST
AF2589	SEQ ID NO: 300	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTET PLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVRAEIMRSFSLSTNLQESLSRKEGGSGGGGGSGGGG SGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDIN WVRQAPGQGLEWIGMINPSSGFTSAAQTFQGRVTMTRDTSTSTVYMELSSLRSE DTAVYYCATIKGLGAYYYYGMDVWGQGTITVTVSSASGGGGSGGGG SGGGGSHASDIQMTQSPSSLSASVGDRTITCRASQSIDRYLNWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQSYSPPLTFGGGKVEIKGKPIP NPLLGLDST
AF2592	SEQ ID NO: 301	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTET PLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVRAEIMRSFSLSTNLQESLSRKEGGSGGGGGSGGGG SGGGGSGVQLVQSGAEVKKPGASVKVSCKASGGTFSSYASIS WVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARSLFTIFGVEVAFDIWGQGTITVTVSSASGGGGSGGGG SGGGGSHASDIQMTQSPSSLSASVGDRTITCRASQSIIDRLAWYQQKPGKAPKLLIYKASSLES GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVDIKGKPIP NPLLGLDST
AF2594	SEQ ID NO: 302	MSTSTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQE EFGNQFQKAE TIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTEL YQQLNDLEACVIQGVGVGTET PLMKEDSILAVRKYFQRITLYLKEKK YSPCAWEVVRAEIMRSFSLSTNLQESLSRKEGGSGGGGGSGGGG SGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGK GLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED TAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASGGGGSGGGGSGGGG SHASDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIY SASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQGHYTPPTFGQGT KVEIKGKPIP NPLLGLDST

EXAMPLE 33

Selection and Binding of LRRC15 and IFN α Specific Dual Binding Antibodies

[0177] This example describes isolation of sensor domains of the present disclosure, specifically, selection of LRRC15 and IFN α specific dual binding antibodies (DBAs). Anti-LRRC15 and anti-IFN α DBAs were isolated from the IFN α Tumbler antibody phage display

library described in EXAMPLE 31. The selection was similar to the protocol described in EXAMPLE 1, using one round of IFN α selection (IFN α 2b, GenScript, Z03002, biotinylated using standard protocols) and one round of LRRC15 selection (LRRC15-hFc, Sino Biologicals, 15786-H02H).

[0178] After a first round of selection in phage on 100 nM IFN α and a second round on 100 nM LRRC15, the resulting library of DBAs was subcloned into a yeast surface display vector and transformed into yeast for further screening using standard protocols. The yeast library was sorted four times for binding to LRRC15 and IFN α . In each round of sorting, the library was labeled with either LRRC15-Fc-biotin or IFN α -biotin, then with Streptavidin-PE (Abcam #ab239759) and sorted based on PE fluorescence on a Sony MA900 cell sorter. The four sorts were carried out with labelling at 100 nM LRRC15-Fc-biotin, 1000 nM IFN α -biotin, 10 nM LRRC15-Fc-biotin, and 10 nM LRRC15-Fc-biotin. Plasmids were rescued from the yeast after the final sort using a Zymoprep Yeast Plasmid Miniprep II kit (Zymo research D2004) and transformed into DH5a *E. coli* for cloning. Ninety-six colonies were picked for Sanger sequencing, from which twenty-four unique clones were identified and screened for IFN α and LRRC15 binding. The scFv DNA sequence for each clone, including c-myc and V5 tags, was amplified by PCR using a forward primer containing a T7 promoter and a translation initiation site, and a reverse primer containing a T7 terminator. Proteins were expressed using the PUREfrex2.1 cell-free transcription/translation system as described in previous examples. The scFv samples were subjected to ELISA analysis to detect LRRC15 and IFN α binding. **FIG. 28A** shows the ELISA binding data for six exemplary scFvs to LRRC15. Because the IFN α binding affinity was too low to detect by ELISA for some scFvs, the binding to IFN α was also measured by Biolayer Interferometry (OctetRED96e) as described in Example 5. Results and antibody sequences are tabulated in **FIG. 28B**. All six show binding to both LRRC15 and IFN α , with binding to LRRC15 detectable at a lower concentration of the antigen. Protein complex sequences are provided in **TABLE 31**.

TABLE 31 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
A03	SEQ ID NO: 262	MSTSTQVQLVQSGAEVKKPGASVKVSCKASGYFTGYIMHWVRQAPGQGLEW MGWMDPNDDADYAQRFQGRVTMTTRDTSTSTVYMEISSLRSEDVAVYYCASLA AAGPYYYYGMDVWGQGTITVSSASGGGGSGGGGSGGGGSHASDIQMTQSPS SLSASVGDRTITCRASQSINNYLNWYQQKPGKAPKLLIYGASNLETGVPSRFSGSG SGTDFTLTISLQPEDFATYYCQSYGTPLTFGGGKVEIKRAAAGSGSEQKLISEED LGKPIPNPLLGLDST

Protein Complex	SEQ ID NO:	Sequence
i47_A11	SEQ ID NO: 314	MSTSTQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGTINPSDGDITYA QKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVGGWGIY YYYGMDVWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCRASQSINSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYTVPFSFGQGTKLEIKRAAAGSGSEQKLISEEDLGKPIPNPLLGLDST
i47_A12	SEQ ID NO: 315	MSTSTQVQLVQSGAEVKKPGSSVKVSCKASGYTFINNDINWVRQAPGQGLEWMGGTIPIFGVHIYA QKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVSSVGAGAYYYYGMDVWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSLPYTFGQGT RLEIKRAAAGSGSEQKLISEEDLGKPIPNPLLGLDST
B03	SEQ ID NO: 263	MSTSTQVQLVQSGAEVKKPGASVEVSCKASGGTFSSYAINWVRQAPGQGLEWMGWIDPKSGDITYA QKFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCASGGSYSPWYFDLWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCRASQSISSWLAWYQQKSGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAYSFPFTFGPGTKVDIKRAAAGSGSEQKLISEEDLGKPIPNPLLGLDST
B07	SEQ ID NO: 264	MSTSTQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWMDPNNDADYA QRFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCASLAAGPYYYYGMDVWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCQASQDISNYLNWYQQKPGKAPKLLIYGASILEAGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSAPITFGQGT RLEIKRAAAGSGSEQKLISEEDLGKPIPNPLLGLDST
B11	SEQ ID NO: 265	MSTSTQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYDINWVRQAPGQGLEWLGTVPLFGISHYA QKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVSSVGAGAYYQGLDVWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYLPPYSFGQGTKLEIKRAAAGSGSEQKLISEEDLGKPIPNPLLGLDST
AF372	SEQ ID NO: 258	MSTSTEKLISEEDLEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGT LTVVSSASGGGGSGGGGSGGGGSHASDIQMTQSPSSLSASVGD RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGSGLNDIFEAQKIEWHEGKPIPNPLLGLDST

EXAMPLE 34**Regulated IFNAR2 (IFN α Receptor 2) Binding by a LRRC15-IFN α Dual Binding****Antibody (DBA) Cytokine Complex**

[0179] This example describes LRRC15 dependent binding of IFN to the receptor IFNAR2 by LRRC15/IFN DBA-cytokine complexes. The cytokine complexes of this example are composed

of a LRRC15-IFN- α DBA IgG with IFN- α linked to the N-terminus of one heavy chain (a schematic of the structure is shown in **FIG. 9B**). DBA-cytokine complexes AF4581 (SEQ ID NO: 266-268), AF4586 (SEQ ID NO: 269-271), AF4587 (SEQ ID NO: 266-267, 272) and AF4588 (SEQ ID NO: 273-275) were chosen for analysis. Two cytokine complexes with the same structure were included as controls: AF4305 (SEQ ID NO: 294-296), which is based on a neutralizing anti-IFN α antibody, and AF4306 (SEQ ID NO: 64, 192, 297), which is based on an anti-Her2 antibody. Protein complex sequences are provided in **TABLE 32**. The six IgG-cytokines were expressed in mammalian cells using standard protocols and added to a 384 well plate at a single dilution. Titrating concentrations of either LRRC15-Fc (SINO Biological), PDL1-Fc (ACROBiosystems) or CEA-Fc (SINO Biological) were added, and the plate was incubated for 30 minutes at room temperature. Eu-labeled IFNAR2 (ACROBiosystems) and Alexa Fluor 647-labeled anti-V5 antibody (Perkin Elmer) were added to all wells and incubated for 24 hours at room temperature. The HTRF signal was then read on an Envision 2105 microplate reader (Perkin Elmer). Results shown in **FIGS. 29A-F** demonstrate IFNAR2 binding increased in a dose dependent manner with the addition of LRRC15 but not with the addition of control protein PDL1 for DBA-cytokine complexes of AF4581, AF4586 and AF4587, demonstrating LRRC15-dependent regulation of IFNAR-binding activity. IFNAR2 binding from AF4588 and the monospecific IFN scFv cytokine complexes AF4305 and AF4306 did not change with the addition of LRRC15 or PD-L1.

[0180] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

TABLE 32 – DBA-cytokine protein complexes, and control protein complexes

Protein Complex	SEQ ID NO:	Sequence
AF4581	SEQ ID NO: 266	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHWV RQAPGQGLEWMGWMDPNNDADYAQRFFQGRVTMTTRDTSTSTVYMESSLRS EDTAVYYCASLAAAGPYYYYGMDVWGQGTITVSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPS

Protein Complex	SEQ ID NO:	Sequence
		QSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI ISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPI QHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRVEKKN WVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 267	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGQGLEWMGWMD PNNDADADYAQRFGQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCASLAAAGPYY YVGMDVWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTL TWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMIISLSPIVTCVVVDVSEDDPD VQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWT NNGKTELNYKNTEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHT TKSFSRTPGK
	SEQ ID NO: 268	DIQMTQSPSSLSASVGDRVITICRASQSINNYLNWYQQKPGKAPKLLIYGASNLET GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYGTPLTFGGGTKEIKRADAAPT VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF4586	SEQ ID NO: 269	CDLPQTHSLGSRRITMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVEVSCASGGTFSSYAINWVR QAPGQGLEWMGWIDPKSGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDT AVYYCASGGSPWYFDLWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLG CLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCN VAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMIISLSPIV TCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGGSYFMYSDLRVEKKNWVERNSYS CSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 270	QVQLVQSGAEVKKPGASVEVSCASGGTFSSYAINWVRQAPGQGLEWMGWIDP KSGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCASGGSPWYFDL WGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPT IKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMIISLSPIVTCVVVDVSEDDPDVQISWF VNNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLGAPI ERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNGKTE LNYKNTEPVLKSDGSYFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRT PGK
	SEQ ID NO: 271	DIQMTQSPSSLSASVGDRVITICRASQSISSWLAWYQQKSGKAPKLLIYAASSLQSG VPSRFGSGSGTDFTLTISLQPEDFATYYCQAYSPFTFGPGTKVDIKRADAAPTV SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDS TYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF4587	SEQ ID NO: 266	CDLPQTHSLGSRRITMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWV

Protein Complex	SEQ ID NO:	Sequence
		RQAPGQGLEWMGWMDPNNDADYAQRFFQGRVTMTTRDTSTSTVYMESSLRS EDTAVYYCASLAAAGPYYYYGMDVWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTG SSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPS QSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI ISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPI QHQDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFMYSDLRVEKKN WVERNSYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 267	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHWVRQAPGQGLEWMGWMDPNNDADYAQRFFQGRVTMTTRDTSTSTVYMESSLRSEDTAVYYCASLAAAGPY YYGMDVWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI ISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNN KDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWT NNGKTELNYKNTEPVLKSDGYSFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHT TKSFSRTPGK
	SEQ ID NO: 272	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYGASILEAG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYAPITFGQGRLEIKRADAAPTV SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWKIDGSEKQNGVLNSWTDQDSKDS TYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
AF4588	SEQ ID NO: 273	CDLPQTHSLGSRRTLMLLAQMRRLSLFSLCKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQNLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLSKEGGGGS GGGGSGGGGSGGGGSGVQLVQSGAEVKKPGSSVKVSCASGYTFTSYDINWVRQ APGQGLEWLGGTVPLFGISHYAQKFQGRVTITADESTSTAYMESSLRSEDTAVYY CVSSVGAGAYYYQGLDVWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCL LVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI ISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDW MSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFMYSDLRVEKKNWVERNSYS CSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 274	QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYDINWVRQAPGQGLEWLGGTVPL FGISHYAQKFQGRVTITADESTSTAYMESSLRSEDTAVYYCVSSVGAGAYYYQGLD VWGQGT LVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG PTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVLMI ISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLG APIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVKDFMPEDIYVEWTNNG KTELNYKNTEPVLKSDGYSFMYSKLTVEKKNWVERNSYSCSVVHEGLHNHHTTKSF SRTPGK
	SEQ ID NO: 275	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG VPSRFGSGSGTDFTLTISLLPEDFATYYCQQSYLPYSFGQGTLEIKRADAAPTVS IFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWKIDGSEKQNGVLNSWTDQDSKDS TYSMSSTLT LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Protein Complex	SEQ ID NO:	Sequence
AF4305	SEQ ID NO: 294	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTAYDINWVR QAPGQGLEWVGIINPGSGSPMYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCVSSVGAGAYYYYQGLDVWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPITCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTC MVTDFMPEDIYVEWTNNGKTELNYKNTEPVLSDGSYFMYSDLRVEKKNWVERN SYSCSVVHEGLHNHHTTESFSRTPGK
	SEQ ID NO: 295	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTAYDINWVRQAPGQGLEWVGIINPGS GSPMYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCVSSVGAGAYYYYQGLDVWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPITCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVK DFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLVEKKNWVERNSYSCSVV HEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
	SEQ ID NO: 296	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPKGAPKLLIYSASNLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTQWTFGQGTKVEIKRADAA PTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKEDEYERHNSYTCEATHKSTSTSPIVKSFNNEC
AF4306	SEQ ID NO: 64	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPKGAPKLLIYSASFLYS GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRADAAP TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKEDEYERHNSYTCEATHKSTSTSPIVKSFNNEC
	SEQ ID NO: 192	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVS SAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPITCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEKEMTKKQVSLTCLVK DFMPEDIYVEWTNNGKTELNYKNTEPVLKSDGSYFMYSKLVEKKNWVERNSYSCSVV HEGLHNHHTTKSFSRTPGGGGSGGGSHHHHHH
	SEQ ID NO: 297	CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVL HEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNLEACVIQGVGTETPLMK EDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKEGGGGS GGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYY CSRWGGDGFYAMDYWGQGTLLTVSSAKTTAPSVYPLAPVCGDTTGSSVT LGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNAAGGPSVFIFPPKIKDVL MISLSPITCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLGAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVT D

Protein Complex	SEQ ID NO:	Sequence
		FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSDLRVEKKNWVERNSYSCS VVHEGLHNHHTTESFSRTPGK

CLAIMS

WHAT IS CLAIMED IS:

1. A complex comprising:
 - a) a therapeutic domain;
 - b) a linker; and
 - c) a sensor domain,wherein the therapeutic domain is linked to the sensor domain by the linker, and wherein the sensor domain is configured to bind the therapeutic domain and a marker.
2. The complex of claim 1, wherein the sensor domain is bound to the therapeutic domain in an absence of the marker.
3. The complex of claim 1, wherein when the sensor domain binds to the marker, the therapeutic domain is blocked from binding the sensor domain.
4. The complex of any one of claims 1 or 2, wherein when the therapeutic domain binds to the sensor domain, the activity of the therapeutic domain is reduced.
5. The complex of any one of claims 1 or 3, wherein when the sensor domain binds to the marker, the therapeutic domain is configured to exhibit therapeutic activity.
6. The complex of any one of claims 1, 3, or 5, wherein when the sensor domain binds to the marker, the therapeutic domain is therapeutically active.
7. The complex of any one of claims 1-6, wherein an affinity of the sensor domain for the therapeutic domain comprises a condition dependence.
8. The complex of claim 7, wherein the condition dependence is selected from the group consisting of pH, temperature, salinity, and osmolarity.
9. The complex of any one of claims 1-8, wherein the sensor domain comprises an antibody.
10. The complex of claim 9, wherein the antibody is an antibody fragment or an antibody derivative.
11. The complex of any one of claims 1-10, wherein the complex comprises an Fc domain.
12. The complex of any one of claims 1-11, wherein the complex comprises a domain that improves kinetic properties.
13. The complex of any one of claims 1-12, wherein the complex comprises a serum circulation half-life of at least 12, 24, or 48 hours.
14. The complex of any one of claims 1-13, wherein the complex comprises a plurality of separately expressed subunits.
15. The complex of any one of claims 1-14, wherein the complex includes two heavy chains and two light chains.

16. The complex of any one of claims 1-15, wherein the complex comprises a second therapeutic domain.
17. The complex of claim 16, wherein said second therapeutic domain is different than said therapeutic domain.
18. The complex of claim 16, wherein said second therapeutic domain is identical to said therapeutic domain.
19. The complex of any one of claims 1-18, wherein the complex comprises a second sensor domain.
20. The complex of claim 19, wherein said sensor domain and said second sensor domain target said therapeutic domain.
21. The complex of claim 20, wherein said sensor domain and said second sensor domain comprise similar affinities for said therapeutic domain.
22. The complex of claim 21, wherein said sensor domain and said second sensor domain comprise affinities for said therapeutic domain which differ by at least one order of magnitude.
23. The complex of either of claims 21 or 22, wherein said second sensor domain targets the marker.
24. The complex of any one of claims 21 or 22, wherein said second sensor domain does not target the marker.
25. The complex of any one of claims 19-24, wherein said second sensor domain targets a second marker.
26. The complex of claim 25, wherein the activity of said therapeutic domain is requisite upon binding of said sensor domain to said marker and said second sensor domain to said second marker.
27. The complex of either of claims 25 or 26, wherein said marker and said second marker are associated with a same cell type.
28. The complex of claim 27, wherein said cell type is a diseased cell type.
29. The complex of any one of claims 23-28, wherein said second sensor domain does not target said therapeutic domain.
30. The complex of any one of claims 23-29, wherein said second sensor domain targets said second therapeutic domain.
31. The complex of claim 29, wherein said second sensor domain does not target a therapeutic domain.
32. The complex of any one of claims 1-31, wherein the complex is a regulated therapeutic protein.

33. The complex of any one of claims 1-32, wherein the therapeutic domain comprises a cytokine, a chemokine, an antibody, an antibody fragment, a peptide agonist, a peptide antagonist, an enzyme, a soluble receptor, a growth factor, a protein toxin, a soluble ligand, a small molecule, or any combination thereof.
34. The complex of any one of claims 9-33, wherein the antibody or the antibody fragment comprises an IgG, a single domain antibody fragment, a nanobody, an scFab, or a single chain variable fragment (scFv).
35. The complex of any one of claims 1-34, wherein the therapeutic domain comprises an IL-2 receptor agonist.
36. The complex of claim 35, wherein the IL-2 receptor agonist is IL-2, IL-15, or variants or fusions thereof.
37. The complex of any one of claims 1-36, wherein the therapeutic domain comprises IFN α , IFN γ , IL-12, IL-4, IL-8, IL-10, IL-15, IL-18, IL-21, TGF beta, an anti-CD3 antibody, an anti-CD28 antibody or ligand, an antibody to or ligand of CD40, GITR, OX40, CD137, CD27, or Death Receptors, the extracellular domain of TGFBR2, VEGF-C, kynureninase, IL-7, TNF, MICA, MICB, CD47, an anti-CTLA4 antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody.
38. The complex of any one of claims 1-37, wherein the therapeutic domain binds to the sensor domain.
39. The complex of any one of claims 1-38, wherein the therapeutic domain, the linker, and the sensor domain are expressed as single peptide respectively.
40. The complex of any one of claims 1-39, wherein the linker comprises a polypeptide.
41. The complex of any one of claims 1-40, wherein the linker comprises from 2 to 200 amino acids in length.
42. The complex of either of claims 40 or 41, wherein the polypeptide of the linker lacks a human protease cleavage site.
43. The complex of any one of claims 1-42, wherein the linker is: attached to a heavy chain of the sensor domain, attached to a light chain of the sensor domain, is a fusion with an N-terminus of the sensor domain, or is a fusion with a C-terminus of the sensor domain.
44. The complex of any one of claims 1-42, wherein the linker is: attached to a heavy chain of the therapeutic domain, attached to a light chain of the therapeutic domain, is a fusion with an N-terminus of the therapeutic domain, or is a fusion with a C-terminus of the therapeutic domain.
45. The complex of any one of claims 1-44, wherein the activity of the therapeutic domain is reduced when bound to the sensor domain.

46. The complex of any one of claims 1-45, wherein the therapeutic domain is inactive when bound to the sensor domain.
47. The complex of any one of claims 1-46, wherein the sensor domain blocks the activity of the therapeutic domain when bound to the therapeutic domain.
48. The complex of any one of claims 1-47, wherein the therapeutic domain is active when the sensor domain is bound to the marker.
49. The complex of any one of claims 1-48, wherein an affinity of the sensor domain for the marker is equal to or greater than an affinity of the sensor domain for the therapeutic domain.
50. The complex of any one of claims 1-49, wherein an affinity of the sensor domain for the marker is at least 2 times, 5 times, 10 times, 100 times, 1000 times, 10000, or 100000 times greater than an affinity of the sensor domain for the therapeutic domain.
51. The complex of any one of claims 1-50, wherein the sensor domain is an antibody or a fragment thereof.
52. The complex of any one of claims 1-51, wherein the sensor domain comprises one or both antigen binding domains of a bispecific antibody.
53. The complex of any one of claims 1-51, wherein the sensor domain comprises two or more antigen binding domains of a bispecific antibody.
54. The complex of any one of claims 1-51, wherein the sensor domain comprises three or more antigen binding domains of a bispecific antibody
55. The complex of claim 52, wherein the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and is capable of binding to the marker, and a second antigen binding domain that is capable of binding to the marker.
56. The complex of claim 52, wherein the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and the marker and a second antigen binding domain that is capable of binding to a second marker.
57. The complex of claim 52, wherein the bispecific antibody comprises a first antigen binding domain that is capable of binding to the therapeutic domain and the marker and a second antigen binding domain that is capable of binding to the therapeutic domain and a second marker.
58. The complex of any one of claims 52-57, wherein the bispecific antibody comprises a single therapeutic domain.
59. The complex of any one of claims 54-56, wherein the therapeutic domain is IFN α , the first marker is ATP, and the second marker is CEA.

60. The complex of any one of claims 1-57, wherein the sensor domain binds to an IL-2 receptor agonist and to PD-1.
61. The complex of claim 58, wherein the IL-2 receptor agonist is IL-2, IL-15, or variants or fusions thereof.
62. The complex of any one of claims 1-61, wherein the sensor domain is configured to bind the therapeutic domain, the marker, and a second marker.
63. The complex of claim 62, wherein a single Fab of the sensor domain is configured to bind the therapeutic domain, the marker, and the second marker.
64. The complex of either of claims 62 or 63, wherein the sensor domain is configured to bind a third marker.
65. The complex of claim 64, wherein said single Fab of the sensor domain is configured to bind to said third marker.
66. The complex of any one of claims 1-65, wherein the sensor domain binds to IFN α and PD-L1.
67. The complex of any one of claims 1-66, wherein the marker is a surface protein, a cell surface marker, or soluble ATP.
68. The complex of any one of claims 1-67, wherein the marker is a secreted protein.
69. The complex of any one of claims 1-67, wherein the marker is expressed by a cancer cell.
70. The complex of any one of claims 1-67, wherein the marker is expressed by an immune cell.
71. The complex of any one of claims 1-70, wherein the marker is PD-1.
72. The complex of any one of claims 1-70, wherein the marker is PD-L1.
73. The complex of any one of claims 1-70, wherein the marker is CEACAM5.
74. The complex of any one of claims 1-70, wherein the marker is FAP.
75. The complex of any one of claims 1-70, wherein the marker is LRRC15.
76. The complex of any one of claims 1-70, wherein the marker is expressed by a stromal cell.
77. The complex of any one of claims 1-70, wherein the marker is expressed by an endothelial cell.
78. The complex of any one of claims 1-70, wherein the marker is a metabolite.
79. The complex of any one of claims 1-70, wherein the marker is adenosine, AMP, ADP, or ATP.
80. The complex of any one of claims 1-70, wherein the marker is kynurenine.
81. The complex of any one of claims 1-80, wherein the sensor domain comprises a complementarity determining region selected from **TABLE 13**.
82. The complex of any one of claims 1-81, wherein the sensor domain is selected from **TABLE 13**.

83. The complex of any one of claims 1-82, wherein the complex is selected from **TABLE 15**.
84. The complex of any one of claims 1-83, wherein the sensor domain comprises a complementarity determining region having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 1 – SEQ ID NO: 20, SEQ ID NO: 142 – SEQ ID NO: 173, or SEQ ID NO: 238-252.
85. The complex of any one of claims 1-83, wherein the sensor domain has at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 21 – SEQ ID NO: 27, SEQ ID NO: 31 – SEQ ID NO: 39, or SEQ ID NO: 127 – SEQ ID NO: 141.
86. The complex of any one of claims 1-83, wherein the protein complex has at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or 100% sequence identity to any one of SEQ ID NO: 41, SEQ ID NO: 44, SEQ ID NO: 80 – SEQ ID NO: 112, SEQ ID NO: 174-175, SEQ ID NO: 181-182, SEQ ID NO: 195-196, SEQ ID NO: 205-206, SEQ ID NO: 210-212, SEQ ID NO: 220-223, SEQ ID NO: 226-231, SEQ ID NO: 259-261, SEQ ID NO: 266-282, or SEQ ID NO: 289- 293.
87. A method comprising administering the complex of any one of claims 1-86 to a subject in need thereof.
88. A method of treating a subject in need thereof comprising administering the complex of any one of claims 1-86 to the subject in need thereof.
89. The method of claim 88, wherein the administering comprises intravenous, intramuscular, or subcutaneous administration.
90. The method of any one of claims 88-89, wherein the subject in need thereof has cancer.
91. The method of any one of claims 88-90, wherein the subject in need thereof has an autoimmune disease.
92. The method of any one of claims 88-91, wherein the subject in need thereof has a viral disease.
93. The method of any one of claims 88-82, wherein the therapeutic domain treats the subject in need thereof.
94. The method of any one of claims 88-83, wherein the subject in need thereof is a mammal.
95. The method of claim 94, wherein the subject in need thereof is a human.
96. A composition comprising a recombinant nucleic acid encoding the complex of any of claims 1-86.
97. A pharmaceutical composition comprising the complex of any of claims 1-86 and a pharmaceutically acceptable excipient.

98. A pharmaceutical composition comprising the composition of claim 96 and a pharmaceutically acceptable excipient.

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FIG. 1A

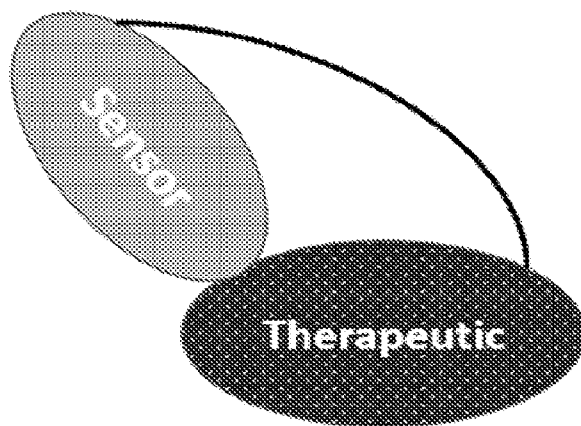
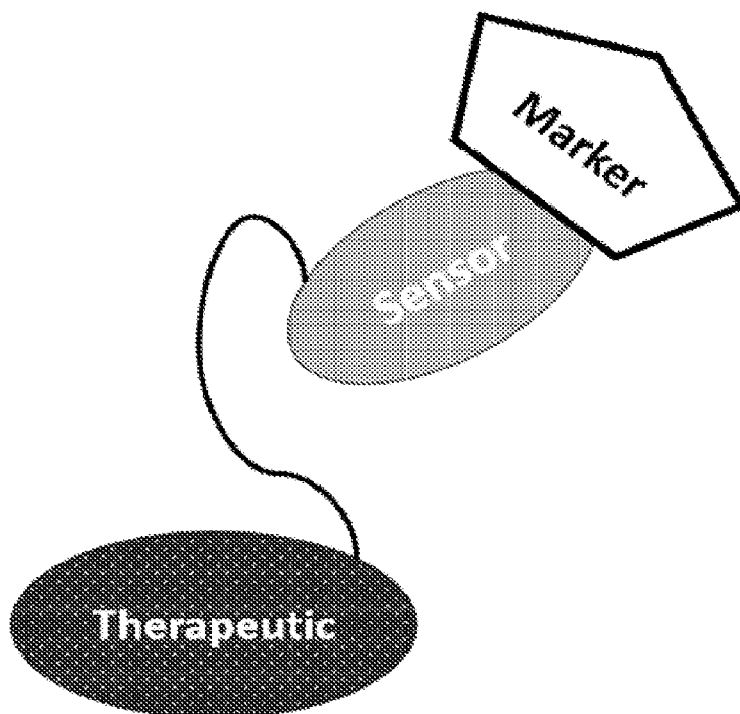


FIG. 1B



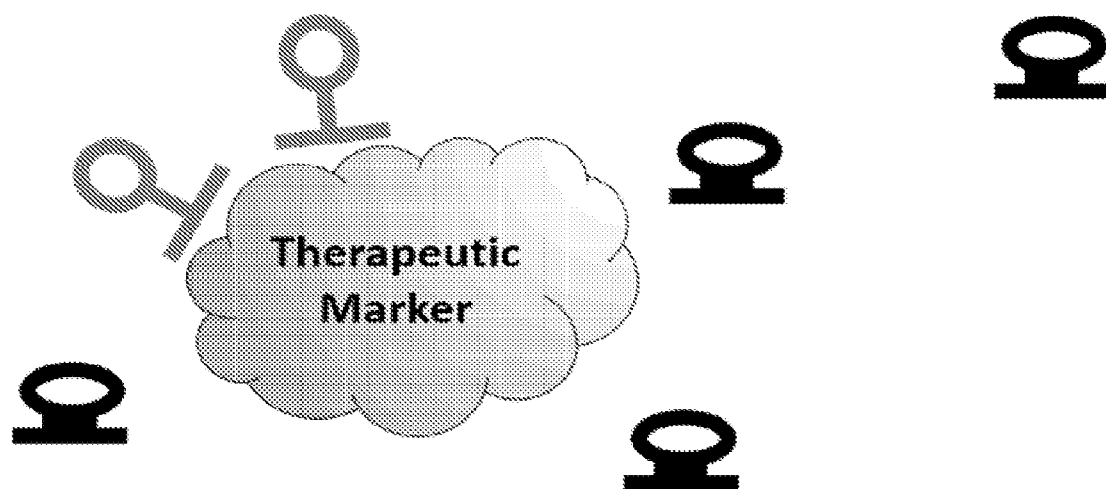
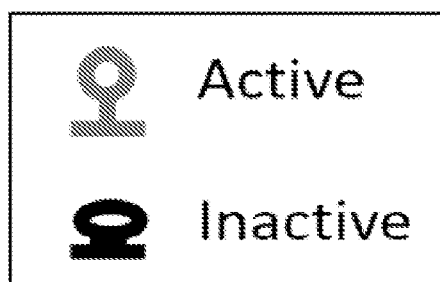


FIG. 2

CA 03177843 2022- 11- 3

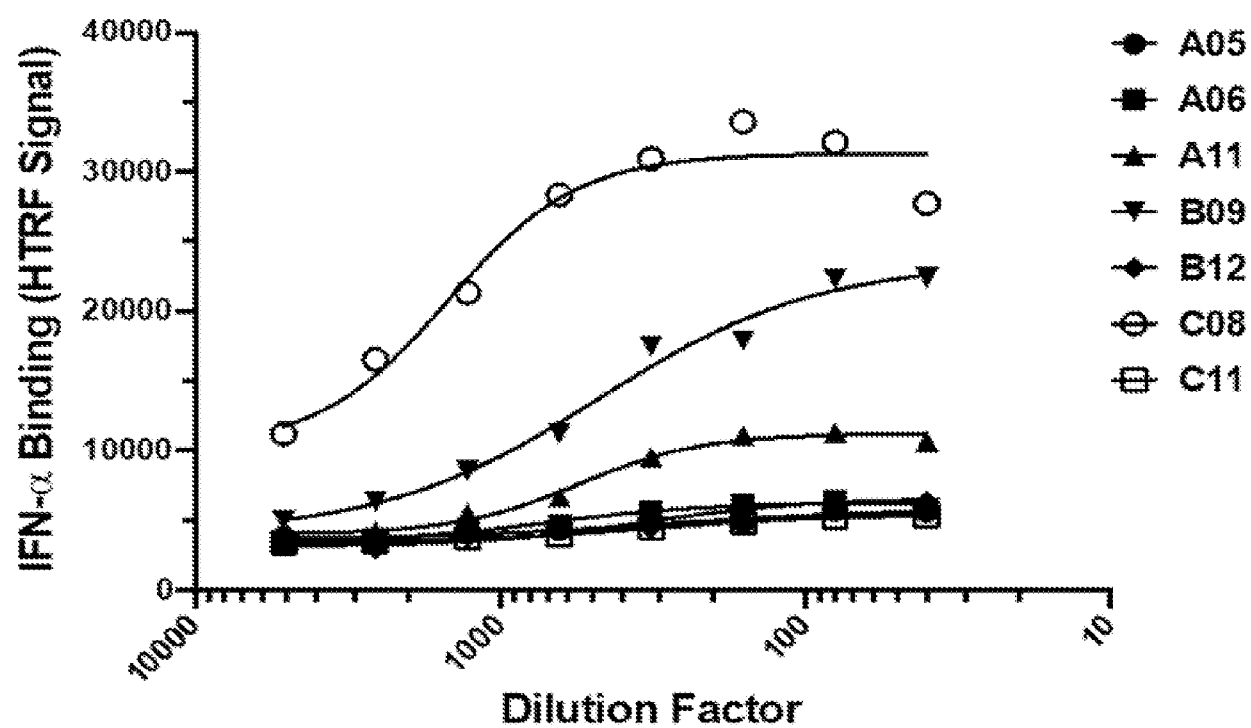


FIG. 4

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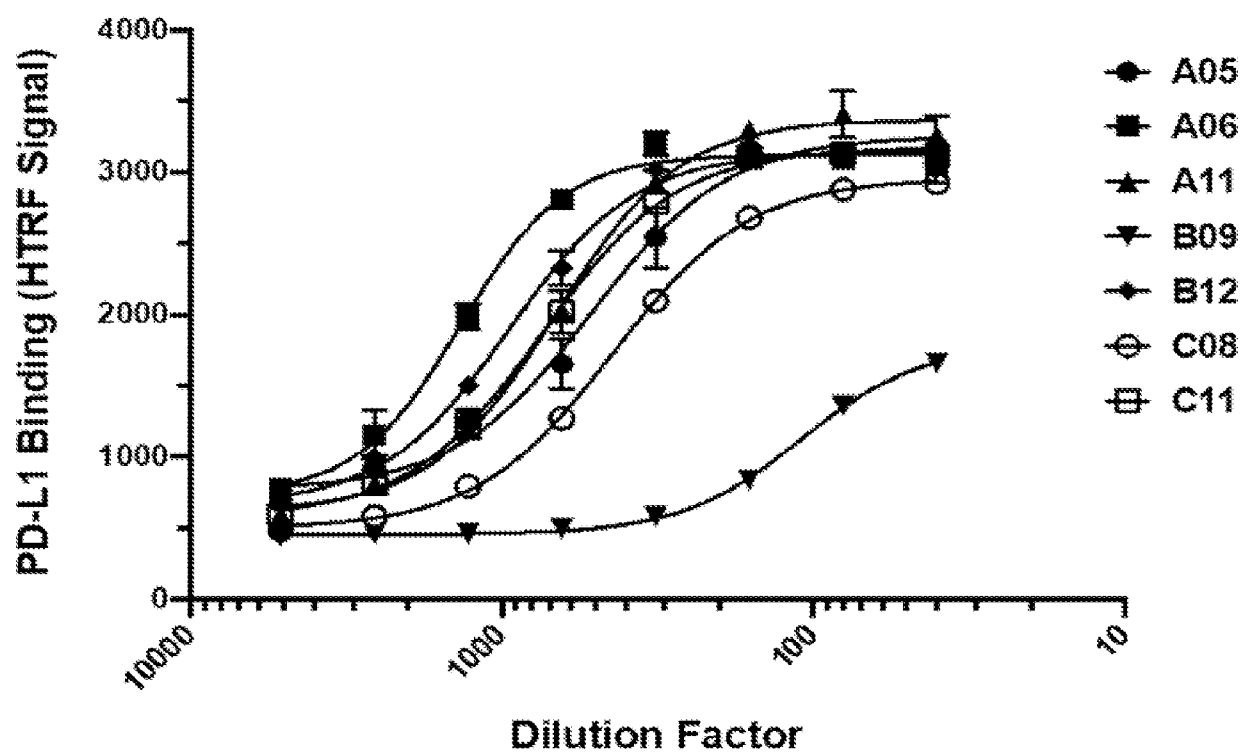


FIG. 5

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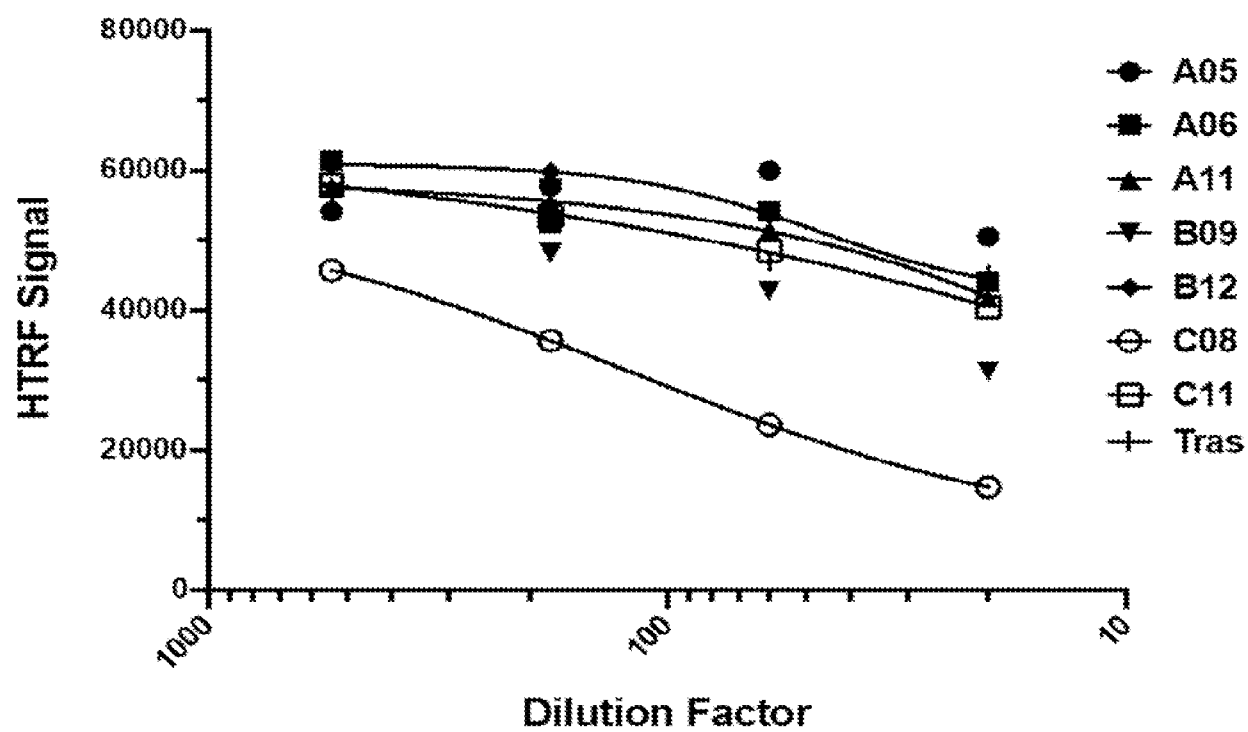


FIG. 6

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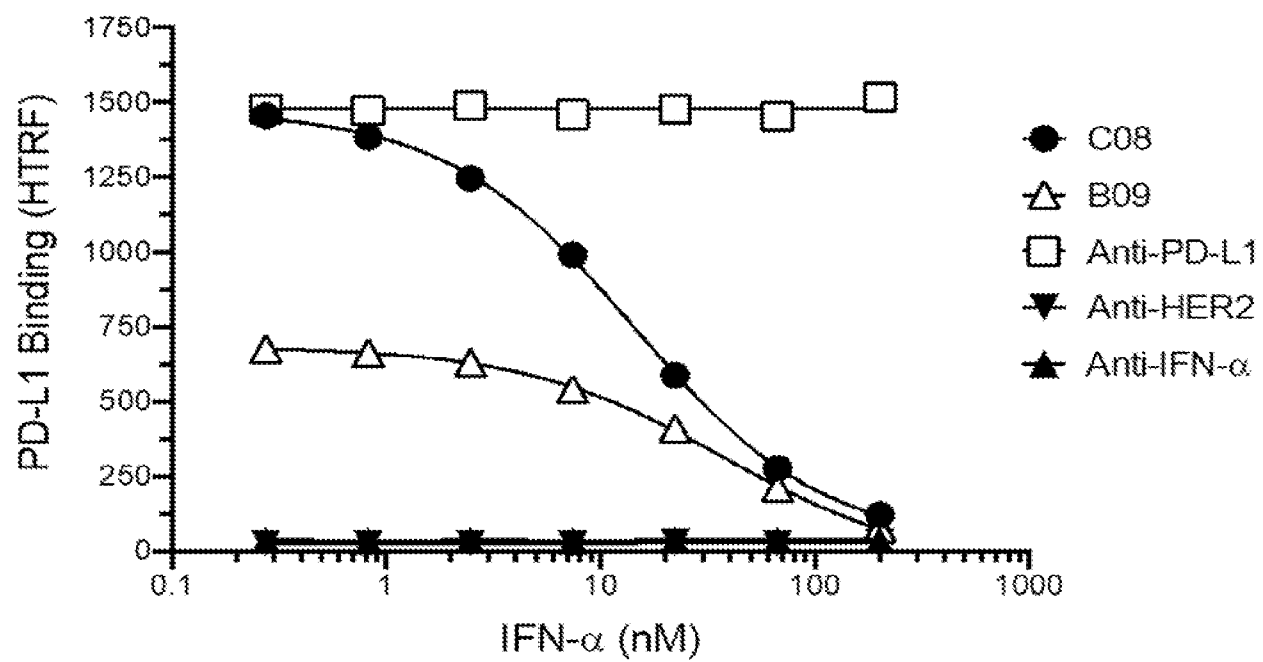
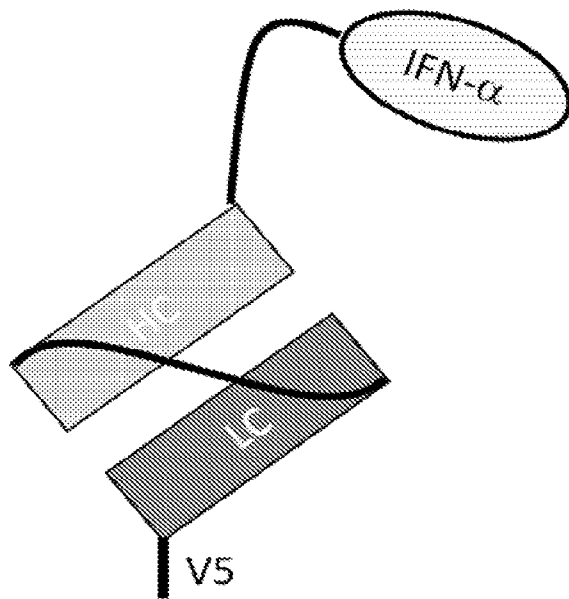


FIG. 7



MSTSTCDLPQTHSLGSRRTLML
 LAQMRRISLFSCLKDRHDFGFP
 QEEFGNQFQKAETIPVLHEMIQ
 QIFNLFSTKDSSAAWDETLLDK
 FYTELYQQQLNDLEACVIQGVGV
 TETPLMKEDSILAVRKYFQRIT
 LYLKEKKYSPCAWEVVRAEIMR
 SFSLSSTNLQESLRSKE
GGGGSGGGGSGGGGSGGGGS
 QVQLVQSGAEVKKPGASVKVSC
 KASGYTFSNYYVHWVRQAPGQG
 LEWMGWMDPNSGGTGYAHQFQG
 RVTMTRDTSTSTVYMELSSLRS
 EDTAVYYCAKEVFSGWYDYWGQ
 GTLVTVSS
ASGGGSGGGGSGGGGSHAS
 DIQMTQSPSSLSASVGDRVIT
 CRASQSISSYLNWYQQKPGKAP
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 QQSYSTPYTFGGQGTKVEIK
GKPIPNPLLGLDST

FIG. 8

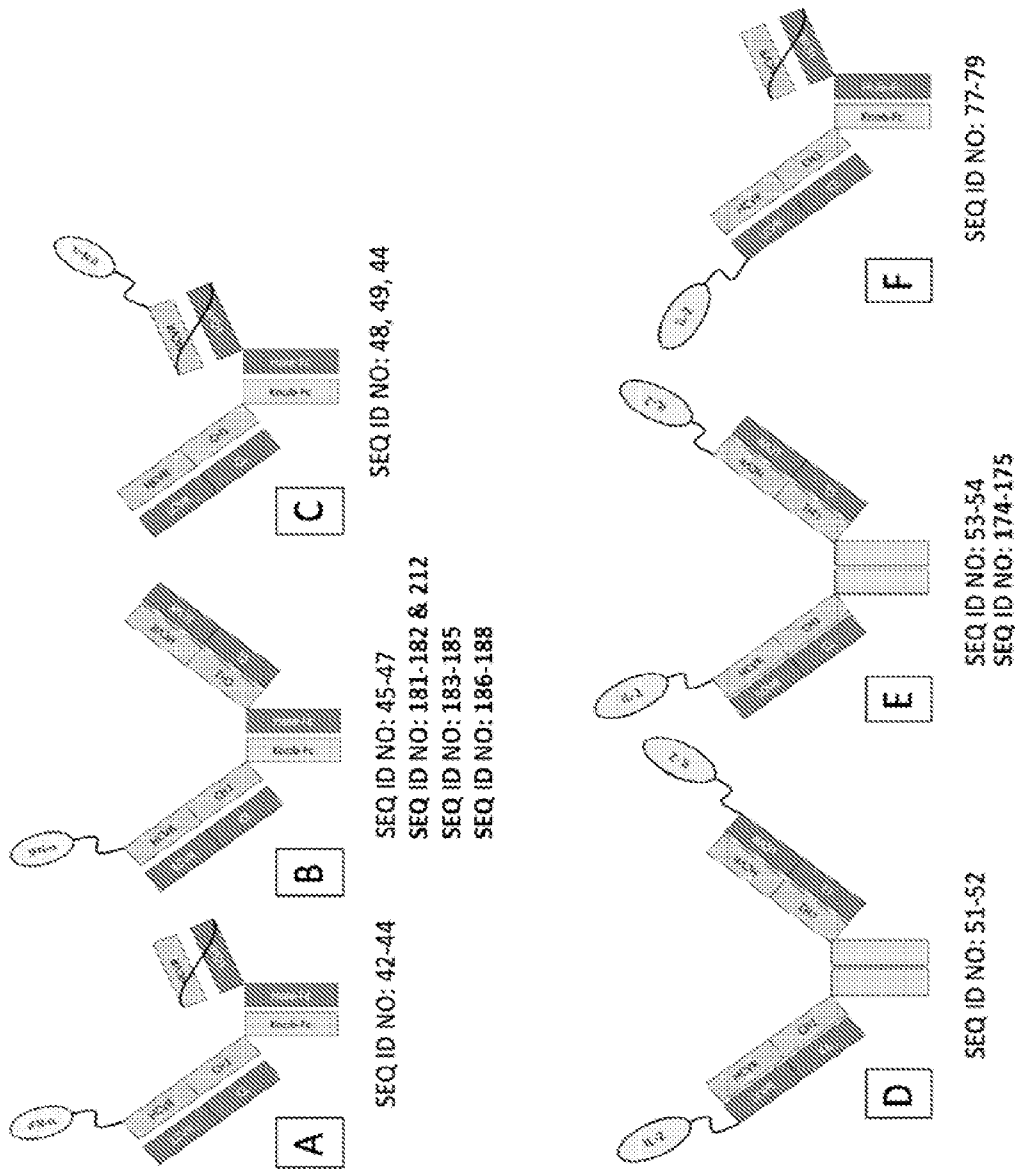


FIG. 9

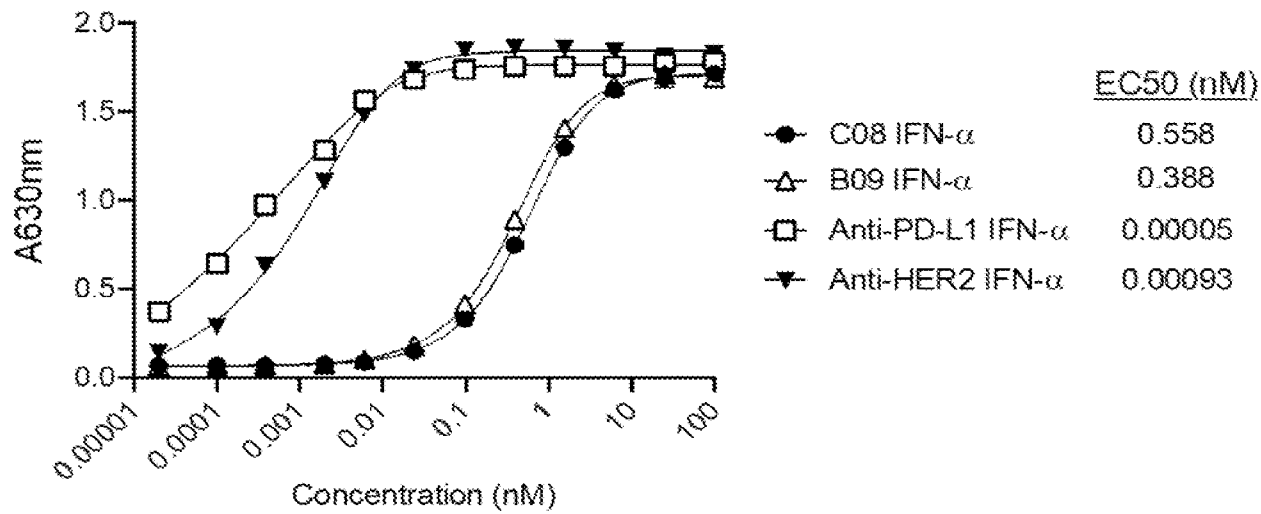


FIG. 10

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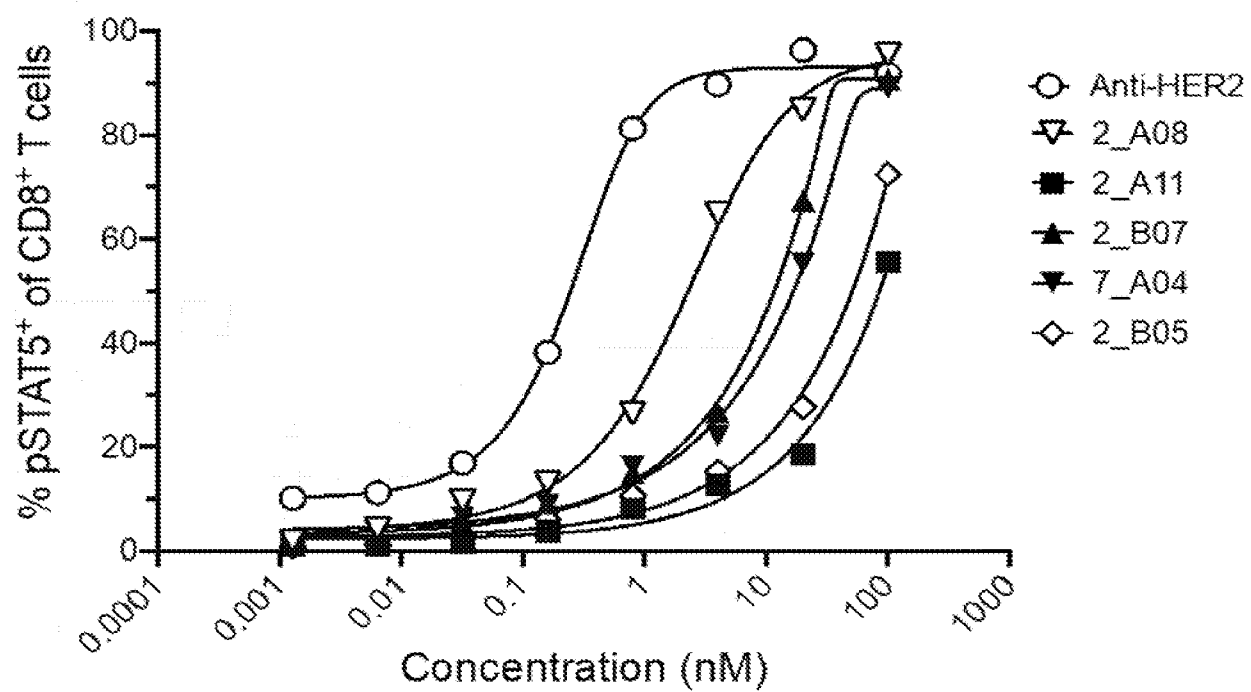


FIG. 11

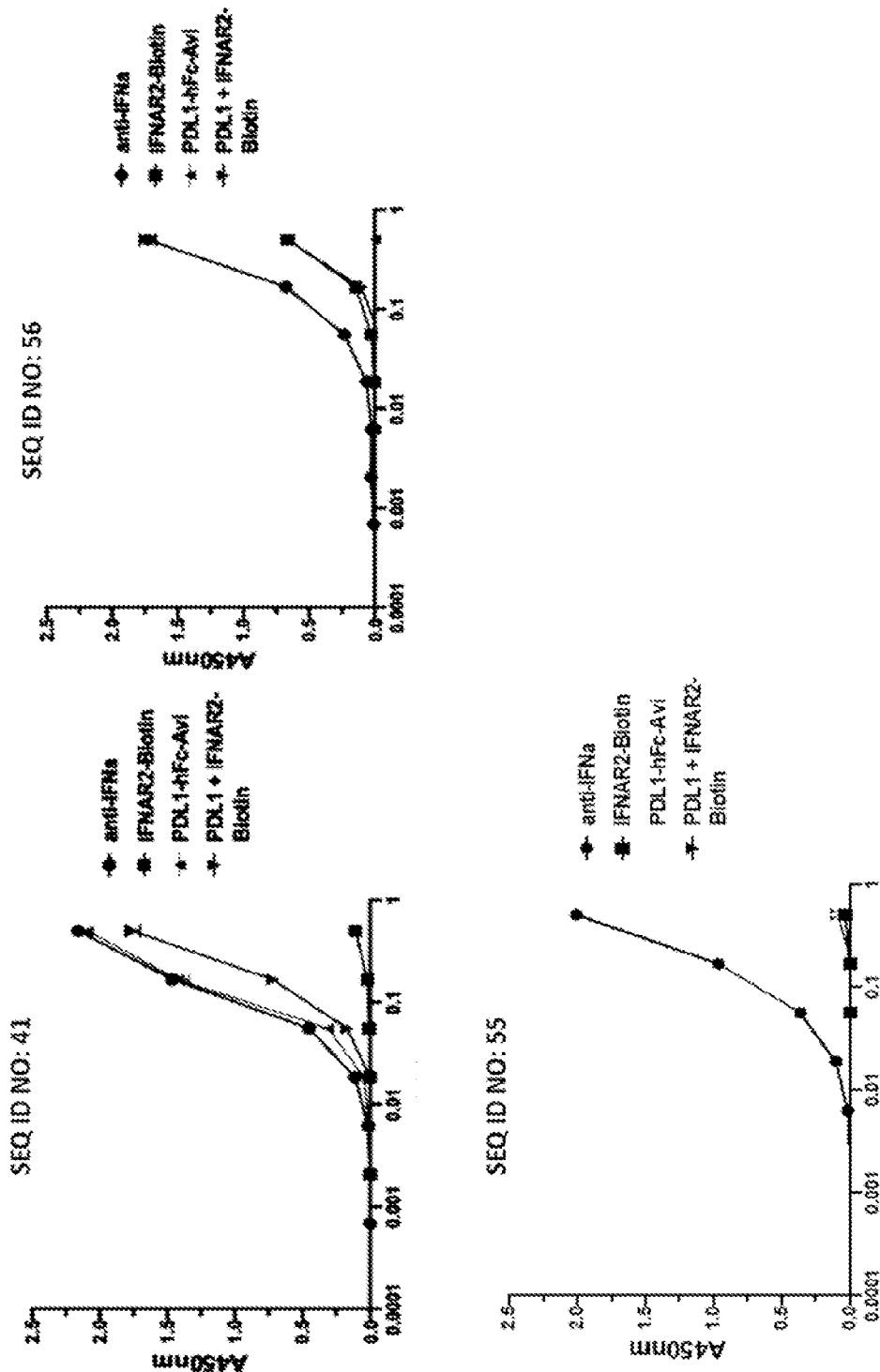


FIG. 12

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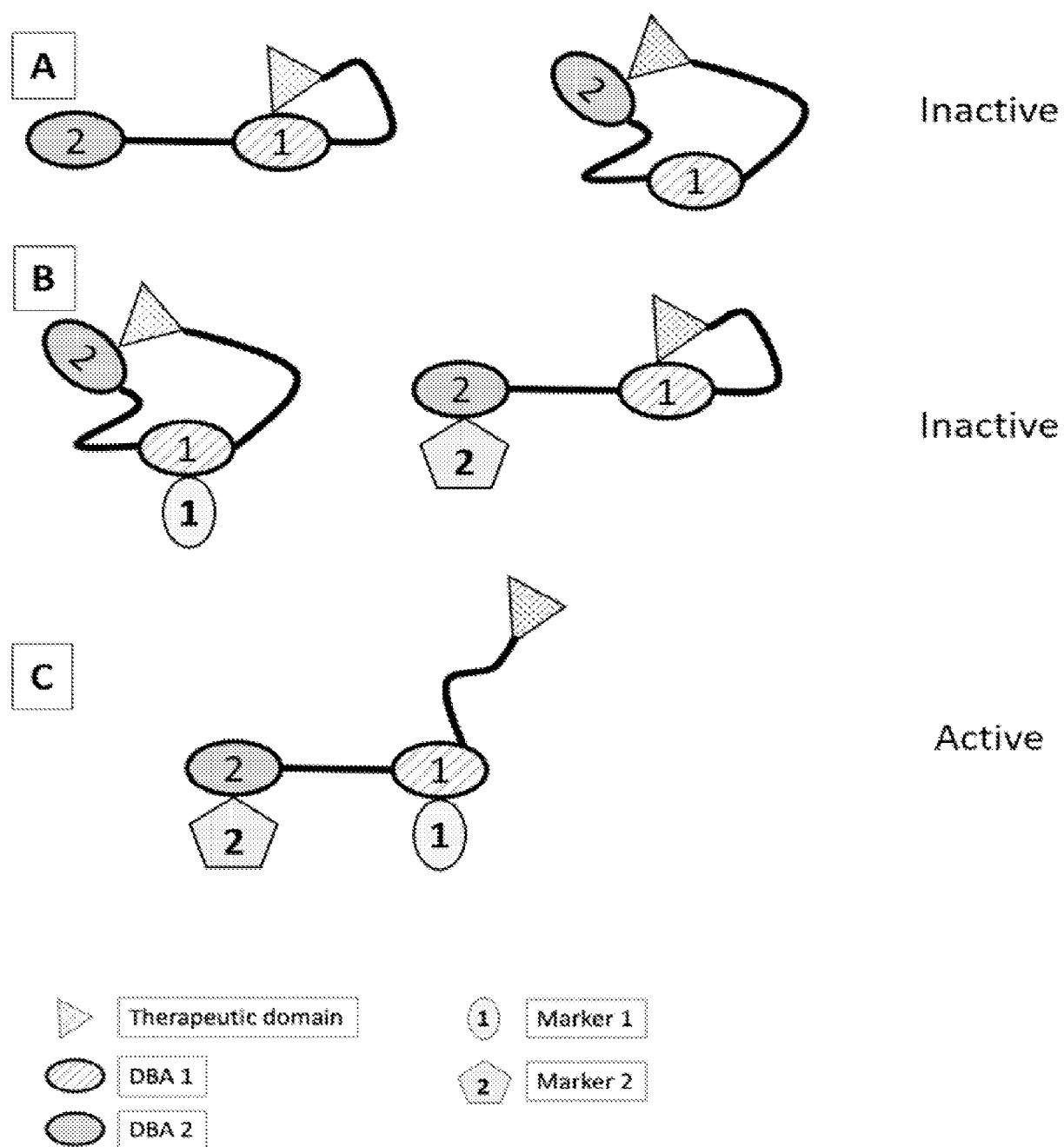


FIG. 13

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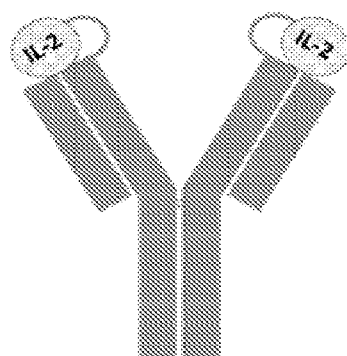


FIG. 14 A

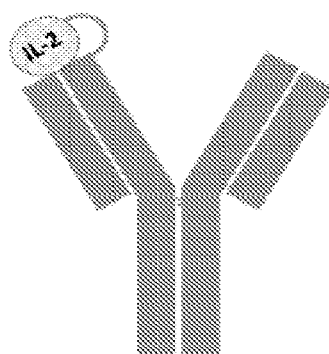


FIG. 14B

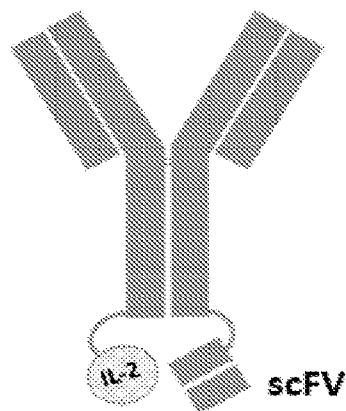


FIG. 14C

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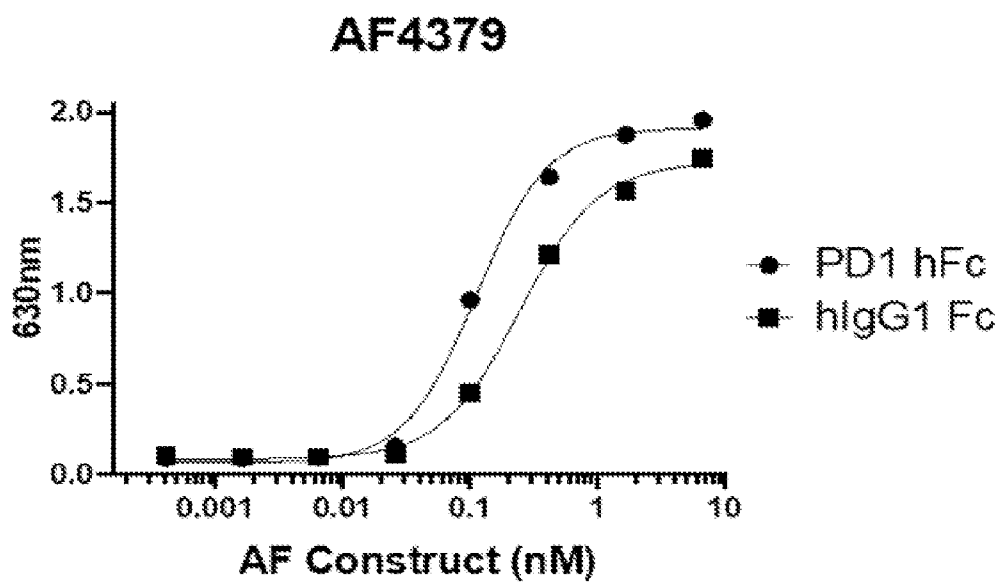


FIG. 15A

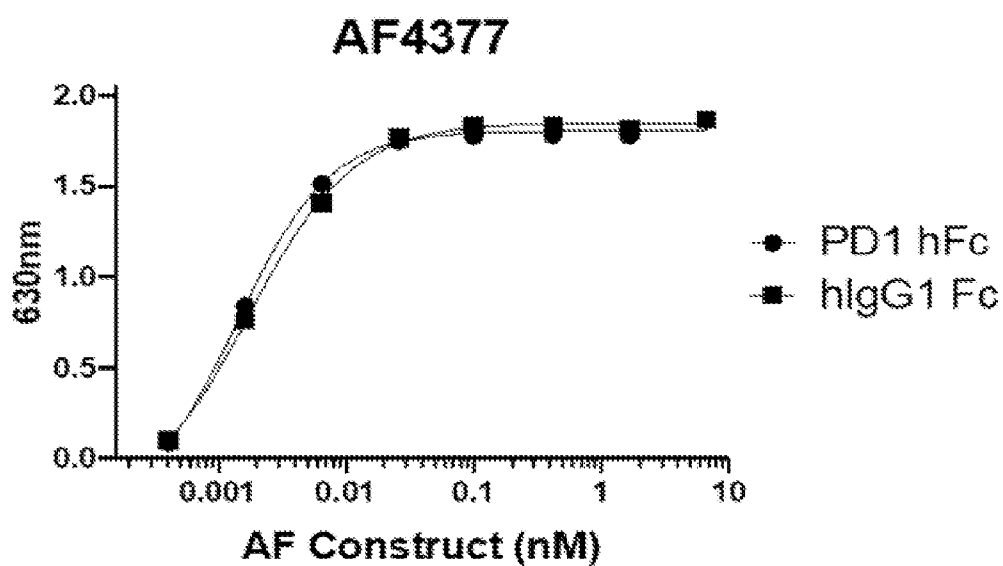


FIG. 15B

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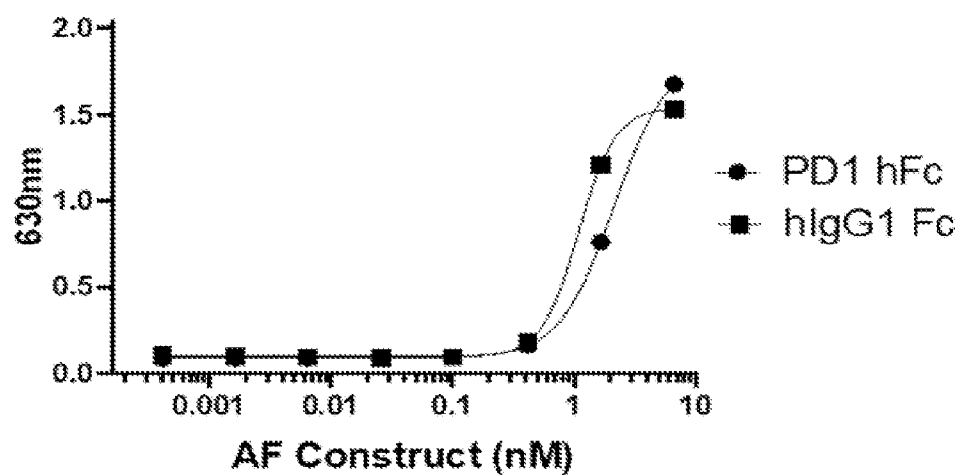
AF4378

FIG. 15C

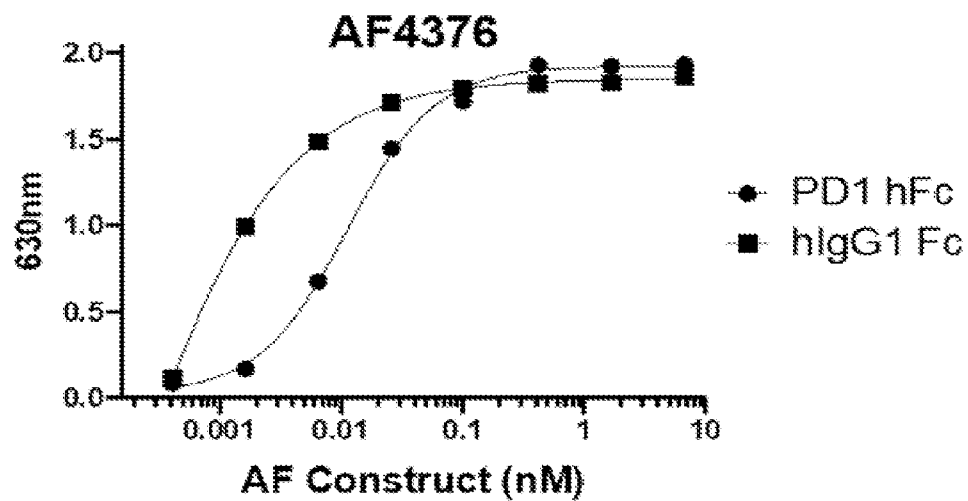


FIG. 15D

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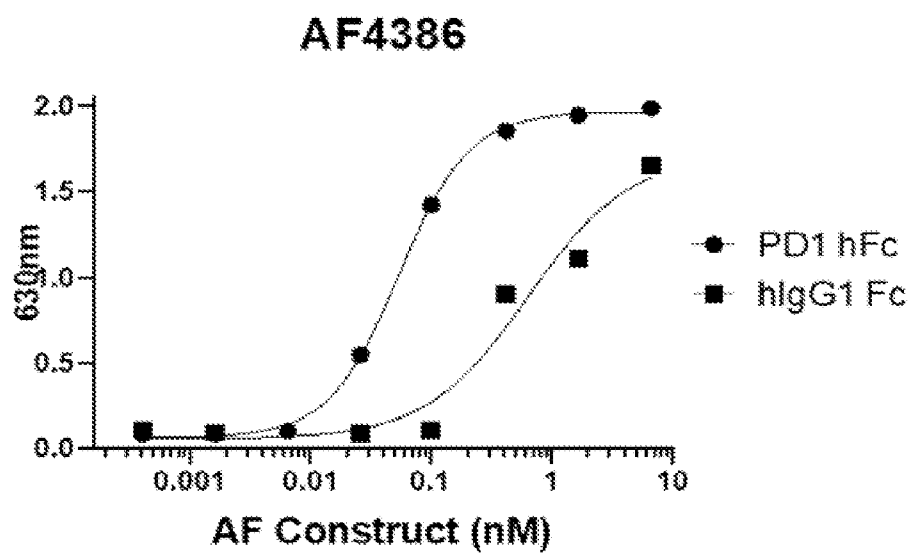


FIG. 16A

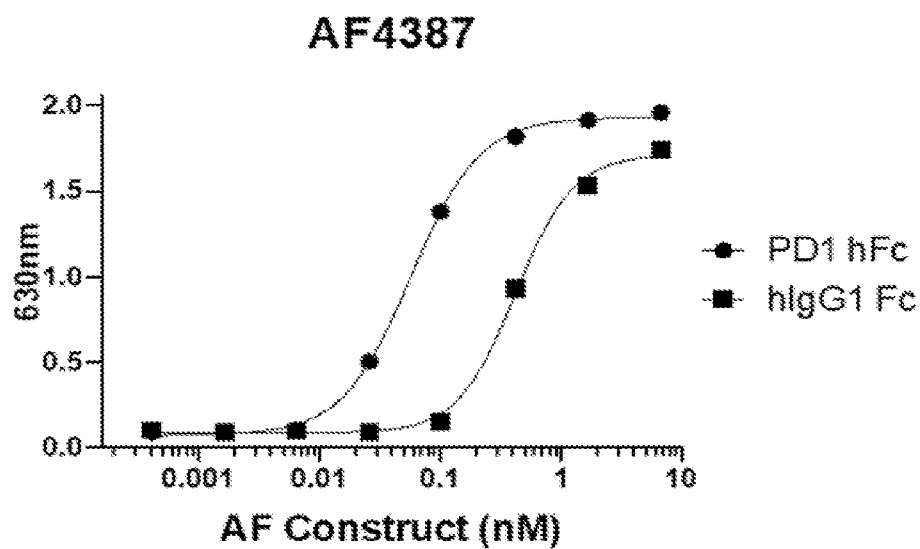


FIG. 16B

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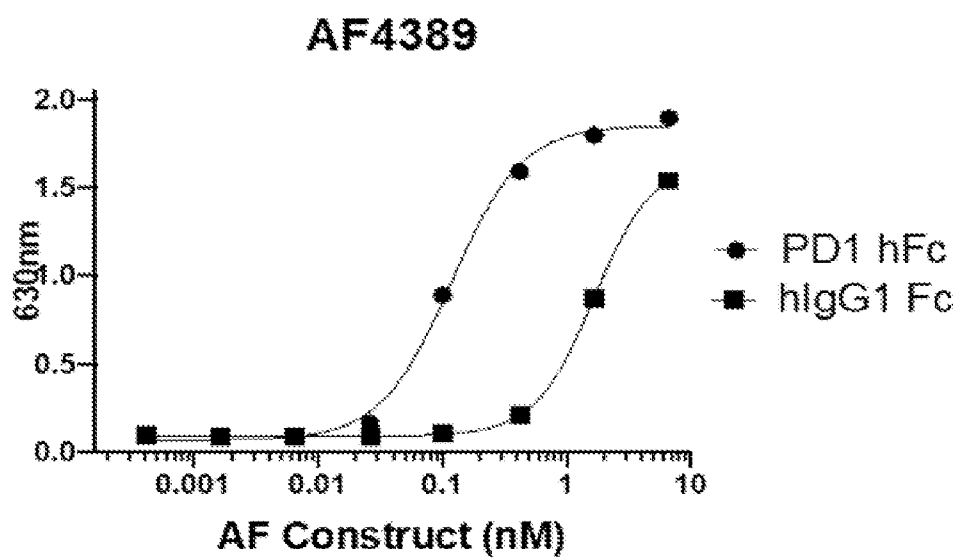


FIG. 16C

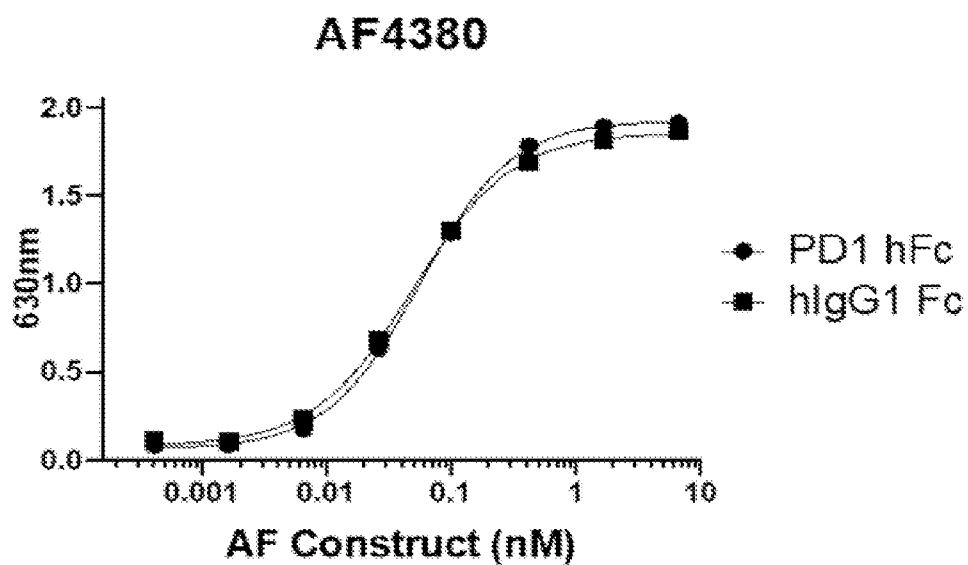


FIG. 16D

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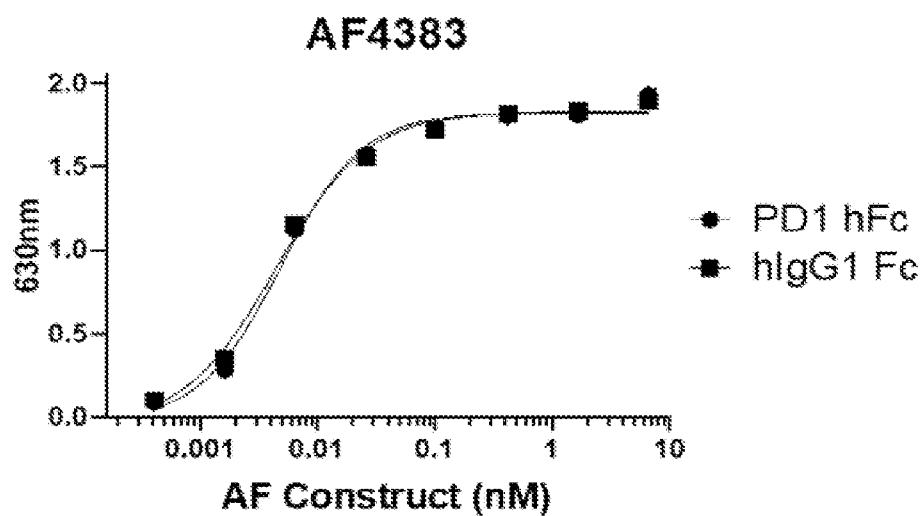


FIG. 16E

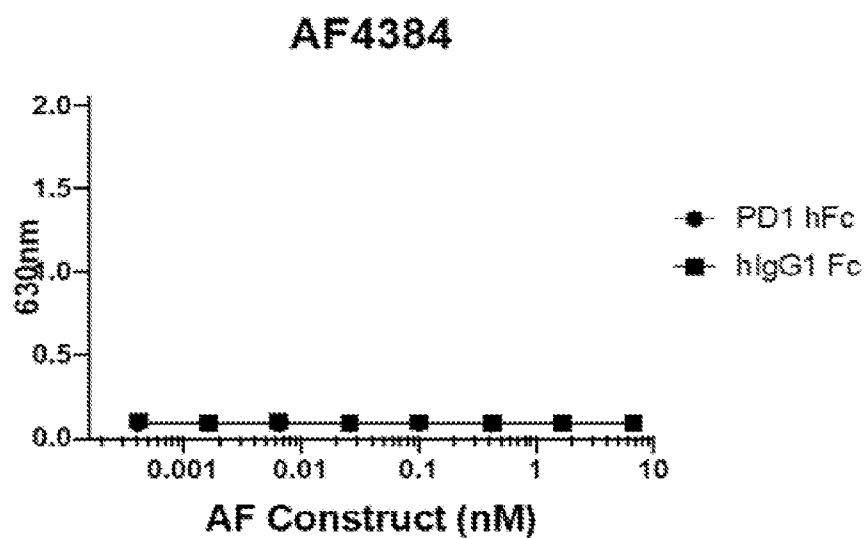


FIG. 16F

Fab: Her2

PD1

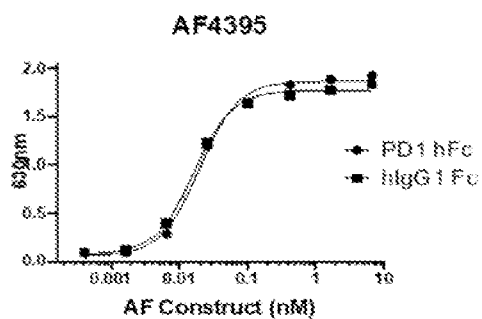
scFvPD1/IL2 DBA
2B07 variant

FIG. 17A

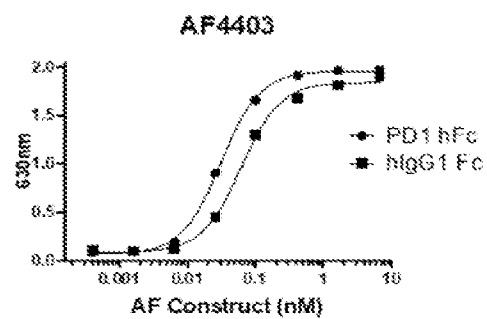


FIG. 17B

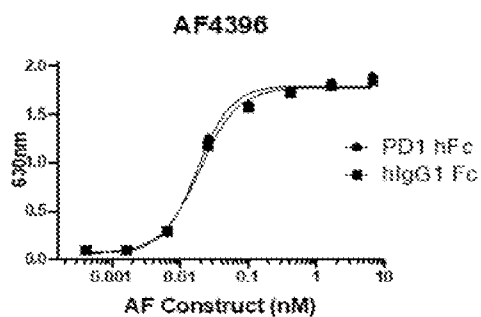
PD1/IL2 DBA
7A04 variant

FIG. 17C

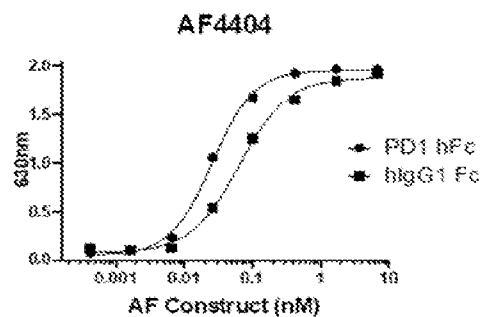


FIG. 17D

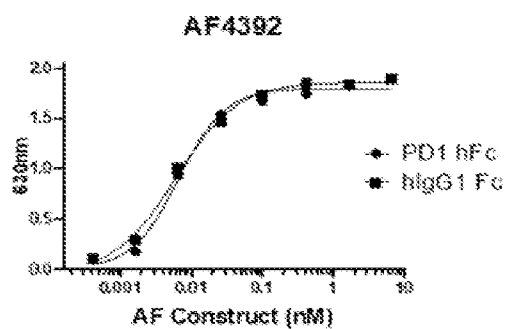
Fab:**Her2****PD1****scFv****Her2**

FIG. 17E

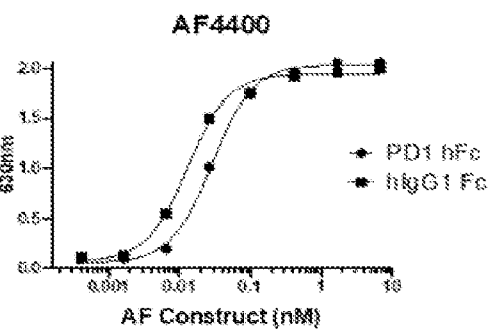


FIG. 17F

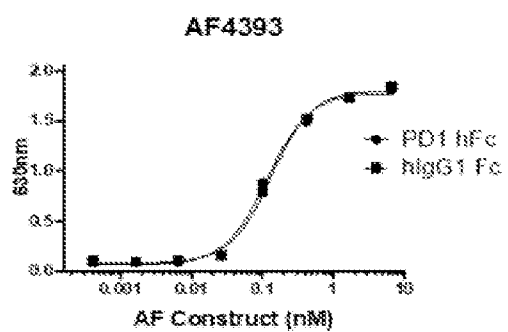
IL-2

FIG. 17G

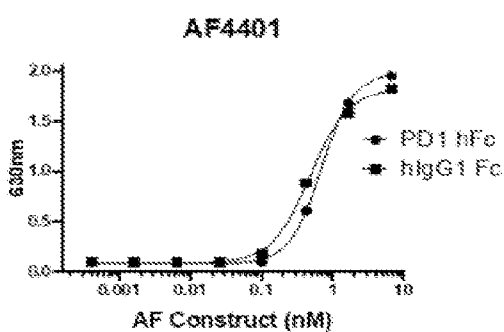


FIG. 17H

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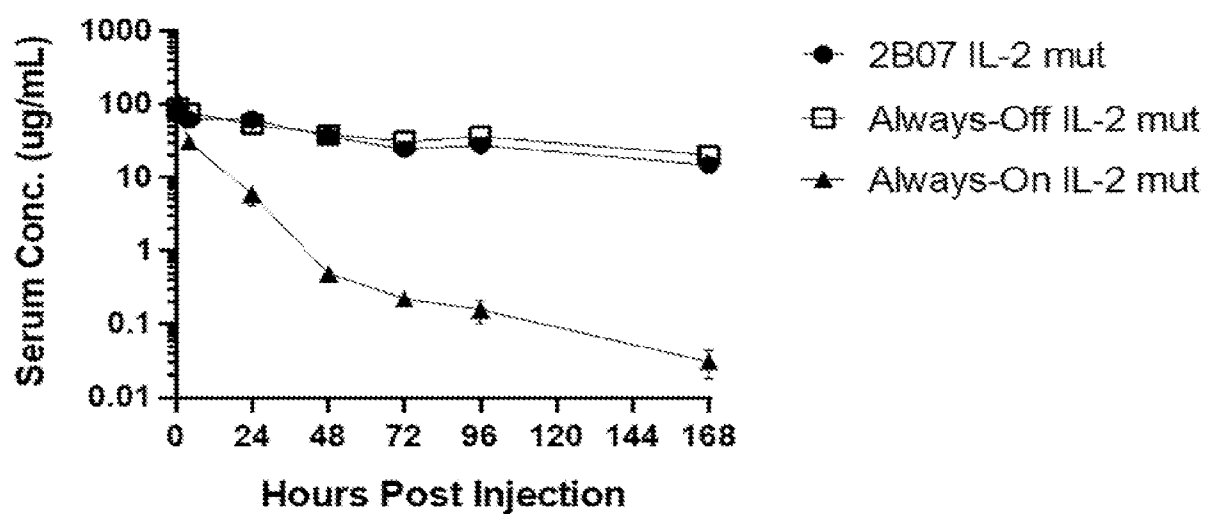
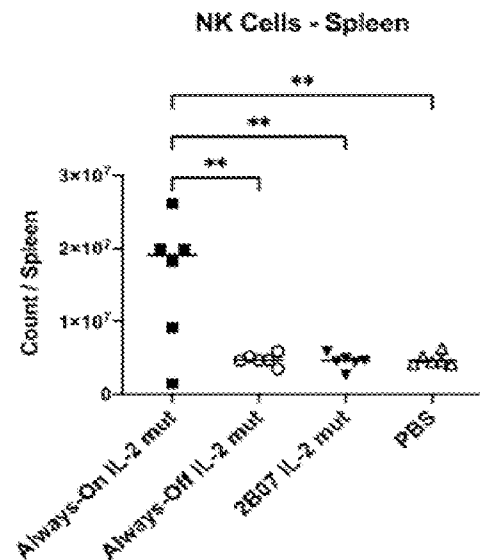
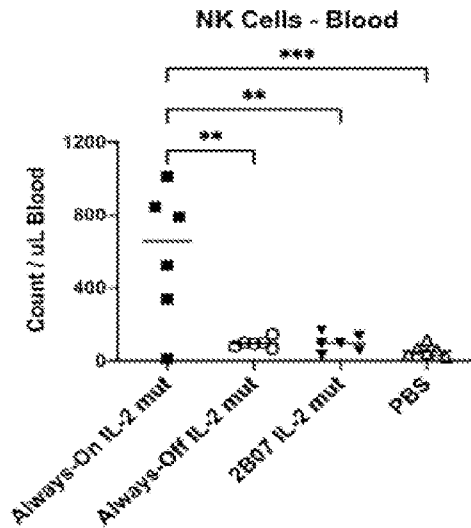
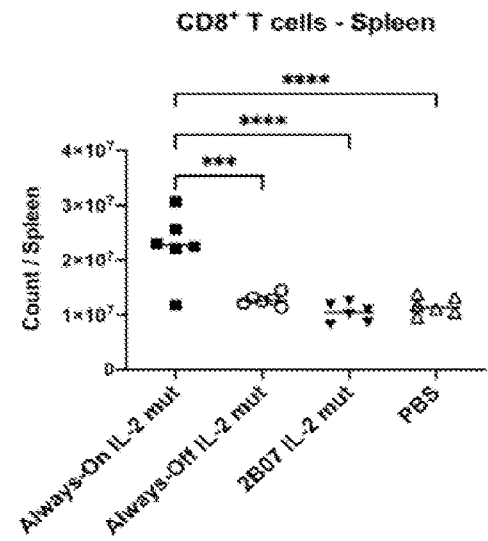
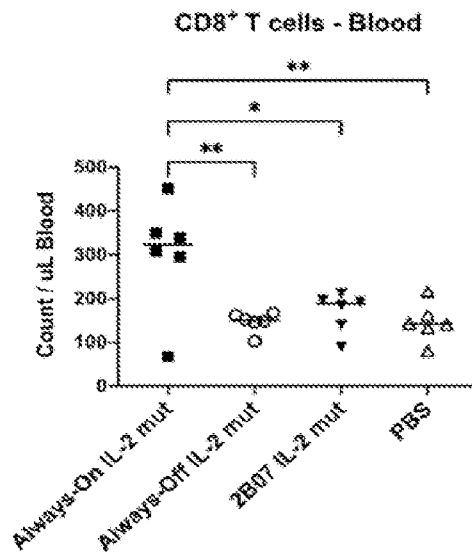


FIG. 18



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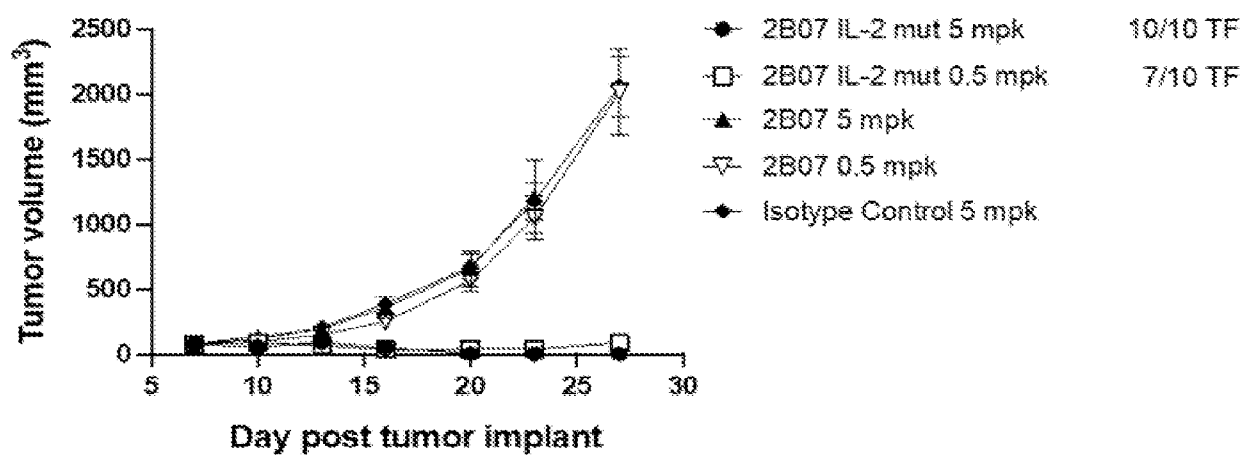


FIG. 20

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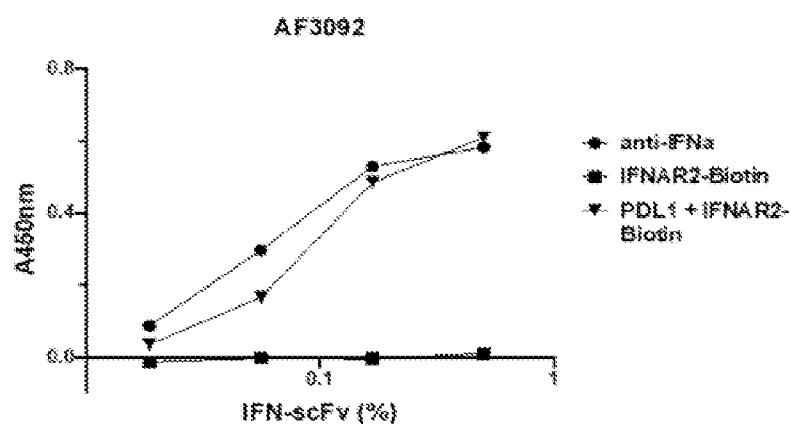


FIG. 21A

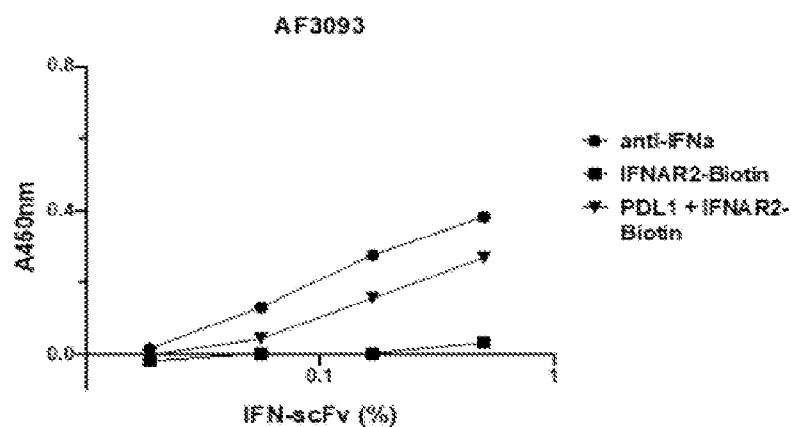


FIG. 21B

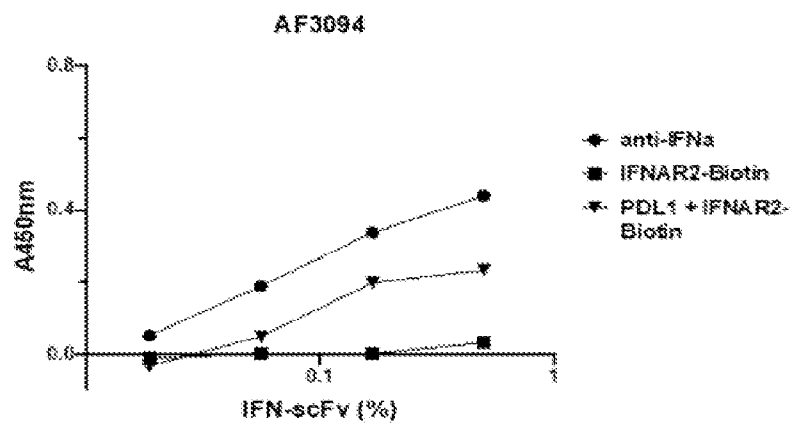


FIG. 21C

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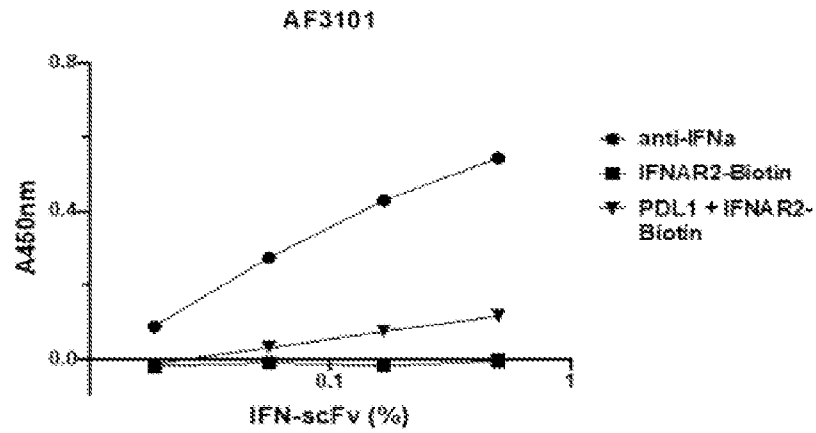


FIG. 21D

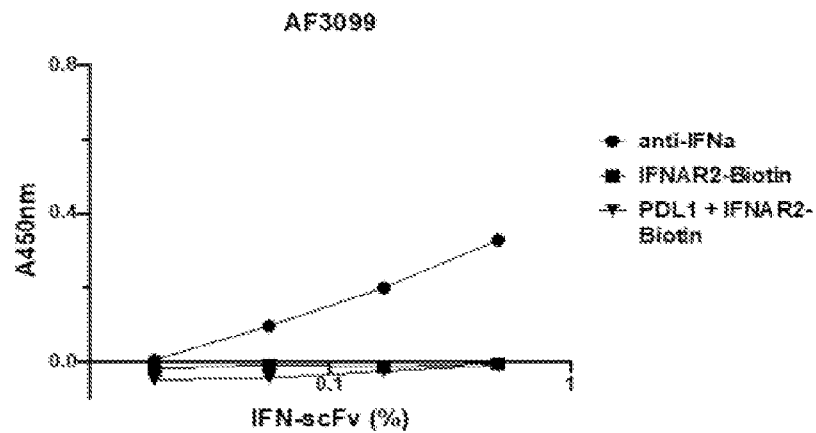


FIG. 21E

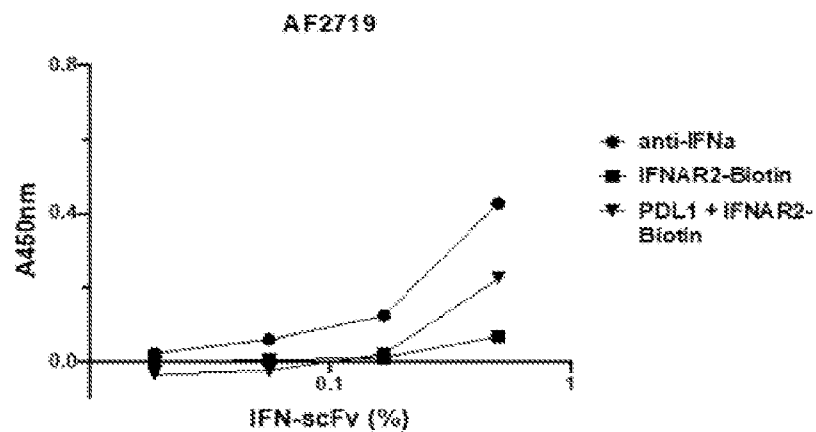


FIG. 21F

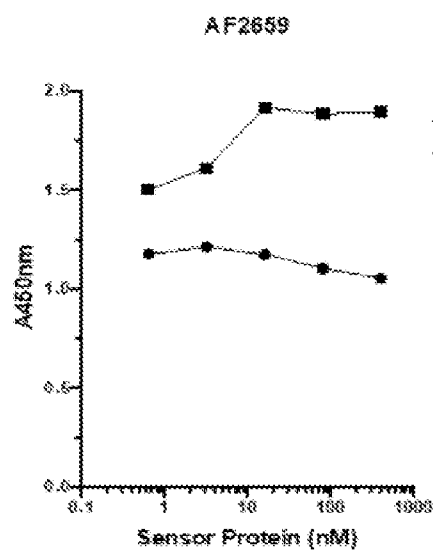


FIG. 22A

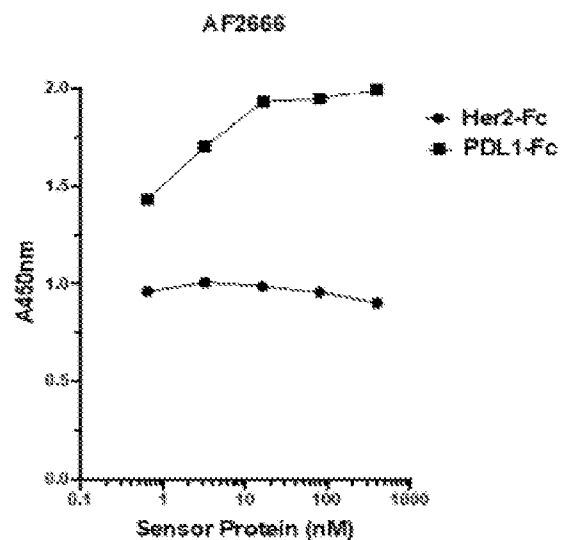


FIG. 22B

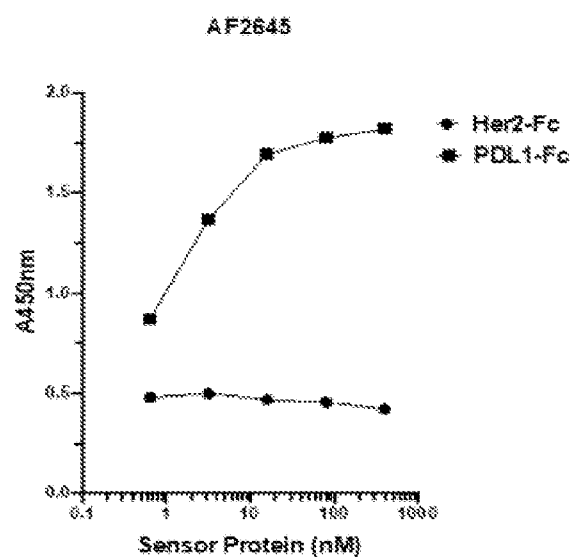


FIG. 22C

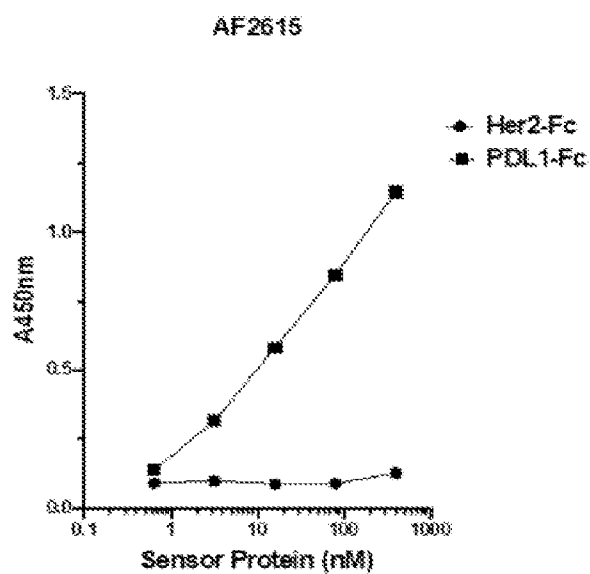


FIG. 22D

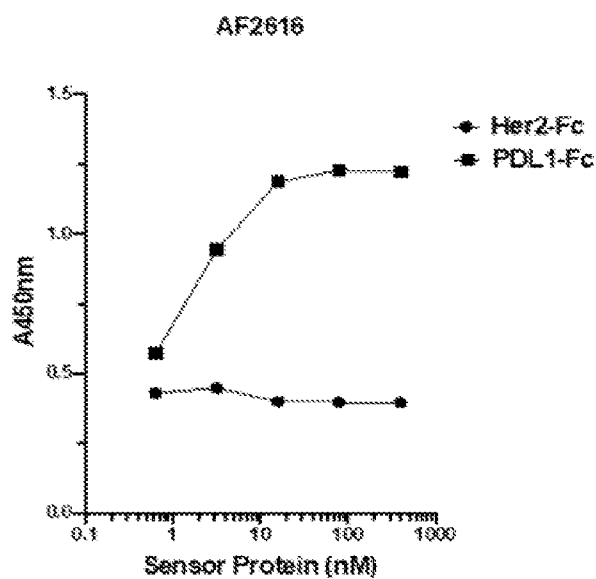


FIG. 22E

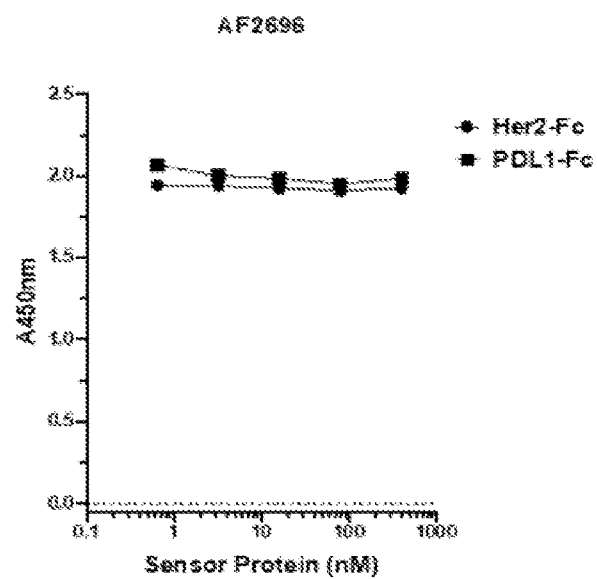


FIG. 22F

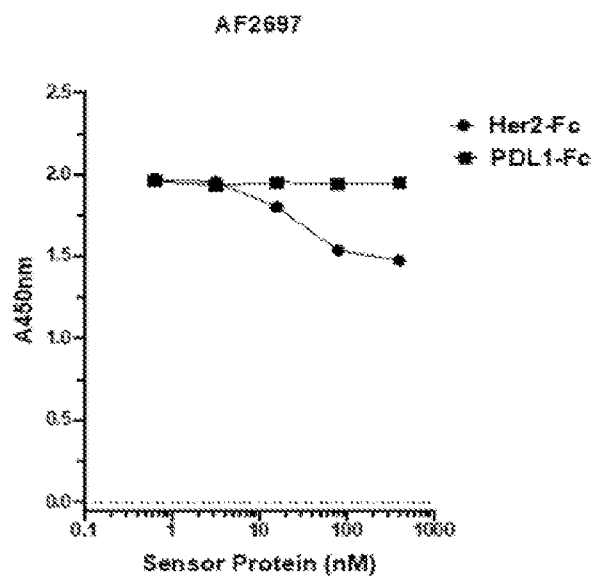


FIG. 22G

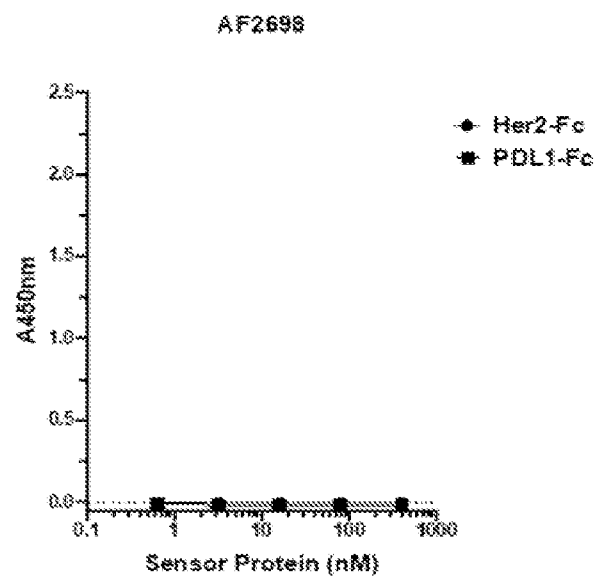


FIG. 22H

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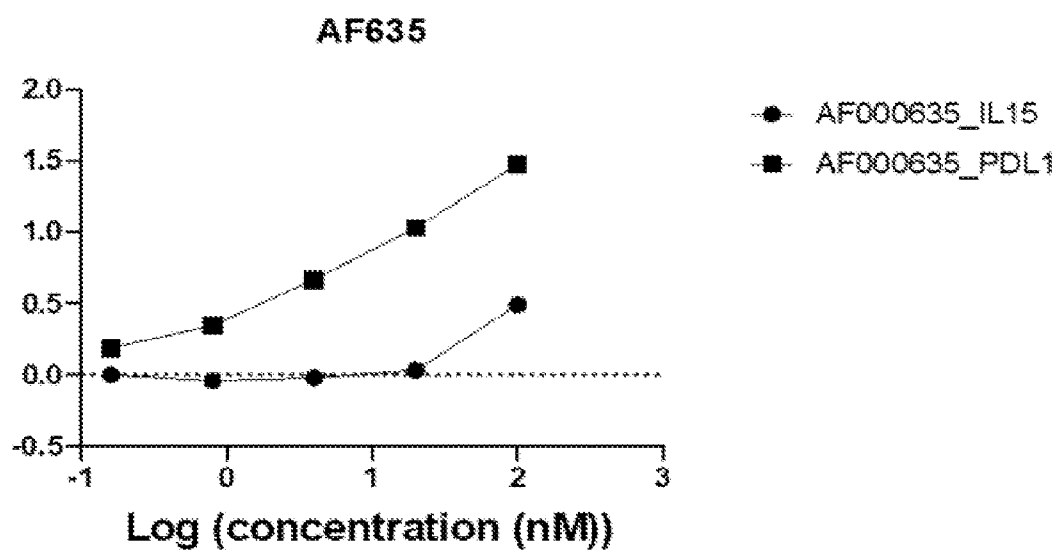


FIG. 23A

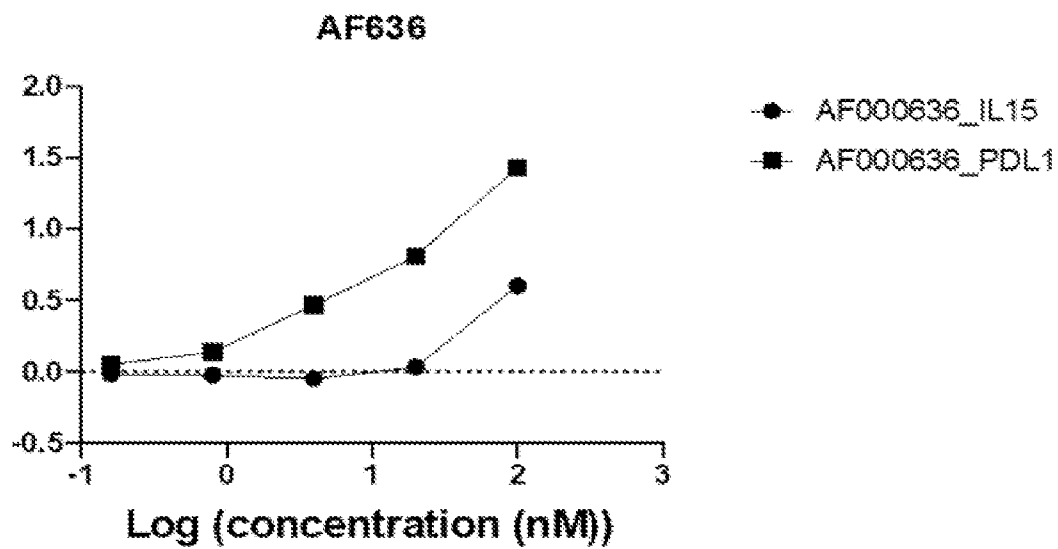


FIG. 23B

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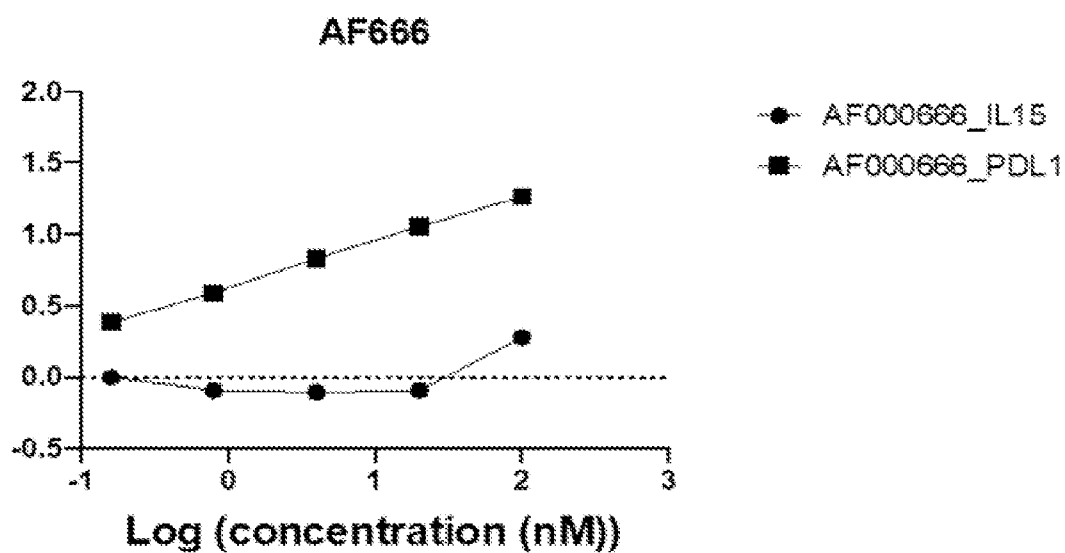


FIG. 23C

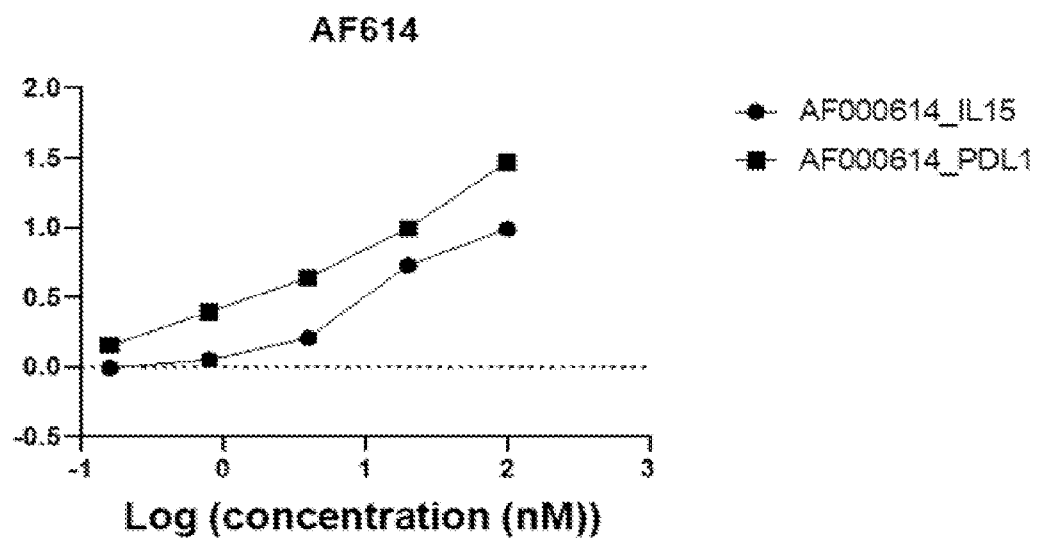


FIG. 23D

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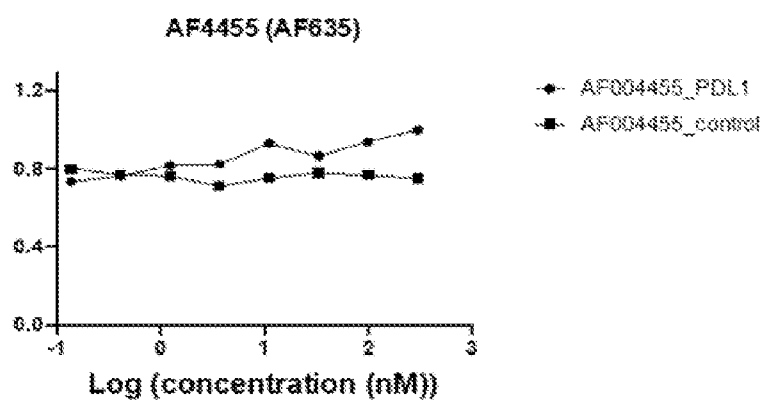


FIG. 24A

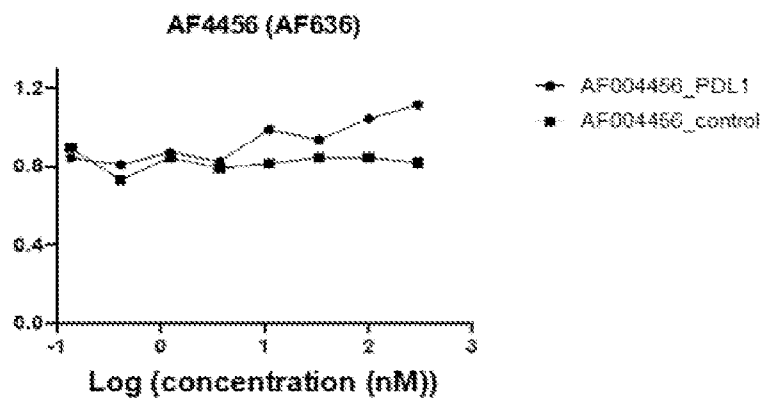


FIG. 24B

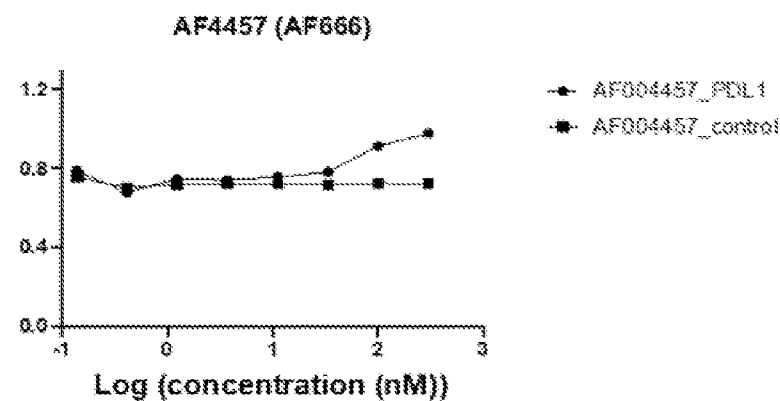


FIG. 24C

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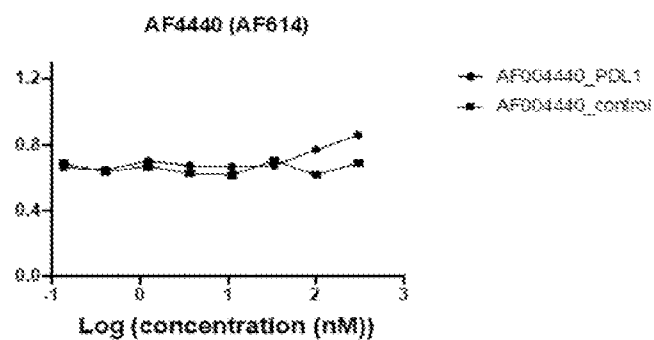


FIG. 24D

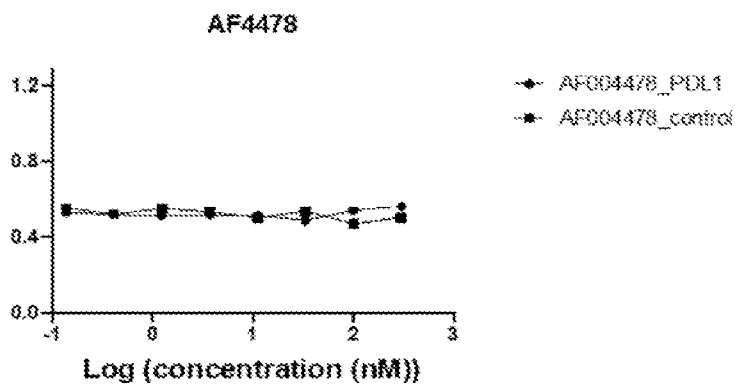


FIG. 24E

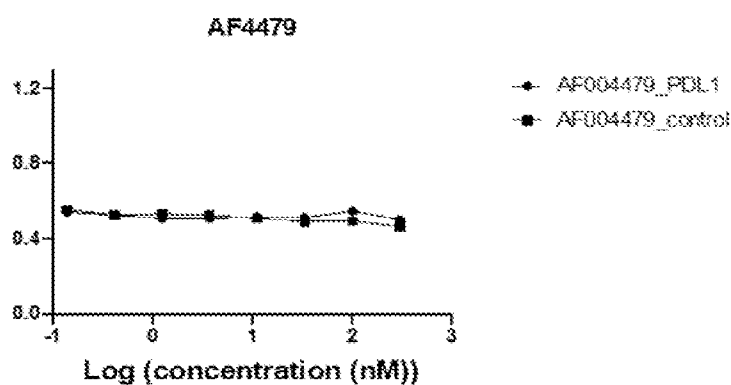


FIG. 24F

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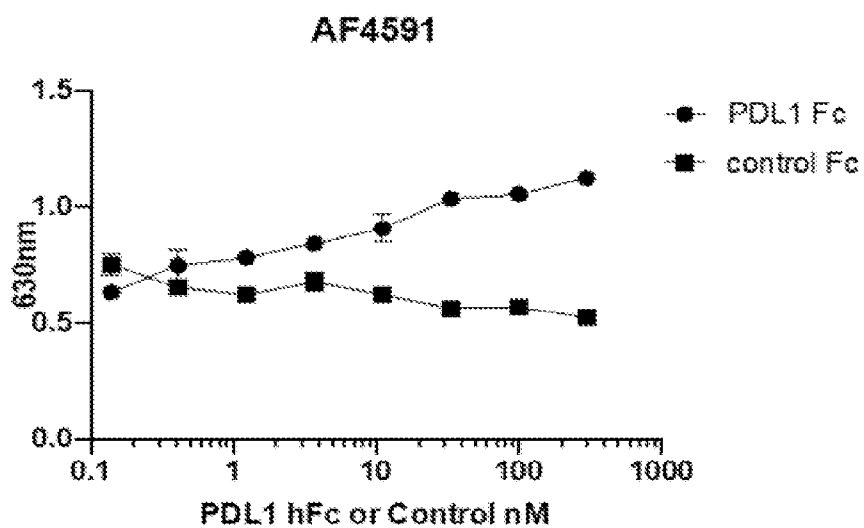


FIG. 25A

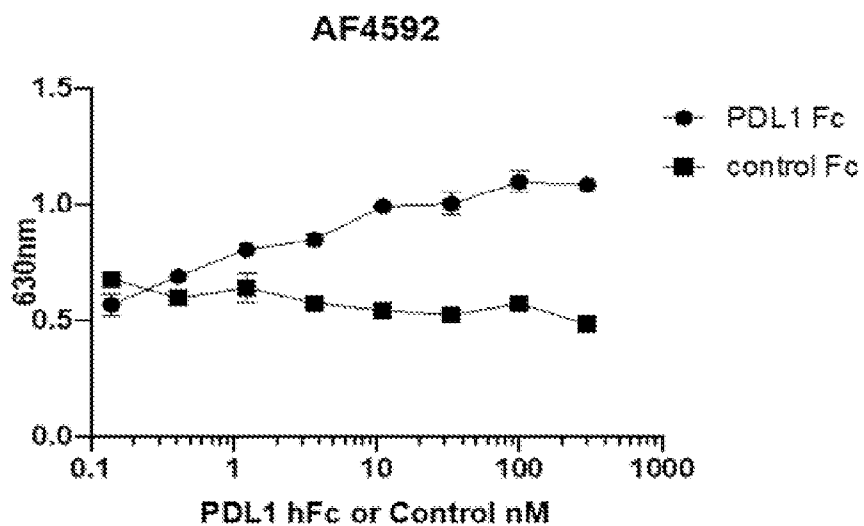


FIG. 25B

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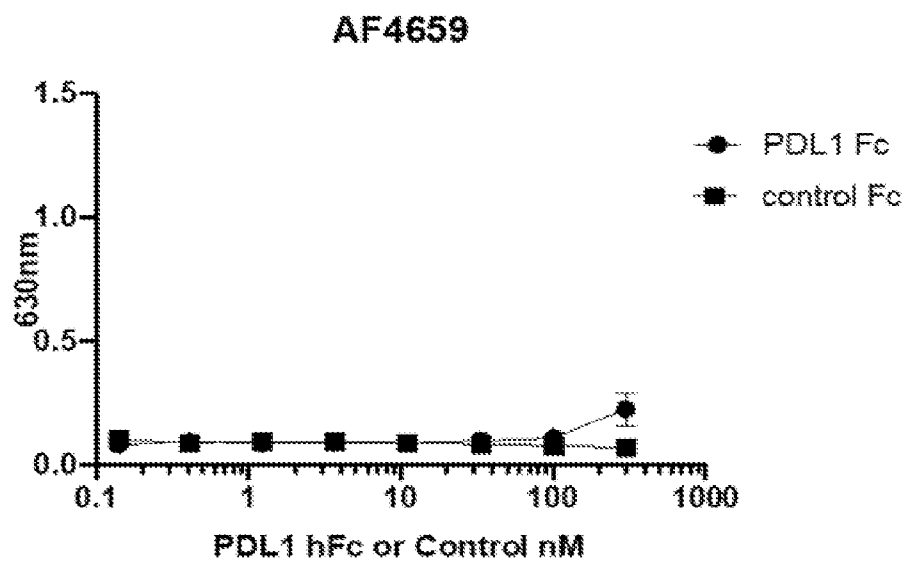


FIG. 25C

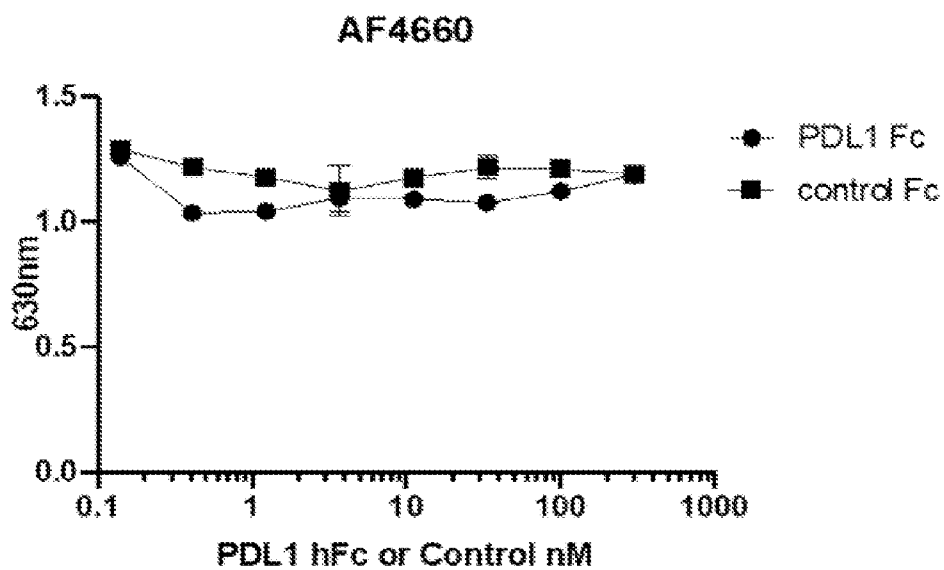


FIG. 25D

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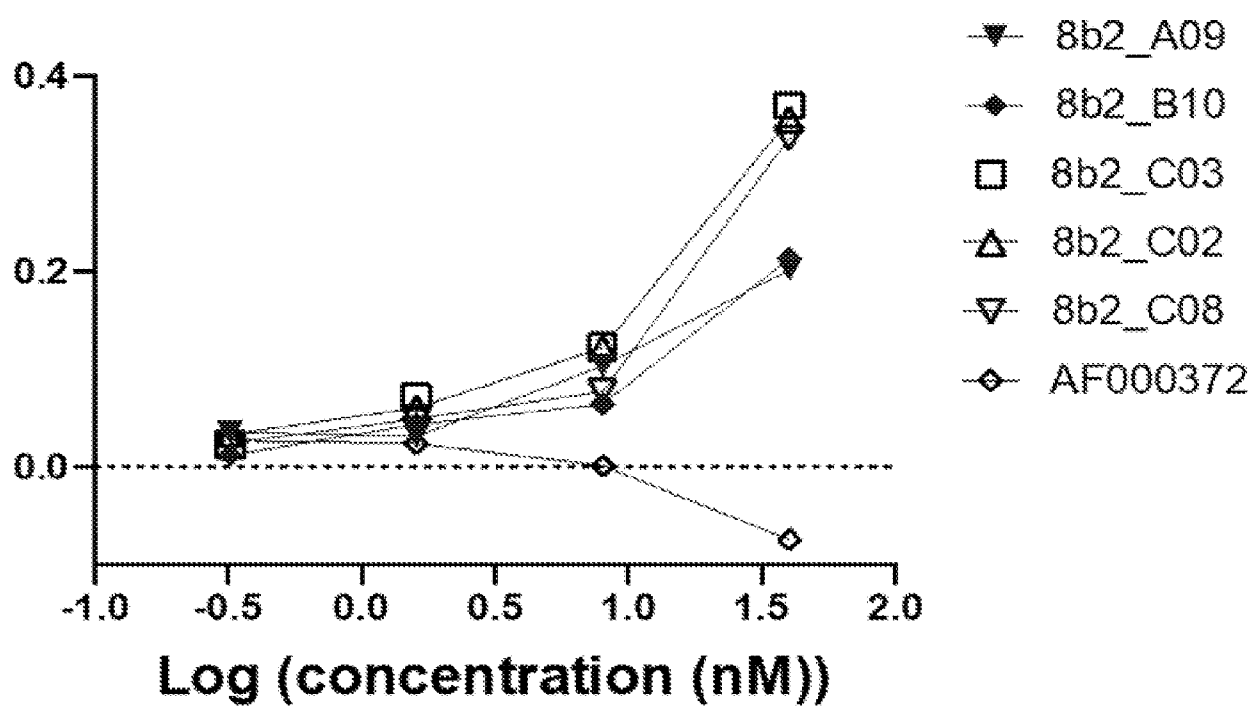


FIG. 26

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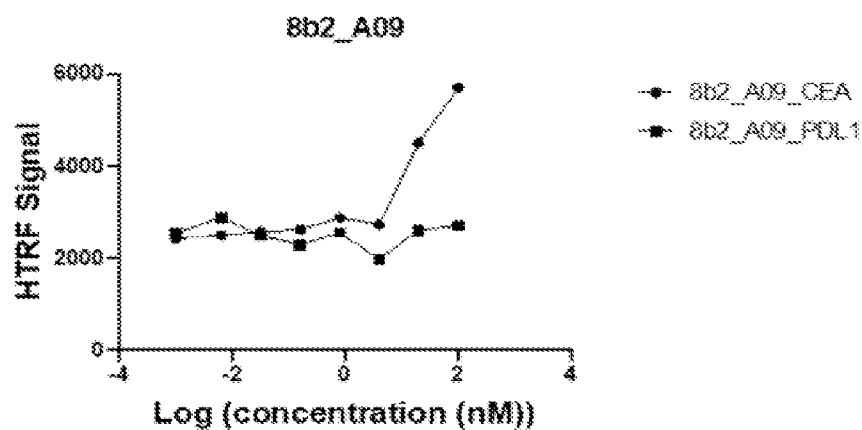


FIG. 27A

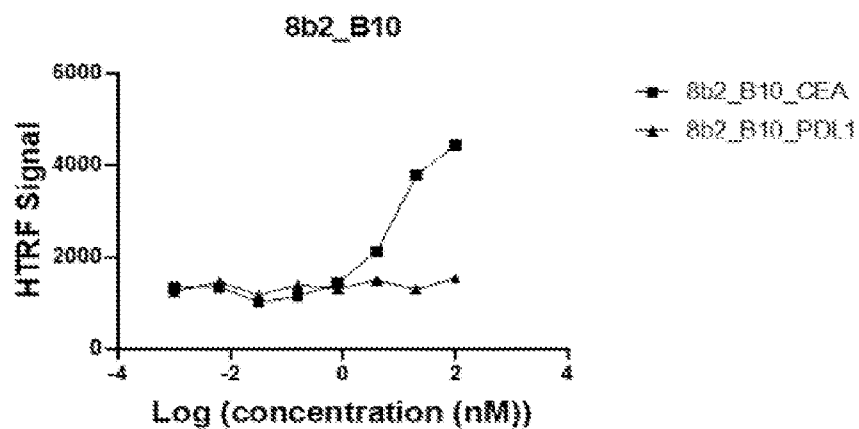


FIG. 27B

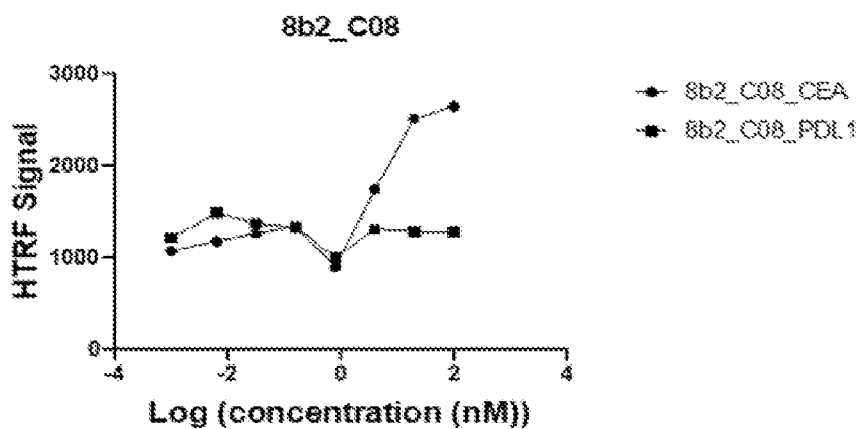


FIG. 27C

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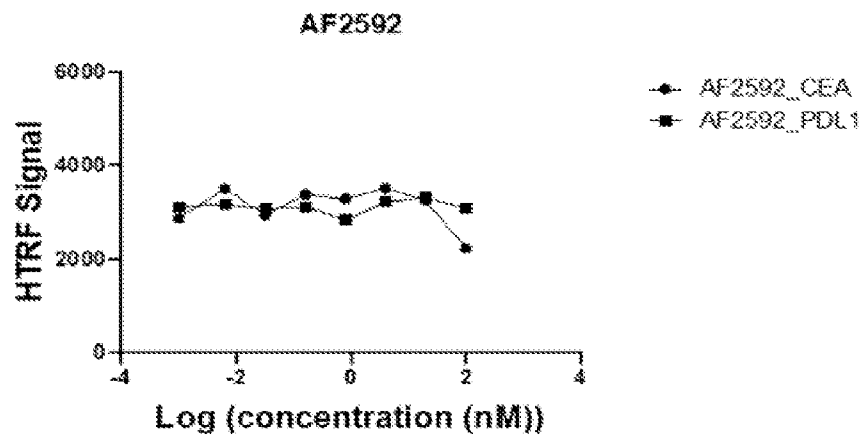


FIG. 27D

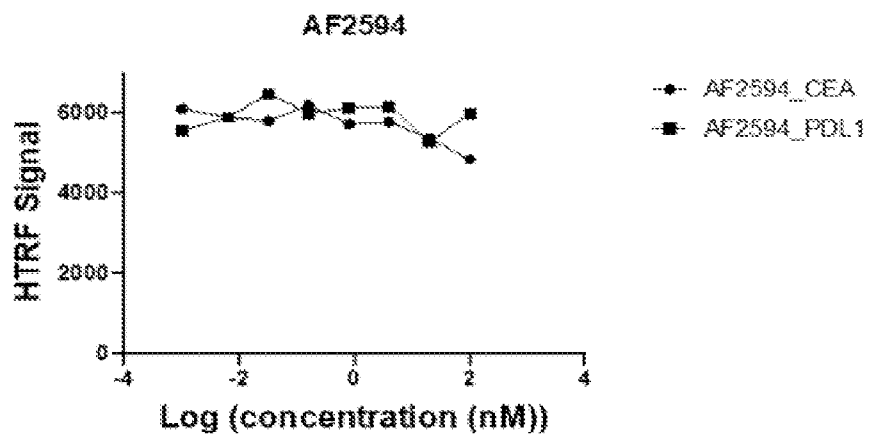


FIG. 27E

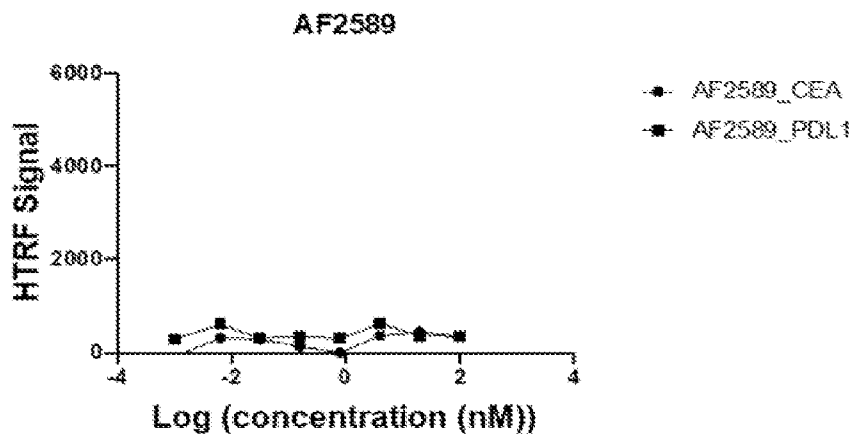


FIG. 27F

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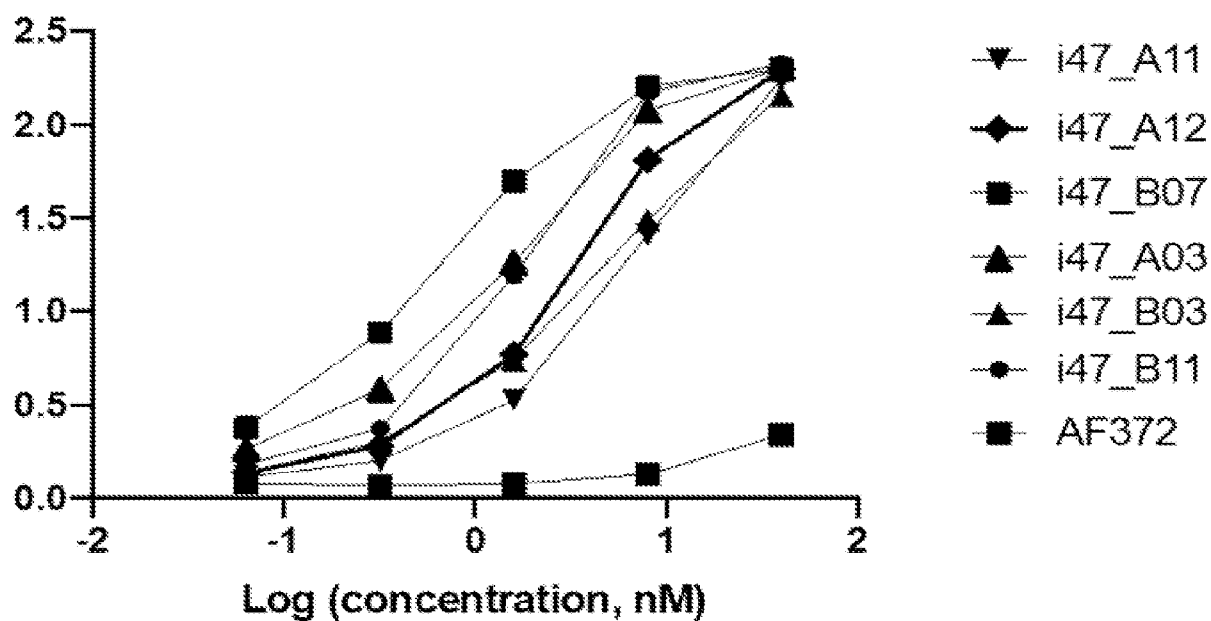


FIG. 28A

CloneID	IFN α binding (@5uM)	ELISA	SEQUENCES
i47_A03	+	-	SEQ ID NO: 262
i47_A11	+	-	N/A
i47_A12	+	-	N/A
i47_B03	+	-	SEQ ID NO: 263
i47_B07	+	-	SEQ ID NO: 264
i47_B11	+	-	SEQ ID NO: 264
AF317	(KD < 10nM)	+++	SEQ ID NO: 257
AF372	-	-	SEQ ID NO: 258

FIG. 28B

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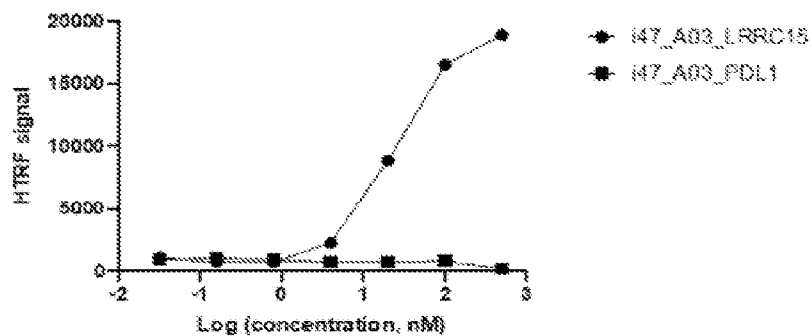


FIG. 29A

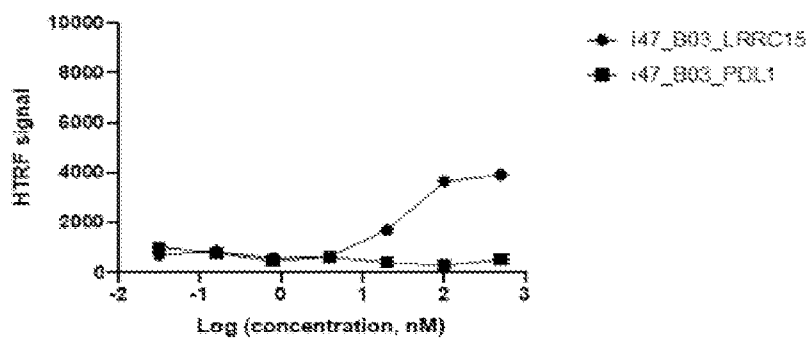


FIG. 29B

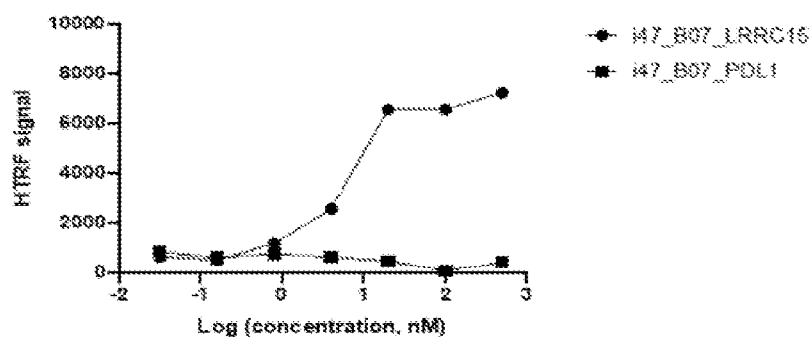


FIG. 29C

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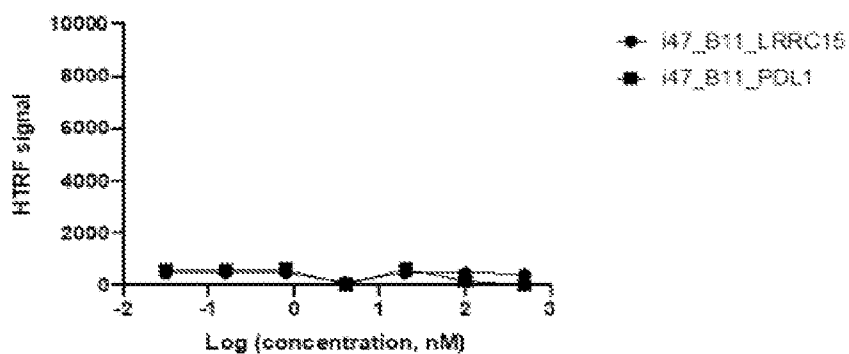


FIG. 29D

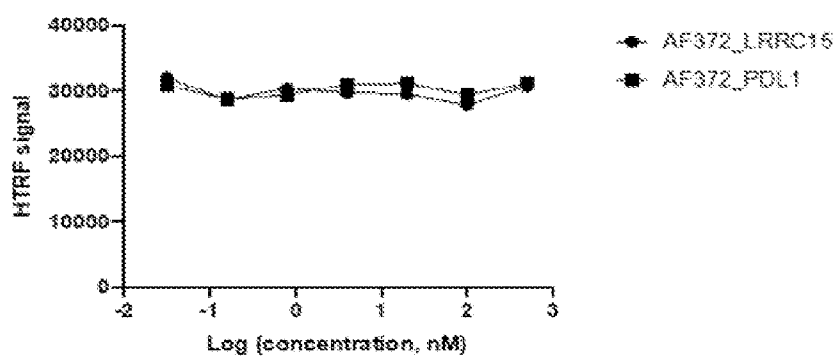


FIG. 29E

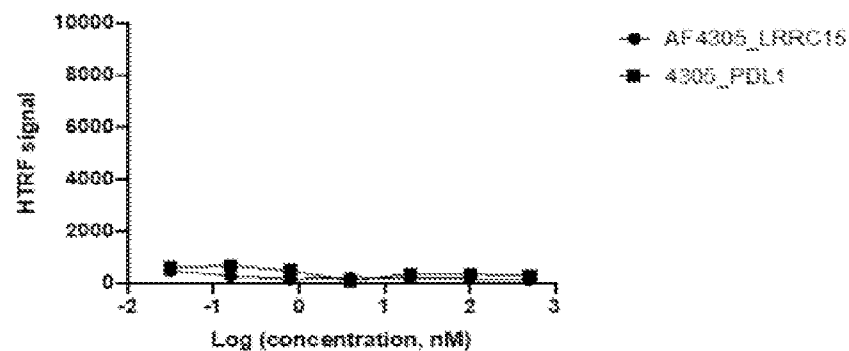


FIG. 29F

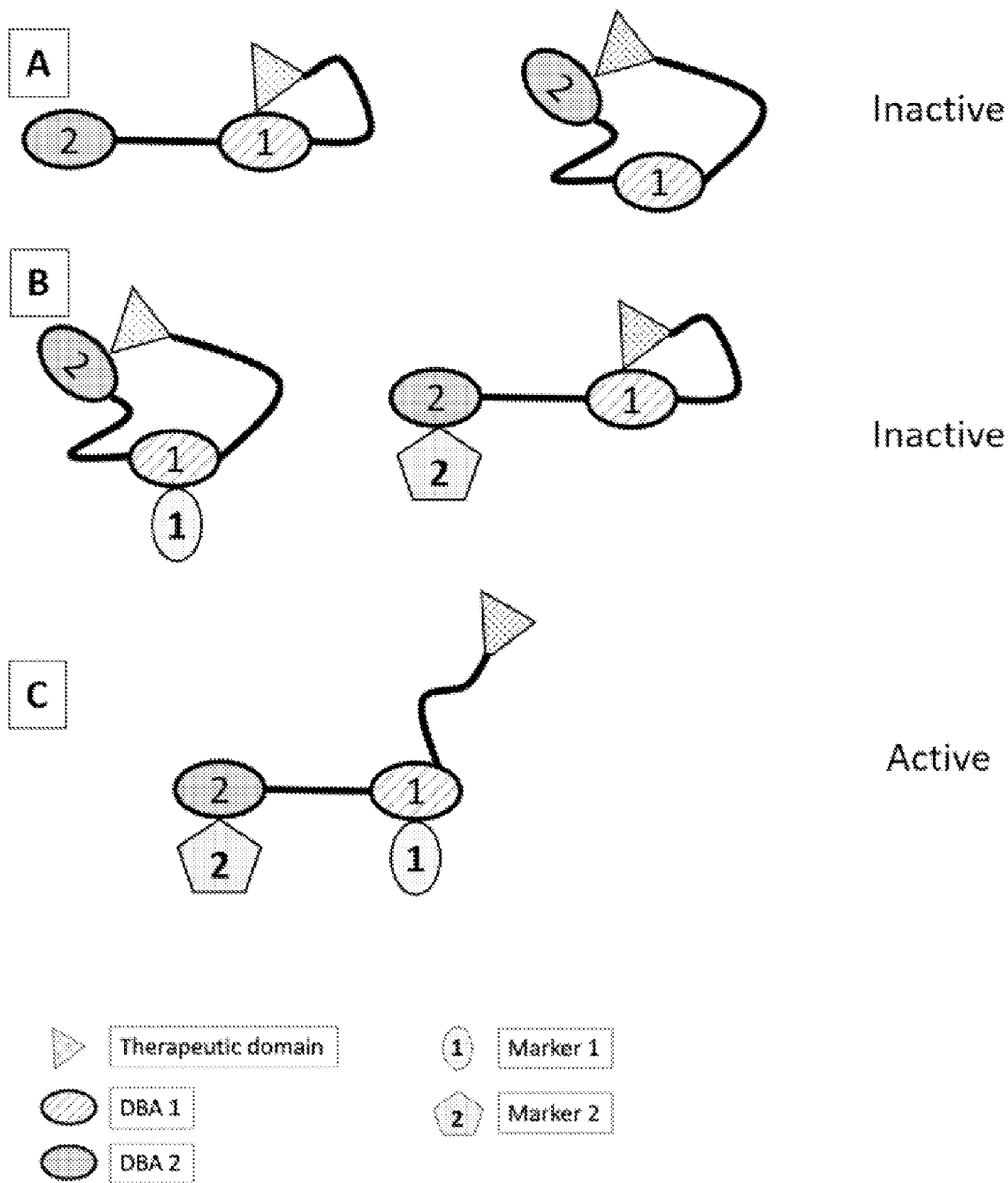


FIG. 13