

(12) STANDARD PATENT APPLICATION (11) Application No. AU 2026202096 A1
(19) AUSTRALIAN PATENT OFFICE

- (54) Title
Methods and systems for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking
- (51) International Patent Classification(s)
C07K 16/30 (2006.01) **A61P 35/00** (2006.01)
A61K 39/00 (2006.01)
- (21) Application No: **2026202096** (22) Date of Filing: **2026.03.18**
- (43) Publication Date: **2026.04.09**
(43) Publication Journal Date: **2026.04.09**
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ABSTRACT

Methods and apparatuses are described for performing a patient-specific immunotherapy procedure. A computing device receives a request to create transfected T cells for a patient. The computing device generates a patient-specific identifier associated with the cell order request. The computing device initiates a process to create transfected T cells for infusion into the patient's bloodstream, comprising: performing a leukapheresis procedure on a sample of the patient's blood to collect T cells from the sample, transferring the collected T cells to a container, labeling the container with the patient-specific identifier, transmitting the collected T cells to a manufacturing facility, creating transfected T cells from the collected T cells using a cell modification technique, receiving the transfected T cells from the manufacturing facility, and infusing the transfected T cells into the patient's bloodstream. The computing device records a tracking event for each step, including the patient-specific identifier, to generate a chain of custody of the patient's T cells.

2026202096 18 Mar 2026

METHODS AND SYSTEMS FOR PERFORMING A PATIENT-SPECIFIC IMMUNOTHERAPY PROCEDURE WITH CHAIN-OF-CUSTODY AND CHAIN-OF-IDENTITY BIOLOGICAL SAMPLE TRACKING

RELATED APPLICATIONS

[0001] This application is a divisional application of Australian patent application no. 2023201386, which is a divisional application of Australian patent application no. 2018334279, the entire disclosures of all of which are incorporated herein by reference. This application claims priority to U.S. Provisional Patent Application No. 62/559,330, filed September 15, 2017, and to U.S. Provisional Patent Application No. 62/566,912, filed October 2, 2017, all of which are incorporated by reference in their entirety.

TECHNICAL FIELD

[0002] This application relates generally to methods and apparatuses, including computer program products, for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking

BACKGROUND

[0003] In recent years, advances in medical technology have led to the emerging use of immunotherapies to treat different types of illnesses and diseases, including various forms of cancer. Generally, immunotherapy is the treatment of disease by stimulating or suppressing an immune response. Often, modified versions of a patient's own biological material, such as immune cells, are reintroduced into the patient in order to initiate and/or supplement the immune response.

[0004] For example, engineered immune cells have been shown to possess desired qualities in therapeutic treatments, particularly in oncology. Two main types of engineered immune cells are those that contain chimeric antigen receptors (termed "CARs" or "CAR-Ts") and T-cell receptors ("TCRs"). These engineered cells are engineered to endow them with antigen specificity while retaining or enhancing their ability to recognize and kill a target cell. Chimeric antigen receptors may comprise, for example, (i) an antigen-specific

component (“antigen binding molecule”), (ii) an extracellular domain, (iii) one or more costimulatory domains, and (iv) one or more activating domains. Each domain may be heterogeneous, that is, comprised of sequences derived from (or corresponding to) different protein chains.

[0005] Because many patients that undergo immunotherapy are critically ill, a crucial factor in the efficacy of such immunotherapy procedures is the ability to provide the modified biological material to the patient as quickly as possible, so that the therapeutic benefits may be maximized. Also, because many types of immunotherapy are tailored for the specific patient (i.e., using the patient’s own cells), it is important to ensure that the patient’s biological material is accurately tracked throughout the immunotherapy process—from extraction, to modification, and then to infusion back into the patient—to avoid delays in manufacturing, mislabeling of material, and misidentification of the patient. However, existing immunotherapy procedures generally lack a technical mechanism to track the patient’s biological material automatically and to ensure that the biological material is tied to the specific patient’s identity throughout the manufacturing process.

SUMMARY

[0006] Therefore, what is needed are methods and systems for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking. The techniques described herein provide the specific technical advantage over existing systems of providing a continuous and automatic chain of custody and chain of identity for a patient-specific biological sample during an immunotherapy procedure, to create a computerized information portal that interested parties—such as the patient, physician, manufacturer, and other medical personnel— may use to quickly understand and track the current phase of the immunotherapy procedure and the status of the patient’s

biological sample during the procedure. Such advanced tracking is an improvement over existing systems that do not have technological solutions for maintaining a chain of custody and chain of identity—resulting in delays during the manufacturing process which, for a patient dealing with a life-threatening illness, may be immeasurably severe.

[0007] The invention, in one aspect, features a method of performing a patient-specific immunotherapy procedure. A computing device receives a cell order request to create transfected T cells for a patient. The computing device generates a patient-specific identifier associated with the cell order request, the patient-specific identifier comprising a patient identity element, a sales order identifier, and a cell order lot number. The computing device initiates a process to create transfected T cells for infusion into the patient's bloodstream, the process comprising: performing a leukapheresis procedure on a sample of the patient's blood to collect T cells from the sample, transferring the collected T cells to a container, labeling the container with the patient-specific identifier, transmitting the collected T cells to a manufacturing facility, creating transfected T cells from the collected T cells using a cell modification technique, receiving the transfected T cells from the manufacturing facility, and infusing the transfected T cells into the patient's bloodstream. The computing device records a tracking event for each step in the process, each tracking event including the patient-specific identifier. The tracking events comprise a chain of custody of the patient's T cells during the process.

[0008] The invention, in another aspect, features a method of tracking a cell order during an immunotherapy procedure. A computing device receives a cell order request for creating transfected T cells for a patient. The computing device generates a patient-specific identifier associated with the cell order request, the patient-specific identifier comprising a patient identity element, a sales order identifier, and a cell order lot number. The computing device monitors a process to create transfected T cells for infusion into the patient's

bloodstream, the process comprising: receiving indicia that a leukapheresis procedure has been performed on a sample of the patient's blood to collect T cells from the sample, receiving indicia that the collected T cells have been transferred to a container, receiving indicia that the container has been labeled with the patient-specific identifier, receiving indicia that the collected T cells have been transmitted to a manufacturing facility, receiving indicia that transfected T cells have been created from the collected T cells using a cell modification technique, receiving indicia that the transfected T cells have been received from the manufacturing facility, and receiving indicia that the transfected T cells have been infused into the patient's bloodstream. The computing device records a tracking event when an indicia is received, each tracking event including the patient-specific identifier. The computing device maintains a chain of custody of the patient's T cells by storing the tracking events during the process.

[0009] The invention, in another aspect, features a method of performing a patient-specific immunotherapy procedure. A cell order request to create transfected T cells for a patient is received. An event tracking module executed on a processor generates a patient-specific identifier associated with the cell order request. A process to create transfected T cells for infusion into the patient's bloodstream is initiated, comprising: performing a leukapheresis procedure on a sample of the patient's blood to collect T cells from the sample, transferring the collected T cells to a container, labeling the container with the patient-specific identifier, transmitting the collected T cells to a manufacturing facility, creating transfected T cells from the collected T cells using a cell modification technique, receiving the transfected T cells from the manufacturing facility, and infusing the transfected T cells into the patient's bloodstream. The event tracking module receives, from a first client device located at the point of the leukapheresis procedure, a first tracking event that confirms the leukapheresis procedure and contains the patient-specific identifier. The event tracking

module integrates the first tracking event in a data structure pertaining to the patient-specific identifier, where the data structure is stored in a database and the integrating step records a first timestamp with the first tracking event. The event tracking module receives, from a second client device located at the manufacturing facility, a second tracking event that confirms the receipt of the collected T cells at the manufacturing facility and contains the patient-specific identifier. The event tracking module integrates the second tracking event in the data structure pertaining to the patient-specific identifier, where the integrating step records a second timestamp with the second tracking event.

[0010] The invention, in another aspect, features a method of performing a patient-specific immunotherapy procedure. A tracking module executed on a processor receives a cell order request to create transfected T cells for a patient. The tracking module generates a patient-specific identifier associated with the cell order request, the patient-specific identifier identifying a patient, and a cell order lot. A database generates a data record for tracking the cell order, the data record identified in the database according to the patient-specific identifier. The tracking module receives a first tracking event indicating that the collected T cells are ready for shipment to a manufacturing facility. The data record corresponding to the patient-specific identifier is updated in accordance with the first tracking event. The tracking module receives, based on the container having been received by the manufacturing facility, a second tracking event indicating that the collected T cells have been received by a manufacturing facility. The data record corresponding to the patient-specific identifier is updated in accordance with the second tracking event. The tracking module receives, based on the manufacturing facility having created transfected T cells from the collected T cells using a cell modification technique, a third tracking event indicating that the transfected T cells have been created. The data record corresponding to the patient-specific identifier is updated in accordance with the third tracking event. ;The tracking module receives, based on

the transfected T cells having been received from the manufacturing facility, a fourth tracking event indicating that the transfected T cells have been received. The data record corresponding to the patient-specific identifier is updated in accordance with the fourth tracking event. The tracking module receives, based on the transfected T cells having been infused into the patient's bloodstream, a fifth tracking event indicating that the transfected T cells have been infused into the patient's bloodstream. The data record corresponding to the patient-specific identifier is updated in accordance with the fifth tracking event, where each of the first, second, third, fourth, and fifth tracking events contains the patient-specific identifier, a timestamp, and an event identifier, and where the data record corresponding to the patient-specific identifier stores, in an ordered sequence, the first, second, third, fourth, and fifth tracking events when the data record is updated in accordance with the respective events.

[0011] Any of the above aspects may include one or more of the following features:

[0012] In some embodiments, the transfected T cells are created by transfecting the collected T cells with a polynucleotide encoding a chimeric antigen receptor (CAR), the CAR comprising an antigen binding molecule that specifically binds to a target molecule. Preferably, the antigen binding molecule is a single chain variable fragment (scFv).

[0013] It is envisioned that in some embodiments, the target molecule is a blood borne cancer-associated antigen. The blood borne cancer-associated antigens of the present invention are associated with one or more cancers selected from the group consisting of: acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), chronic myelomonocytic leukemia (CMML), juvenile myelomonocytic leukemia, atypical chronic myeloid leukemia, acute promyelocytic leukemia (APL), acute monoblastic leukemia, acute erythroid leukemia, acute megakaryoblastic leukemia, lymphoblastic leukemia, B-lineage acute lymphoblastic leukemia, B-cell chronic lymphocytic leukemia, B-cell non-Hodgkin's

lymphoma, myelodysplastic syndrome (MDS), myeloproliferative disorder, myeloid neoplasm, myeloid sarcoma), and Blastic Plasmacytoid Dendritic Cell Neoplasm (BPDCN).

[0014] In some embodiments, the target molecule is a viral infection-associated antigen. The viral infections of the present invention may be caused by any virus, including, for example, HIV.

[0015] The chimeric antigen receptors (CARs) of the present invention may further comprise at least one costimulatory domain. The costimulatory domains of the present invention include, but are not limited to, a signaling region, or other suitable portion, of CD28, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1 (CD11a/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT, (TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNF receptor proteins, an Immunoglobulin protein, cytokine receptor, integrins, Signaling Lymphocytic Activation Molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof.

[0016] Preferably, the costimulatory domain comprises CD28. CD28 costimulatory domains of the present invention comprise, for example, a sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, and SEQ ID NO. 8.

[0017] In other embodiments, the costimulatory domain comprises CD8. CD8 costimulatory domains of the present invention comprise, for example, SEQ ID NO. 14.

[0018] The chimeric antigen receptors (CARs) of the present invention may further comprise at least one activating domain. The activating domains of the present invention comprise, for example, CD3. Preferably, the CD3 activating domains comprise CD3 zeta. CD3 zeta activating domains of the present invention comprise, for example, SEQ ID NO. 10.

[0019] In a preferred embodiment, the chimeric antigen receptor (CAR) comprises all or part of: an anti-CD19 scFv, CD28, and CD3 zeta.

[0020] In additional preferred embodiments, the chimeric antigen receptor (CAR) comprises:

- all or part of: an anti-CD19 scFv, CD8, and 4-1BB;
- all or part of: an anti-BCMA scFv and CD8;
- all or part of: an anti-CD19 scFv, CD28, and 4-1BB;
- all or part of: an anti-CD22 scFv and CD8;
- all or part of: an anti-CD19 scFv, CD28, and EGFRt/19-28z/4-1BBL;
- all or part of: an anti-MUC16 scFv, and CD28;
- all or part of: an anti-CD171;
- all or part of: an anti-CD123, and CD28;
- all or part of: an anti-BCMA, CD8, and 4-1BB;
- all or part of: an anti-CD19 and CD28;
- all or part of: an anti-CD19 and CD8; or,

- all or part of: CD28.

[0021] In a further preferred embodiment, the CAR comprises a leader sequence (CSF2RA), an anti-CD19 scFv, a Whitlow linker, a CD28 spacer, a CD28 costimulatory domain, and CD3 zeta. One example of such a CAR is encoded by the nucleotide sequence of SEQ ID NO. 146 and the amino acid sequence of SEQ ID NO. 147.

[0022] In an additional preferred embodiment, the CAR comprises a leader sequence (CD8), an anti-CD19 scFv, a Whitlow linker, a CD28T spacer, a CD28 costimulatory domain, and CD3 zeta. One example of such a CAR is encoded by the nucleotide sequence of SEQ ID NO. 148 and the amino acid sequence of SEQ ID NO. 149.

[0023] In another preferred embodiment, the CAR comprises a leader sequence (CD8a), an anti-CD19 scFv, a Whitlow linker, a CD8a spacer and transmembrane domain, a CD28 costimulatory domain, and CD3 zeta. One example of such a CAR is encoded by the nucleotide sequence of SEQ ID NO. 150 and the amino acid sequence of SEQ ID NO. 151.

[0024] In a further preferred embodiment, the CAR comprises a leader sequence (CD8), an anti-CLL-1 scFv, a G4S linker, a Minispacer, a CD28T (extracellular / transmembrane region of CD28), CD28 (an intracellular costimulatory region of CD28), and CD3 zeta. One example of such a CAR is encoded by the nucleotide sequence of SEQ ID NO. 154 and the amino acid sequence of SEQ ID NO. 155.

[0025] In an additional preferred embodiment, the CAR comprises a leader sequence (CD8a), an anti-BCMA scFv, a Whitlow linker, a CD28T spacer, a CD28 costimulatory domain, and CD3 zeta. One example of such a CAR is encoded by the nucleotide sequence of SEQ ID NO. 156 and the amino acid sequence of SEQ ID NO. 157.

[0026] In some embodiments, the transfected T cells are created by transfecting the collected T cells with a polynucleotide encoding a T cell receptor (TCR). The TCRs of the present invention may bind to a tumor-associated antigen. Tumor-associated antigens are

associated with one or more cancers selected from the group consisting of: adrenocortical carcinoma, anal cancer, bladder cancer, bone cancer, brain cancer, breast cancer, carcinoid cancer, carcinoma, cervical cancer, colon cancer, endometrial cancer, esophageal cancer, extrahepatic bile duct cancer, extracranial germ cell cancer, eye cancer, gallbladder cancer, gastric cancer, germ cell tumor, gestational trophoblastic tumor, head and neck cancer, hypopharyngeal cancer, islet cell carcinoma, kidney cancer, large intestine cancer, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer, lymphoma, malignant mesothelioma, Merkel cell carcinoma, mycosis fungoides, myelodysplastic syndrome, myeloproliferative disorders, nasopharyngeal cancer, neuroblastoma, oral cancer, oropharyngeal cancer, osteosarcoma, ovarian epithelial cancer, ovarian germ cell cancer, pancreatic cancer, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pituitary cancer, plasma cell neoplasm, prostate cancer, rhabdomyosarcoma, rectal cancer, renal cell cancer, transitional cell cancer of the renal pelvis and ureter, salivary gland cancer, Sezary syndrome, skin cancers, small intestine cancer, soft tissue sarcoma, stomach cancer, testicular cancer, thymoma, thyroid cancer, urethral cancer, uterine cancer, vaginal cancer, vulvar cancer, and Wilms' tumor.

[0027] In certain aspects, the present application may be suitable for target molecule to hematologic cancer. In some embodiments, the cancer is of the white blood cells. In other embodiments, the cancer is of the plasma cells. In some embodiments, the cancer is leukemia, lymphoma, or myeloma. In certain embodiments, the cancer is acute lymphoblastic leukemia (ALL) (including non T cell ALL), acute lymphoid leukemia (ALL), and hemophagocytic lymphohistocytosis (HLH)), B cell prolymphocytic leukemia, B-cell acute lymphoid leukemia ("BALL"), blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloid leukemia (CML), chronic or acute granulomatous disease, chronic or acute

leukemia, diffuse large B cell lymphoma, diffuse large B cell lymphoma (DLBCL), follicular lymphoma, follicular lymphoma (FL), hairy cell leukemia, hemophagocytic syndrome (Macrophage Activating Syndrome (MAS), Hodgkin's Disease, large cell granuloma, leukocyte adhesion deficiency, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, monoclonal gammopathy of undetermined significance (MGUS), multiple myeloma, myelodysplasia and myelodysplastic syndrome (MDS), myeloid diseases including but not limited to acute myeloid leukemia (AML), non-Hodgkin's lymphoma (NHL), plasma cell proliferative disorders (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, plasmacytomas (e.g., plasma cell dyscrasia; solitary myeloma; solitary plasmacytoma; extramedullary plasmacytoma; and multiple plasmacytoma), POEMS syndrome (Crow-Fukase syndrome; Takatsuki disease; PEP syndrome), primary mediastinal large B cell lymphoma (PMBCL), small cell- or a large cell-follicular lymphoma, splenic marginal zone lymphoma (SMZL), systemic amyloid light chain amyloidosis, T-cell acute lymphoid leukemia (TALL), T-cell lymphoma, transformed follicular lymphoma, Waldenstrom macroglobulinemia, or a combination thereof.

[0028] In additional preferred embodiments, the TCR comprises an AV38-2 variable alpha chain, a BV7-2 variable beta chain, a murine constant alpha domain, a murine constant beta domain, TRAJ40, Furin-SG SG-P2A, and TRBJ1-3. One example of such a TCR is encoded by the nucleotide sequence of SEQ ID NO. 152 and the amino acid sequence of SEQ ID NO. 153.

[0029] In further preferred embodiments, the TCR comprises a TCR beta chain variable region, a TCR beta chain constant region, P2A peptide (with Furin cleavage site and linker), a TCR alpha chain variable region, and a TCR alpha chain constant region. One example of such a TCR is encoded by the nucleotide sequence of SEQ ID NO. 158 and the

amino acid sequence of SEQ ID NO. 159. Another example of such a TCR is encoded by the nucleotide sequence of SEQ ID NO. 160 and the amino acid sequence of SEQ ID NO. 161.

[0030] In other embodiments, the TCRs of the present invention bind to a viral infection-associated antigen. Viral infections of the present invention may be caused by any virus, including, for example, HIV.

[0031] Polynucleotides of the present invention may be a component of a vector. Suitable vectors include, but are not limited to, retroviral vectors, DNA vectors, plasmids, RNA vectors, adenoviral vectors, adenovirus associated vectors, lentiviral vectors, or any combination thereof. Preferably, the vector is a lentiviral vector. The lentiviral vectors of the present invention include, but are not limited to, pGAR and derivatives thereof.

[0032] In some embodiments, initiating a process to create transfected T cells further comprises requesting a timeslot for performing the leukapheresis procedure from a remote computing device, receiving indicia responsive to the request for a timeslot that a timeslot is available to perform the leukapheresis procedure, and confirming acceptance of the available timeslot with the remote computing device.

[0033] In some embodiments, initiating a process to create transfected T cells further comprises receiving indicia that the transfected T cells have been shipped from a first site after being created and receiving indicia that the transfected T cells have been received at a second site before being infused, where the computing device records a tracking event upon receiving the indicia that the transfected T cells have been shipped, and the computing device records a tracking event upon receiving the indicia that the transfected T cells have been received at a second site.

[0034] In some embodiments, the patient identity element comprises a first patient ID associated with the immunotherapy procedure and a second patient ID associated with a facility that administers one or more of: the leukapheresis procedure or the infusion of the

transfected T cells. In some embodiments, the computing device stores the tracking events in an ordered sequence. In some embodiments, the ordered sequence is arranged in chronological order.

[0035] Other aspects and advantages of the invention will become apparent from the following detailed description, taken in conjunction with the accompanying drawings, illustrating the principles of the invention by way of example only.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] The advantages of the invention described above, together with further advantages, may be better understood by referring to the following description taken in conjunction with the accompanying drawings. The drawings are not necessarily to scale, emphasis instead generally being placed upon illustrating the principles of the invention.

[0037] FIG. 1A is a block diagram of a system for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking.

[0038] FIG. 1B is a detailed block diagram of a system for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking.

[0039] FIG. 2 is a flow diagram of a computerized method of performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking.

[0040] FIGS. 3A and 3B are exemplary screenshots generated by a user interface module to receive patient-specific information during a patient-specific immunotherapy procedure.

[0041] FIGS. 4A to 4D are exemplary screenshots generated by a user interface module to receive confirmation of extraction and infusion sites, and to schedule an appointment, during a patient-specific immunotherapy procedure.

[0042] FIGS. 5A and 5B are exemplary screenshots generated by a user interface module to display a chain of custody for biological material during a patient-specific immunotherapy procedure.

DETAILED DESCRIPTION

[0043] FIG. 1A is a block diagram of a system 100 for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking. The system of FIG. 1A includes a plurality of client computing devices 102a-102d, a communications network 104, a server computing device 106 with a user interface module 108a, an event tracking module 108b, and a chain of custody module 108c, and a database 110.

[0044] The client computing devices 102a-102d are connected to the communications network 104 in order to communicate with the server computing device 106 to provide input and receive output relating to the process of performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking as described herein. In some embodiments, each client computing device 102a-102d may be coupled to a respective display device for, e.g., providing a detailed graphical user interface (GUI) that receives input for and presents output resulting from the methods and systems described herein. For example, the client computing device 102a-102d may connect to the user interface module 108a of server computing device 106, which provides, e.g., a web-based portal for users of the client computing devices 102a-102c to access functionality associated with the methods described herein.

[0045] Exemplary client devices 102a-102d include but are not limited to desktop computers, laptop computers, tablets, mobile devices, smartphones, and internet appliances. It should be appreciated that other types of computing devices that are capable of connecting to the components of the system of FIG. 1A may be used without departing from the scope of invention. It also should be appreciated that each of the client computing devices 102a-102d may be associated with a different user type—for example, client computing device 102a may be associated with a patient accessing the system of FIG. 1A to generate a user profile and receive updates on a patient-specific immunotherapy procedure; client computing device 102b may be associated with a physician who is treating the patient and who accesses the system of FIG. 1A to initiate an immunotherapy procedure for the patient; client computing device 102c may be associated with a hospital or other facility that is administering the immunotherapy procedure to the patient; and client computing device 102d may be associated with a manufacturing facility that is creating patient-specific immunotherapy product (as will be described herein) for use in the immunotherapy procedure.

[0046] The communications network 104 enables the other components of the system 100 to communicate with each other in order to conduct the process of performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking as described herein. The network 104 may be a local network, such as a LAN, or a wide area network, such as the Internet and/or a cellular network. In some embodiments, the network 104 is comprised of several discrete networks and/or sub-networks (*e.g.*, cellular to Internet) that enable the components of the system of FIG. 1A to communicate with each other.

[0047] The server computing device 106 is a combination of hardware and software modules that includes specialized hardware and/or software modules that execute on a processor and interact with memory modules of the server computing device 106 to perform

functions for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking as described herein. The server computing device 106 includes a user interface module 108a, an event tracking module 108b, and a chain of custody module 108c (as mentioned above) that execute on and/or interact with the processor of the server computing device 106.

[0048] In some embodiments, the user interface module 108a, the event tracking module 108b, and the chain of custody module 108c are specialized sets of computer software instructions programmed onto one or more dedicated processors in the server computing device 106 and may include specifically-designated memory locations and/or registers for executing the specialized computer software instructions. Although the modules 108a-108c are shown in FIG. 1A as executing within the same server computing device 106, in some embodiments the functionality of the modules 108a-108c may be distributed among a plurality of server computing devices. As shown in FIG. 1A, the server computing device 106 enables the modules 108a-108c to communicate with each other in order to exchange data for the purposes of performing the described functions. It should be appreciated that any number of computing devices, arranged in a variety of architectures, resources, and configurations (e.g., cluster computing, virtual computing, cloud computing) may be used without departing from the scope of the invention. The exemplary functionality of the modules 108a-108c is described in detail below.

[0049] The database 110 is a computing device (or in some embodiments, a set of computing devices) coupled to the server computing device 106 and is configured to receive, generate, and store specific segments of data relating to the process of performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking as described herein. In some embodiments, all or a portion of the database 110 may be integrated with the server computing device 106 or be located on a separate

computing device or devices. The database 110 may comprise one or more databases configured to store portions of data used by the other components of the system of FIG. 1A, as will be described in greater detail below. In some embodiments, the database 110 comprises an enterprise business suite, such as Oracle E-Business Suite (EBS), that includes various modules that enable a spectrum of functionality to support the methods and systems described herein—including logistics, supply chain, transportation, CRM, and other types of modules.

[0050] FIG. 1B is a detailed block diagram of the system of FIG. 1A for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking. As shown in FIG. 1B, the server computing device 106 is the central component in the overall hardware architecture, interfacing with client computing devices 102a-102e and database 110, and also interfacing with a scheduling module 114 and a physician master data feed 116. In some embodiments, the server computing device 106 and the corresponding modules 108a-108c leverage the Salesforce platform, available from Salesforce.com, Inc. of San Francisco, California, to integrate certain of the functions described herein. The client computing devices 102a-102e communicate with the server computing device 106 to perform patient enrollment in the immunotherapy procedure and to monitor the chain-of-custody and chain-of-identity tracking (e.g., via browser-based user interfaces) as described herein.

[0051] For example, client computing device 102a may be associated with the patient undergoing the immunotherapy procedure and may include browser software and email software to enable the patient to both monitor the tracking and to electronically sign documents required to participate in the immunotherapy procedure (e.g., via DocuSign or other similar technology). Similarly, the client computing devices 102b-102d may be located at different hospitals where a treating physician may enroll a patient in the immunotherapy

procedure, place a cell order with the system, and monitor the chain-of-custody and chain-of-identity tracking using the browser software. The client computing devices 102b-102d also include a single-sign-on (SSO) module that enables the devices to authenticate to the server computing device 106 (e.g., using SAML 2.0 supported SSO or a specific username/password for the server). The client computing device 102e may be located at an administration or manufacturing site to enable an administrator of the server computing device 106 to communicate with the server, receive communications such as emails from other participants in the system, and monitor the chain-of-custody and chain-of-identity tracking using the browser software.

[0052] As described above, the database 110 may comprise an enterprise business suite that manages the data for the server computing device 106 and includes modules to enable chain-of-custody and chain-of-identity tracking and logistics for the biological sample. For example, the database 110 may transmit approved customer sites to the server 106 upon request, receive cell order entry data from the server 106, and provide cell order booking and apheresis lot update information to the server 106.

[0053] The scheduling module 114 may be integrated into the server computing device 106 or reside on a separate computing device. The scheduling module 114 may authenticate to and communicate with the server computing device 106 to receive certain information about the cell order and immunotherapy procedure (e.g., patient ID, apheresis site, infusion site, and product code) and provide calendaring and scheduling functionality to the server 106 (e.g., enabling a treating physician to select an apheresis date/time and provide an estimated delivery date/time for the biological sample once it has gone through the manufacturing process). Also, the server computing device 106 may communicate with a physician master data feed 116 (e.g., provided using the Veeva™ CRM platform integrated with the Heroku™ application) to receive certain information about treating physicians.

[0054] FIG. 2 is a flow diagram of a computerized method 200 of performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking, using the system of FIG. 1A and/or the system of FIG. 1B. As will be appreciated, the methods and systems described herein are presented in the context of performing a patient-specific immunotherapy procedure. As used herein, “patient-specific immunotherapy procedure” means any procedure that uses molecular or cellular components of the immune system to target and/or destroy cancer, pathogenic, or other disease-causing cells. An immunotherapy procedure is “patient-specific” if it utilizes components of a patient’s immune system to treat that patient’s own cancer, pathology, or other disease.

[0055] As used herein, the terms “patient” and “subject” are used interchangeably and include human and non-human animals, as well as those with formally diagnosed disorders, those without formally recognized disorders, those receiving medical attention, those at risk of developing disorders, etc. In addition to humans, categories of animals within the scope of the present invention include, for example, agricultural animals, domestic animals, laboratory animals, etc. Some examples of agricultural animals include cows, pigs, horses, goats, etc. Some examples of domestic animals include dogs, cats, etc. Some examples of laboratory animals include rats, mice, rabbits, guinea pigs, etc.

[0056] The term “leukapheresis” refers to a specific form of apheresis which involves the selective separation and removal of leukocytes from a blood sample. During leukapheresis, the removed blood is passed through a cell separation device which separates nucleated white blood cells, including T cells, from red blood cells and plasma. The separated T cells may then be collected to be used in the cell modification techniques of the present invention. In certain embodiments, the red blood cells and plasma are returned to the individual as part of the separation process. In additional embodiments, the red blood cells and plasma are discarded or stored for further analysis.

[0057] As used herein, the terms “T cell” and “T lymphocyte” are interchangeable. T cells are a subset of lymphocytes defined by their development in the thymus and by heterodimeric receptors associated with the proteins of the CD3 complex. T cells of the present invention include, but are not limited to, naïve T cells, cytotoxic T cells, helper T cells, suppressor T cells, regulatory T cells, memory T cells, NKT cells, $\gamma\delta$ cells, CD8 $\alpha\alpha$ cells, lymphokine activated cells, TCR-expressing cells, subtypes thereof, and any other cell type which may express chimeric receptor chain.

[0058] T cells may be engineered to possess specificity to one or more desired targets. For example, T cells may be transduced with DNA or other genetic material encoding an antigen binding molecule, such as one or more single chain variable fragment (“scFv”) of an antibody, in conjunction with one or more signaling molecules, and/or one or more activating domains, such as CD3 zeta. In addition to the CAR-T cells’ ability to recognize and destroy the targeted cells, successful T cell therapy benefits from the CAR-T cells’ ability to persist and maintain the ability to proliferate in response to antigen.

[0059] As used herein, the term “cell modification technique” includes, but is not limited to, transfection and transduction. The term “transfection” and grammatical variations thereof, refer to the introduction of foreign or exogenous DNA into a cell. A number of transfection techniques are well known in the art and are disclosed herein. See, *e.g.*, Graham *et al.*, 1973, *Virology* 52:456; Sambrook *et al.*, 2001, *Molecular Cloning: A Laboratory Manual*, *supra*; Davis *et al.*, 1986, *Basic Methods in Molecular Biology*, Elsevier; Chu *et al.*, 1981, *Gene* 13:197. Transfection techniques include, but are not limited to, calcium phosphate-DNA co-precipitation, DEAE-dextran-mediated transfection, cationic lipid-mediated delivery, polybrene-mediated transfection, electroporation, sonoporation, microinjection, liposome fusion, lipofection (lipid transfection), polymer transfection, nanoparticles, polyplexes, receptor-mediated gene delivery, delivery mediated by polylysine,

histone, chitosan, and peptides, protoplast fusion, retroviral infection, and biolistics (e.g. Gene Gun). The term “transduction” and grammatical variations thereof refer to the process whereby foreign DNA is introduced into a cell via viral vector. See Jones *et al.*, (1998). Genetics: principles and analysis. Boston: Jones & Bartlett Publ.

[0060] As used herein, the term “infuse” and grammatical variations thereof mean to introduce a solution into a body through a blood vessel. An infusion of the present invention includes, but is not limited to, therapeutic introduction of a fluid other than whole blood into a blood vessel. For example, transfected T cells of the present invention may be infused into a patient’s bloodstream, for example, intramuscularly, intravenously, intraarterially, intraperitoneally, or subcutaneously.

[0061] It will be appreciated that chimeric antigen receptors (CARs or CAR-Ts) are, and T cell receptors (TCRs) may, be genetically engineered receptors. These engineered receptors may be readily inserted into and expressed by immune cells, including T cells in accordance with techniques known in the art. With a CAR, a single receptor may be programmed to both recognize a specific antigen and, when bound to that antigen, activate the immune cell to attack and destroy the cell bearing that antigen. When these antigens exist on tumor cells, an immune cell that expresses the CAR may target and kill the tumor cell.

[0062] CARs may be engineered to bind to an antigen (such as a cell-surface antigen) by incorporating an antigen binding molecule that interacts with that targeted antigen. An “antigen binding molecule” as used herein means any protein that binds a specified target molecule. Antigen binding molecules include, but are not limited to antibodies and binding parts thereof, such as immunologically functional fragments. Peptibodies (*i.e.*, Fc fusion molecules comprising peptide binding domains) are another example of suitable antigen binding molecules.

[0063] The term “immunologically functional fragment” (or “fragment”) of an

antigen binding molecule is a species of antigen binding molecule comprising a portion (regardless of how that portion is obtained or synthesized) of an antibody that lacks at least some of the amino acids present in a full-length chain but which is still capable of specifically binding to an antigen. Such fragments are biologically active in that they bind to the target antigen and may compete with other antigen binding molecules, including intact antibodies, for binding to a given epitope. In some embodiments, the fragments are neutralizing fragments. In one aspect, such a fragment will retain at least one CDR present in the full-length light or heavy chain, and in some embodiments will comprise a single heavy chain and/or light chain or portion thereof. These fragments may be produced by recombinant DNA techniques, or may be produced by enzymatic or chemical cleavage of antigen binding molecules, including intact antibodies.

[0064] Immunologically functional immunoglobulin fragments include, but are not limited to, scFv fragments, Fab fragments (Fab', F(ab')₂, and the like), one or more CDR, a diabody (heavy chain variable domain on the same polypeptide as a light chain variable domain, connected via a short peptide linker that is too short to permit pairing between the two domains on the same chain), domain antibodies, and single-chain antibodies. These fragments may be derived from any mammalian source, including but not limited to human, mouse, rat, camelid or rabbit. As will be appreciated by one of skill in the art, an antigen binding molecule may include non-protein components.

[0065] In some embodiments, the antigen binding molecule binds to an antigen on a tumor cell. In some embodiments, the antigen binding molecule binds to an antigen on a cell involved in a hyperproliferative disease or to a viral or bacterial antigen. In further embodiments, the antigen binding molecule is an antibody or fragment thereof, including one or more of the complementarity determining regions (CDRs) thereof. In further embodiments, the antigen binding molecule is a single chain variable fragment (scFv).

[0066] Preferably, the antigen binding molecule is an antibody fragment thereof. More preferably, the antigen binding molecule comprises one or more single chain variable fragment (“scFv”). An scFv is a single chain antibody fragment having the variable regions of the heavy and light chains of an antibody linked together. See U.S. Patent Nos. 7,741,465, 6,319,494, PCT application WO88/01649, and U.S. Patent Nos. 4,946,778 and 5,260,203, the disclosures of which are incorporated by reference in their entirety, as well as Eshhar *et al.*, *Cancer Immunol Immunotherapy* (1997) 45: 131-136. An scFv retains the parent antibody's ability to specifically interact with a target antigen. scFvs are preferred for use in chimeric antigen receptors because they may be engineered to be expressed as part of a single chain along with the other CAR components. *Id.* See also Krause *et al.*, *J. Exp. Med.*, Volume 188, No. 4, 1998 (619–626); Finney *et al.*, *Journal of Immunology*, 1998, 161: 2791–2797.

[0067] It will be appreciated that the antigen binding molecule is typically contained within the extracellular portion of the CAR such that it is capable of recognizing and binding to the antigen of interest. Bispecific and multispecific CARs are contemplated within the scope of the invention, with specificity to more than one target of interest.

[0068] In certain embodiments, the polypeptide structure of the antigen binding molecules is based on antibodies, including, but not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as “antibody mimetics”), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions (sometimes referred to herein as “antibody conjugates”), and fragments thereof, respectively. In some embodiments, the antigen binding molecule comprises or consists of avimers.

[0069] An antigen binding molecule is said to “specifically bind” its target antigen when the dissociation constant (K_d) is $\sim 1 \times 10^{-7}$ M. The antigen binding molecule specifically binds antigen with “high affinity” when the K_d is $1-5 \times 10^{-9}$ M, and with “very high affinity”

when the K_d is $1-5 \times 10^{-10}$ M. In one embodiment, the antigen binding molecule has a K_d of 10^{-9} M. In one embodiment, the off-rate is $<1 \times 10^{-5}$.

[0070] Those of ordinary skill in the art will understand that the target molecules of the present invention may be any molecule, the specificity for which is desired to be transferred to transfected T cells. The terms “target molecule” or “antigen” refers to a molecule or a portion of a molecule capable of being bound by an antigen binding molecule. In certain embodiments, a target may have one or more epitopes.

[0071] Preferably, target molecules of the present invention include, but are not limited to, blood borne cancer-associated antigens. Non-limiting examples of blood borne cancer-associated antigens include antigens associated with one or more cancers selected from the group consisting of acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), chronic myelomonocytic leukemia (CMML), juvenile myelomonocytic leukemia, atypical chronic myeloid leukemia, acute promyelocytic leukemia (APL), acute monoblastic leukemia, acute erythroid leukemia, acute megakaryoblastic leukemia, lymphoblastic leukemia, B-lineage acute lymphoblastic leukemia, B-cell chronic lymphocytic leukemia, B-cell non-Hodgkin's lymphoma, myelodysplastic syndrome (MDS), myeloproliferative disorder, myeloid neoplasm, myeloid sarcoma), and Blastic Plasmacytoid Dendritic Cell Neoplasm (BPDCN).

In some embodiments, the antigen is selected from a tumor-associated surface antigen, such as 5T4, alphafetoprotein (AFP), B7-1 (CD80), B7-2 (CD86), BCMA, B-human chorionic gonadotropin, CA-125, carcinoembryonic antigen (CEA), carcinoembryonic antigen (CEA), CD123, CD133, CD138, CD19, CD20, CD22, CD23, CD24, CD25, CD30, CD33, CD34, CD4, CD40, CD44, CD56, CD8, CLL-1, c-Met, CMV-specific antigen, CSPG4, CTLA-4, disialoganglioside GD2, ductal-epithelial mucine, EBV-specific antigen, EGFR variant III (EGFRvIII), ELF2M, endoglin, ephrin B2, epidermal growth factor receptor (EGFR),

epithelial cell adhesion molecule (EpCAM), epithelial tumor antigen, ErbB2 (HER2/neu), fibroblast associated protein (fap), FLT3, folate binding protein, GD2, GD3, glioma-associated antigen, glycosphingolipids, gp36, HBV-specific antigen, HCV-specific antigen, HER1-HER2, HER2-HER3 in combination, HERV-K, high molecular weight-melanoma associated antigen (HMW-MAA), HIV-1 envelope glycoprotein gp41, HPV-specific antigen, human telomerase reverse transcriptase, IGF1 receptor, IGF-II, IL-11Ralpha, IL-13R-a2, Influenza Virus-specific antigen; CD38, insulin growth factor (IGF1)-I, intestinal carboxyl esterase, kappa chain, LAGA-Ia, lambda chain, Lassa Virus-specific antigen, lectin-reactive AFP, lineage-specific or tissue specific antigen such as CD3, MAGE, MAGE-A1, major histocompatibility complex (MHC) molecule, major histocompatibility complex (MHC) molecule presenting a tumor-specific peptide epitope, M-CSF, melanoma-associated antigen, mesothelin, mesothelin, MN-CA IX, MUC-1, mut hsp72, mutated p53, mutated p53, mutated ras, neutrophil elastase, NKG2D, Nkp30, NY-ESO-1, p53, PAP, prostate specific antigen (PSA), prostate carcinoma tumor antigen-1 (PCTA-1), prostate-specific antigen, prostatein, PSMA, RAGE-1, ROR1, RU1, RU2 (AS), surface adhesion molecule, surviving and telomerase, TAG-72, the extra domain A (EDA) and extra domain B (EDB) of fibronectin and the A1 domain of tenascin-C (Tn C A1) , thyroglobulin, tumor stromal antigens, vascular endothelial growth factor receptor-2 (VEGFR2), virus-specific surface antigen such as an HIV-specific antigen (such as HIV gp120), as well as any derivate or variant of these surface markers.

[0072] In some embodiments, target molecules of the present invention include viral infection-associated antigens. Viral infections of the present invention may be caused by any virus, including, for example, HIV.

[0073] This list of possible target molecules is not intended to be exclusive and those of ordinary skill in the art will be aware of many additional molecules that would be useful to

target with the chimeric antigen receptors of the present invention.

[0074] Chimeric antigen receptors may incorporate costimulatory (signaling) domains to increase their potency. See U.S. Patent Nos. 7,741,465, and 6,319,494, as well as Krause *et al.* and Finney *et al.* (*supra*), Song *et al.*, Blood 119:696-706 (2012); Kalos *et al.*, Sci Transl. Med. 3:95 (2011); Porter *et al.*, N. Engl. J. Med. 365:725-33 (2011), and Gross *et al.*, Annu. Rev. Pharmacol. Toxicol. 56:59-83 (2016). For example, CD28 is a costimulatory protein found naturally on T-cells. A variety of costimulatory molecules are set forth herein, but it will be appreciated that additional costimulatory molecules are also included within the scope of this invention.

[0075] The complete native amino acid sequence of CD28 is described in NCBI Reference Sequence: NP_006130.1. The complete native CD28 nucleic acid sequence is described in NCBI Reference Sequence: NM_006139.1.

[0076] Certain CD28 domains have been used in chimeric antigen receptors. In accordance with the present invention, it has now been found that a novel CD28 extracellular (hinge) construct, termed “CD28T”, unexpectedly provides certain benefits when utilized in a CAR construct. This construct demonstrates the ability to retain (and at times exceed) the properties of CD28-containing CARs, despite truncation (removal) of multiple amino acids from the extracellular CD28 sequence. These benefits include equivalent or superior cytokine production, equivalent or superior cytolytic activity, and/or equivalent or superior CAR expression levels.

[0077] The nucleotide sequence of the CD28T molecule, including the extracellular domain, and the CD28 transmembrane and intracellular domains is set forth in SEQ ID NO. 1:

CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC
TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGT

GGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCT
GGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTC
CACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAG
ATTTGCTGCCTATCGGAGC

[0078] The corresponding amino acid sequence is set forth in SEQ ID NO. 2:

LDNEKSNGTIIHVKGKHLCP SPLFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVR
SK RSRL LHSDYM NMTPRRPGPT RKHYQPYAPP RDFAA YRS

[0079] The nucleotide sequence of the extracellular portion of CD28T is set forth in
SEQ ID NO. 3:

CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC
TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCA

[0080] The corresponding amino acid sequence of the CD28T extracellular domain is
set forth in SEQ ID NO. 4:

LDNEKSNGTI IHVKGKHLCP SPLFPGPSK

[0081] The nucleotide sequence of the CD28 transmembrane domain is set forth in
SEQ ID NO. 5:

TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCAC
CGTGGCTTTTATAATCTTCTGGGTT

[0082] The amino acid sequence of the CD28 transmembrane domain is set forth in
SEQ ID NO. 6:

FWVLVVVGGV LACYSLLVTV AFIIFWV

[0083] The nucleotide sequence of the CD28 intracellular signaling domain is set
forth in SEQ ID NO. 7:

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC

GCTGCCTATCGGAGC

[0084] The amino acid sequence of the CD28 intracellular signaling domain is set forth in SEQ ID NO. 8:

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

[0085] Additional CD28 sequences suitable for use in the invention include the CD28 nucleotide sequence set forth in SEQ ID NO. 11:

ATTGAGGTGATGTATCCACCGCCTTACCTGGATAACGAAAAGAGTAACGGTACC
ATCATTACGTGAAAGGTAAACACCTGTGTCCTTCTCCCCTCTTCCCCGGGCCAT
CAAAGCCC

[0086] The corresponding amino acid sequence is set forth in SEQ ID NO. 12:

IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKP

[0087] It will be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like comprising at least one isolated nucleic acid sequence of SEQ ID NO. 1 or SEQ ID NO. 3. It will further be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like wherein the extracellular portion consists of at least one isolated nucleic acid sequence of SEQ ID NO. 1 or SEQ ID NO. 3. Additionally, it will be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like wherein the extracellular portion consists essentially of at least one isolated nucleic acid sequence of SEQ ID NO. 1 or SEQ ID NO. 3.

[0088] It will be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like comprising at least one amino acid sequence of SEQ ID NO. 2 or SEQ ID NO. 4. It will further be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like wherein the extracellular portion consists of at least one amino acid sequence of SEQ ID NO. 2 or SEQ ID NO. 4. It will also be appreciated that the invention relates to antigen binding molecules, CARs, TCRs, and the like wherein the

extracellular portion consists essentially of at least one amino acid sequence of SEQ ID NO. 2 or SEQ ID NO. 4.

[0089] Another suitable source of extracellular and/or transmembrane domains may be derived from (or correspond to) some or all of CD8.

[0090] The nucleotide sequence of a suitable CD8 extracellular and transmembrane domain is set forth in SEQ ID NO. 13:

GCTGCAGCATTGAGCAACTCAATAATGTATTTTAGTCACTTTGTACCAGTGTCTT
GCCGGCTAAGCCTACTACCACACCCGCTCCACGGCCACCTACCCCAGCTCCTACC
ATCGCTTCACAGCCTCTGTCCCTGCGCCCAGAGGCTTGCCGACCGGCCGCAGGGG
GCGCTGTTTCATACCAGAGGACTGGATTTCGCCTGCGATATCTATATCTGGGCACC
CCTGGCCGGAACCTGCGGCGTACTCCTGCTGTCCCTGGTCATCACGCTCTATTGT
AATCACAGGAAC

[0091] The corresponding amino acid sequence is set forth in SEQ ID NO. 14:

AAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH
TRGLDFACDIYWAPLAGTCGVLLLSLVITLYCNHRN

[0092] Structurally, it will be appreciated that the domains described herein correspond to locations relative to an immune or other cell. These domains thus may be part of the (i) “hinge” or extracellular (EC) domain, (ii) the transmembrane (TM) domain, and/or (iii) the intracellular/cytoplasmic domain (IC). The intracellular component frequently comprises, in part, an activating domain such as a portion of a member of the CD3 family, preferably CD3 zeta. This domain is capable of activating the T cell upon binding of the antigen binding molecule to its target. It will be appreciated that the intracellular domain typically further comprises one or more costimulatory molecules as described herein.

[0093] A “costimulatory molecule” as used herein refers to a molecule that provides a signal which mediates a T cell response, including, but not limited to, proliferation,

activation, differentiation, and the like. Costimulatory molecules may provide a signal in addition to the primary signal provided by an activating molecule as described herein.

[0094] It will be appreciated that suitable costimulatory domains within the scope of the invention may be derived from (or correspond to) costimulatory molecules, such as, for example, CD28, CD28T, OX40, 4-1BB/CD137, CD2, CD3 (alpha, beta, delta, epsilon, gamma, zeta), CD4, CD5, CD7, CD9, CD16, CD22, CD27, CD30, CD 33, CD37, CD40, CD 45, CD64, CD80, CD86, CD134, CD137, CD154, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1 (CD11a/CD18), CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNF, TNFr, integrin, signaling lymphocytic activation molecule, BTLA, Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, CD83 ligand, or fragments or combinations thereof. It will be appreciated that additional costimulatory molecules, or fragments thereof, not listed above are within the scope of the invention.

[0095] In some embodiments, the costimulatory domain may comprise all or a portion of the 4-1BB nucleic acid sequence set forth in SEQ ID NO. 140, and the corresponding amino acid sequence as set forth in SEQ ID NO. 141. In other embodiments, the

costimulatory domain may comprise all or a portion of the amino acid sequence of OX40 as set forth in SEQ ID NO. 142. See also Hombach *et al.*, *Oncoimmunology*. 2012 Jul. 1; 1(4): 458–466. In still other embodiments, the costimulatory domain may comprise all or a portion of the ICOS molecule as described in Guedan *et al.*, August 14, 2014; Blood: 124 (7) and Shen *et al.*, *Journal of Hematology & Oncology* (2013) 6:33. In still other embodiments, the costimulatory domain may comprise all or a portion of CD27 as described in Song *et al.*, *Oncoimmunology*. 2012 Jul. 1;1(4): 547–549.

[0096] The engineered T cells of the invention comprise an antigen binding molecule (such as an scFv), an extracellular domain (which may comprise a “hinge” domain), a transmembrane domain, and an intracellular domain. The intracellular domain may comprise at least in part an activating domain, preferably comprised of a CD3 family member such as CD3 zeta, CD3 epsilon, CD3 gamma, or portions thereof.

[0097] It will further be appreciated that the antigen binding molecule (*e.g.*, one or more scFvs) is engineered such that it is located in the extracellular portion of the molecule/construct, such that it is capable of recognizing and binding to its target or targets.

[0098] It will be appreciated that the hinge region may contain some or all of a member of the immunoglobulin family such as IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, IgM, or fragment thereof.

[0099] In some embodiments, the extracellular domain is positioned between the antigen binding molecule and the transmembrane domain.

[0100] Extracellular domains of particular use in this invention may be derived from (*i.e.*, comprise) all or some of CD28, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1, CD11a/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT, (TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc

gamma receptor, MHC class 1 molecule, TNF receptor proteins, an Immunoglobulin protein, cytokine receptor, integrins, Signaling Lymphocytic Activation Molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof. The extracellular domain may be derived either from a natural or from a synthetic source.

[0101] Extracellular domains often comprise the hinge portion, sometimes referred to as the “spacer” region. A variety of hinges may be employed in accordance with the invention, including portions or derivatives of the molecules described herein.

[0102] The CAR may be designed with a transmembrane domain that is fused to the extracellular domain of the CAR. It may similarly be fused to the intracellular domain of the CAR. In some instances, the transmembrane domain may be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex. The transmembrane domain may be derived either from a natural or from a synthetic source. Where the source is natural, the domain may be derived from any membrane-bound or transmembrane protein. Transmembrane regions of particular use in this

invention may be derived from (comprise, or correspond to) CD28, CD28T, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1, CD11a/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT, (TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class 1 molecule, TNF receptor proteins, an Immunoglobulin protein, cytokine receptor, integrins, Signaling Lymphocytic Activation Molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof.

[0103] Optionally, short linkers may form linkages between any or some of the extracellular, transmembrane, and intracellular domains of the CAR.

[0104] In other embodiments, the transmembrane domain in the CAR of the invention is a CD8 transmembrane domain. In one embodiment, the CD8 transmembrane domain comprises the transmembrane portion of the nucleic acid sequence of SEQ ID NO: 13. In another embodiment, the CD8 transmembrane domain comprises the nucleic acid sequence that encodes the transmembrane amino acid sequence contained within SEQ ID NO: 14.

[0105] In certain embodiments, the transmembrane domain in the CAR of the

invention is the CD28 transmembrane domain. In one embodiment, the CD28 transmembrane domain comprises the nucleic acid sequence of SEQ ID NO: 5. In one embodiment, the CD28 transmembrane domain comprises the nucleic acid sequence that encodes the amino acid sequence of SEQ ID NO: 6. In another embodiment, the CD28 transmembrane domain comprises the amino acid sequence of SEQ ID NO: 6.

[0106] The intracellular (cytoplasmic) domain of the engineered T cells of the invention may provide activation of at least one of the normal effector functions of the immune cell. Effector function of a T cell, for example, may refer to cytolytic activity or helper activity, including the secretion of cytokines.

[0107] It will be appreciated that suitable intracellular molecules include (*i.e.*, comprise), but are not limited to signaling domains derived from (or corresponding to) CD28, CD28T, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1, CD11a/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT, (TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class 1 molecule, TNF receptor proteins, an Immunoglobulin protein, cytokine receptor, integrins, Signaling Lymphocytic Activation Molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3),

BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof.

[0108] In a preferred embodiment, the intracellular/cytoplasmic domain of the CAR may be designed to comprise the CD3 zeta domain by itself or combined with any other desired intracellular domain(s) useful in the context of the CAR of the invention. For example, the intracellular domain of the CAR may comprise a CD3 zeta chain portion and a portion of a costimulatory signaling molecule. The intracellular signaling sequences within the intracellular signaling portion of the CAR of the invention may be linked to each other in a random or specified order.

[0109] In another preferred embodiment, the intracellular domain is designed to comprise the activating domain of CD3 zeta and a signaling domain of CD28. In another embodiment, the intracellular domain is designed to comprise the activating domain of CD3 zeta and a signaling domain of 4-1BB. In another embodiment, the intracellular domain in the CAR is designed to comprise a portion of CD28 and CD3 zeta, wherein the intracellular CD28 comprises the nucleic acid sequence set forth in SEQ ID NO: 7 and the amino acid sequence set forth in SEQ ID NO. 8. The CD3 zeta nucleic acid sequence is set forth in SEQ ID NO: 9, and the amino acid sequence is set forth in SEQ ID NO. 8.

[0110] “Activation” or “stimulation” as used herein, refers to a primary response induced by binding of an activating molecule with its cognate ligand, wherein the binding mediates a signal transduction event.

[0111] An “activating molecule” or “stimulating molecule” refers to a molecule on a T cell, *e.g.*, the TCR/CD3 complex that specifically binds with a cognate stimulatory ligand present on an antigen present cell. Suitable activating molecules are described herein.

[0112] It will be appreciated that suitable activation domains within the scope of the invention may be derived from (or correspond to) activating / stimulating molecules, such as,

for example, CD3 or CD3 zeta. CD3 is an element of the T cell receptor on native T cells, and has been shown to be an important intracellular activating element in CARs.

[0113] In a preferred embodiment, the CD3 is CD3 zeta, the nucleotide sequence of which is set forth in SEQ ID NO. 9:

AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAAC
CAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGT
ACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAG
CCCTGCCACCTAGG

[0114] The corresponding amino acid of intracellular CD3 zeta is set forth in SEQ ID NO. 10:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR
RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH
MQALPPR

[0115] It will be appreciated that one preferred orientation of the CARs in accordance with the invention comprises an antigen binding molecule (such as scFv) in tandem with an extracellular and/or hinge domain, a costimulatory domain, and an activating domain. It will be further appreciated that multiple domains may be utilized in tandem.

[0116] Exemplary CAR constructs in accordance with the invention are set forth in Table 1:

Table 1

Construct Name	scFv	Hinge Domain	Activating Domain
24C1 CD28T	24C1	CD28T	CD3 zeta

24C1 CD28	24C1	CD28	CD3 zeta
24C1 CD8	24C1	CD8	CD3 zeta
24C8 CD28T	24C8	CD28T	CD3 zeta
24C8 CD28	24C8	CD28	CD3 zeta
24C8 CD8	24C8	CD8	CD3 zeta
20C5.1 CD28T	20C5.1	CD28T	CD3 zeta
20C5.1 CD28	20C5.1	CD28	CD3 zeta
20C5.1 CD8	20C5.1	CD8	CD3 zeta
20C5.2 CD28T	20C5.2	CD28T	CD3 zeta
20C5.2 CD28	20C5.2	CD28	CD3 zeta
20C5.2 CD8	20C5.2	CD8	CD3 zeta

[0117] The term “vector” means any molecule or entity (*e.g.*, nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell. The term “expression vector” or “expression construct” refers to a vector that is suitable for transformation of a host cell and contains nucleic acid sequences that direct and/or control (in conjunction with the host cell) expression of one or more heterologous coding regions operatively linked thereto. An expression construct may include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto.

[0118] The term “host cell” refers to a cell that has been transformed, or is capable of being transformed, with a nucleic acid sequence and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present.

[0119] The term “transformation” refers to a change in a cell's genetic characteristics, and a cell has been transformed when it has been modified to contain new DNA or RNA. For example, a cell is transformed where it is genetically modified from its native state by introducing new genetic material via transfection, transduction, or other techniques. Following transfection or transduction, the transforming DNA may recombine with that of the cell by physically integrating into a chromosome of the cell, or may be maintained transiently as an episomal element without being replicated, or may replicate independently as a plasmid. A cell is considered to have been “stably transformed” when the transforming DNA is replicated with the division of the cell.

[0120] The invention further relates to isolated polynucleotides encoding the chimeric antigen receptors (CARs) and T cell receptors (TCRs) of the present invention, as well as vectors comprising the polynucleotides. Any vector known in the art may be suitable for the present invention. In some embodiments, the vector is a viral vector. In some embodiments, the vector is a retroviral vector (such as pMSVG1), a DNA vector, a murine leukemia virus vector, an SFG vector, a plasmid, a RNA vector, an adenoviral vector, a baculoviral vector, an Epstein Barr viral vector, a papovaviral vector, a vaccinia viral vector, a herpes simplex viral vector, an adenovirus associated vector (AAV), a lentiviral vector (such as pGAR), or any derivative or combination thereof.

[0121] The pGAR sequence is as follows:

CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCA
GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCT
TCCTTTCTCGCCACGTTCCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCC
TTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAG
GGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGA
CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACT

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CAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTTCGGCCT
ATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAAT
ATTAACGCTTACAATTTGCCATTTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGG
CGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT
GCAAGGCGATTAAGTTGGGTAAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAA
ACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGACCCGGGGATGGCG
CGCCAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCG
TTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT
TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAG
TGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGC
CTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATC
TACGTATTAGTCATCGCTATTACCATGCTGATGCGGTTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGT
CAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAAC
AACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTAT
ATAAGCAGAGCTGGTTTAGTGAACCGGGGTCTCTCTGGTTAGACCAGATCTGAGC
CTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTG
CCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGA
GATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAAC
AGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACGCAGGACTCG
GCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCC
AAAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCA
GTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGGTTAAGGCCAG
GGGGAAAGAAAAAATATAAATTAACATATAGTATGGGCAAGCAGGGAGCTA

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GAACGATTTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAA
ATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAACTTAGATCA
TTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAG
ACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAAAGTAAGACC
ACCGCACAGCAAGCCGCCGCTGATCTTCAGACCTGGAGGAGGAGATATGAGGGA
CAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGG
AGTAGCACCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAG
TGGAATAGGAGCTTTGTTCCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGG
CGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGT
GCAGCAGCAGAACAAATTTGCTGAGGGCTATTGAGGCGCAACAGCATCTGTTGCA
ACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTGTGGAAAG
ATACCTAAAGGATCAACAGCTCCTGGGGATTGTTGGGTTGCTCTGGAAACTCATT
TGCACCACTGCTGTGCCTTGAATGCTAGTTGGAGTAATAAATCTCTGGAACAGA
TTTGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAATTACACAA
GCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAAC
AAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTTTAACATAAC
AAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGGTAGGT
TTAAGAATAGTTTTTGTCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATT
CACCATTATCGTTTCAGACCCACCTCCCAACCCCGAGGGGACCCGACAGGCCCG
AAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTTCGATTA
GTGAACGGATCTCGACGGTATCGGTAACTTTTAAAAGAAAAGGGGGGATTGGG
GGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAAC
TAAAGAATTACAAAAACAAATTACAAAATTCAAAATTTTATCGCGATCGCGGAA
TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAA
GGCATGGAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTTAGGAACA

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GAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCC
CCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGT
TTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCT
GTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCT
GCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCCTT
CGAAGTAGATCTTTGTCGATCCTACCATCCACTCGACACACCCGCCAGCGGCCGC
TGCCAAGCTTCCGAGCTCTCGAATTAATTCACGGTACCCACCATGGCCTAGGGAG
ACTAGTCGAATCGATATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGG
TATTCTTAACATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTT
GTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTG
GTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTG
TGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTC
AGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACATCATC
GCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATT
CCGTGGTGTTGTCGGGGAAGCTGACGTCCTTTTCATGGCTGCTCGCCTGTGTTGC
CACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCA
GCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCG
CCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCCTGGTTAA
TTAAAGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTT
TTTAAAAGAAAAGGGGGGACTGGAAGGGCGAATTCCTCCCAACGAAGACAAG
ATCTGCTTTTTTGCTTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAG
CTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAG
TGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCT
CAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGGCATGCCAGACATGATAA
GATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAAATGCT

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TTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT
AAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGG
TGTGGGAGGTTTTTTGGCGCGCCATCGTCGAGGTTCCCTTTAGTGAGGGTTAATT
GCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCT
CACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGC
CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGCTTTCCAG
TCGGGAAACCTGTCTGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGA
GGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT
ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAGGCCAGC
AAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCC
GCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC
TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA
GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGT
TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC
TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC
TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA
CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTG
GTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG
ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAG
ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT
CTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATC
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATC
TAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGG

CACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTC
 GTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATG
 ATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
 GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAG
 TCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
 GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGTTTGGTAT
 GGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATG
 TTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGT
 TGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTC
 ATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCT
 GAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCCGGCGTCAATACGGGATA
 ATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTC
 GGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCC
 ACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTG
 AGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGA
 AATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGT
 TATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCAC

[0122] Suitable additional exemplary vectors include e.g., pBABE-puro, pBABE-neo largeTcDNA, pBABE-hygro-hTERT, pMKO.1 GFP, MSCV-IRES-GFP, pMSCV PIG (Puro IRES GFP empty plasmid), pMSCV-loxp-dsRed-loxp-eGFP-Puro-WPRE, MSCV IRES Luciferase, pMIG, MDH1-PGK-GFP_2.0, TtRMPVIR, pMSCV-IRES-mCherry FP, pRetroX GFP T2A Cre, pRXTN, pLncEXP, and pLXIN-Luc.

[0123] In a further embodiment, a mixture of different expression vectors may be used in genetically modifying a donor population of immune effector cells wherein each

vector encodes a different CAR as disclosed herein. The resulting transduced immune effector cells form a mixed population of engineered cells, with a proportion of the engineered cells expressing more than one different CARs.

[0124] In a preferred embodiment of the present invention, the CAR comprises all or part of an anti-CD19 scFv, CD28, and CD3 zeta.

[0125] Transfected T cells of the present invention may also be created by transfecting the collected T cells with a polynucleotide encoding a T cell receptor (TCR). T cell receptors (TCRs) are molecules found on the surface of T cells that are responsible for recognizing antigen fragments as peptides bound to major histocompatibility complex (MHC) molecules. The TCR is comprised of two different protein chains - in approximately 95% of human TCRs, the TCR consists of an alpha (α) and beta (β) chain. In approximately 5% of human T cells the TCR consists of gamma and delta (γ/δ) chains. Each chain is composed of two extracellular domains: a variable (V) region and a constant (C) region, both of the immunoglobulin superfamily. As in other immunoglobulins, the variable domains of the TCR α -chain and β -chain (or gamma and delta (γ/δ) chains) each have three hypervariable or complementarity determining regions (CDRs). When the TCR engages with antigenic peptide and MHC (peptide/MHC), the T cell becomes activated, enabling it to attack and destroy the target cell.

[0126] The TCRs of the present invention may bind to, for example, a tumor-associated antigen. As used herein, "tumor-associated antigen" refers to any antigen that is associated with one or more cancers selected from the group consisting of: adrenocortical carcinoma, anal cancer, bladder cancer, bone cancer, brain cancer, breast cancer, carcinoid cancer, carcinoma, cervical cancer, colon cancer, endometrial cancer, esophageal cancer, extrahepatic bile duct cancer, extracranial germ cell cancer, eye cancer, gallbladder cancer, gastric cancer, germ cell tumor, gestational trophoblastic tumor, head and neck cancer,

hypopharyngeal cancer, islet cell carcinoma, kidney cancer, large intestine cancer, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer, lymphoma, malignant mesothelioma, Merkel cell carcinoma, mycosis fungoides, myelodysplastic syndrome, myeloproliferative disorders, nasopharyngeal cancer, neuroblastoma, oral cancer, oropharyngeal cancer, osteosarcoma, ovarian epithelial cancer, ovarian germ cell cancer, pancreatic cancer, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pituitary cancer, plasma cell neoplasm, prostate cancer, rhabdomyosarcoma, rectal cancer, renal cell cancer, transitional cell cancer of the renal pelvis and ureter, salivary gland cancer, Sezary syndrome, skin cancers, small intestine cancer, soft tissue sarcoma, stomach cancer, testicular cancer, thymoma, thyroid cancer, urethral cancer, uterine cancer, vaginal cancer, vulvar cancer, and Wilms' tumor.

[0127] In certain aspects, the present application may be suitable for target molecule to hematologic cancer. In some embodiments, the cancer is of the white blood cells. In other embodiments, the cancer is of the plasma cells. In some embodiments, the cancer is leukemia, lymphoma, or myeloma. In certain embodiments, the cancer is acute lymphoblastic leukemia (ALL) (including non T cell ALL), acute lymphoid leukemia (ALL), and hemophagocytic lymphohistocytosis (HLH)), B cell prolymphocytic leukemia, B-cell acute lymphoid leukemia ("BALL"), blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloid leukemia (CML), chronic or acute granulomatous disease, chronic or acute leukemia, diffuse large B cell lymphoma, diffuse large B cell lymphoma (DLBCL), follicular lymphoma, follicular lymphoma (FL), hairy cell leukemia, hemophagocytic syndrome (Macrophage Activating Syndrome (MAS), Hodgkin's Disease, large cell granuloma, leukocyte adhesion deficiency, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, monoclonal gammopathy of undetermined

significance (MGUS), multiple myeloma, myelodysplasia and myelodysplastic syndrome (MDS), myeloid diseases including but not limited to acute myeloid leukemia (AML), non-Hodgkin's lymphoma (NHL), plasma cell proliferative disorders (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, plasmacytomas (e.g., plasma cell dyscrasia; solitary myeloma; solitary plasmacytoma; extramedullary plasmacytoma; and multiple plasmacytoma), POEMS syndrome (Crow-Fukase syndrome; Takatsuki disease; PEP syndrome), primary mediastinal large B cell lymphoma (PMBCL), small cell- or a large cell-follicular lymphoma, splenic marginal zone lymphoma (SMZL), systemic amyloid light chain amyloidosis, T-cell acute lymphoid leukemia (TALL), T-cell lymphoma, transformed follicular lymphoma, Waldenstrom macroglobulinemia, or a combination thereof.

[0128] In some embodiments, the antigen is selected from a tumor-associated surface antigen, such as 5T4, alphafetoprotein (AFP), B7-1 (CD80), B7-2 (CD86), BCMA, B-human chorionic gonadotropin, CA-125, carcinoembryonic antigen (CEA), carcinoembryonic antigen (CEA), CD123, CD133, CD138, CD19, CD20, CD22, CD23, CD24, CD25, CD30, CD33, CD34, CD4, CD40, CD44, CD56, CD8, CLL-1, c-Met, CMV-specific antigen, CSPG4, CTLA-4, disialoganglioside GD2, ductal-epithelial mucine, EBV-specific antigen, EGFR variant III (EGFRvIII), ELF2M, endoglin, ephrin B2, epidermal growth factor receptor (EGFR), epithelial cell adhesion molecule (EpCAM), epithelial tumor antigen, ErbB2 (HER2/neu), fibroblast associated protein (fap), FLT3, folate binding protein, GD2, GD3, glioma-associated antigen, glycosphingolipids, gp36, HBV- specific antigen, HCV-specific antigen, HER1-HER2, HER2-HER3 in combination, HERV-K, high molecular weight-melanoma associated antigen (HMW-MAA), HIV-1 envelope glycoprotein gp41, HPV-specific antigen, human telomerase reverse transcriptase, IGFI receptor, IGF-II, IL-11Ralpha, IL-13R-a2, Influenza Virus-specific antigen; CD38, insulin growth factor (IGFI)-I,

intestinal carboxyl esterase, kappa chain, LAGA-Ia, lambda chain, Lassa Virus-specific antigen, lectin-reactive AFP, lineage-specific or tissue specific antigen such as CD3, MAGE, MAGE-A1, major histocompatibility complex (MHC) molecule, major histocompatibility complex (MHC) molecule presenting a tumor-specific peptide epitope, M-CSF, melanoma-associated antigen, mesothelin, mesothelin, MN-CA IX, MUC-1, mut hsp72, mutated p53, mutated p53, mutated ras, neutrophil elastase, NKG2D, Nkp30, NY-ESO-1, p53, PAP, prostate, prostate specific antigen (PSA), prostate carcinoma tumor antigen-1 (PCTA-1), prostate-specific antigen, prostein, PSMA, RAGE-1, ROR1, RU1, RU2 (AS), surface adhesion molecule, surviving and telomerase, TAG-72, the extra domain A (EDA) and extra domain B (EDB) of fibronectin and the A1 domain of tenascin-C (TnC A1), thyroglobulin, tumor stromal antigens, vascular endothelial growth factor receptor-2 (VEGFR2), virus-specific surface antigen such as an HIV-specific antigen (such as HIV gp120), as well as any derivative or variant of these surface markers.

[0129] The TCRs of the present invention may also bind to a viral infection-associated antigen. Viral infection-associated antigens include antigens associated with any viral infection, including, for example, viral infection caused by HIV.

[0130] To initiate the patient-specific immunotherapy procedure described herein, a physician or other medical personnel at client computing device 102a accesses the user interface module 108a of server computing device 106 (e.g., via a web portal, web site, or other similar platform). The user interface module 108a generates user interface screens and/or elements for presentation to the physician on the client computing device 102a, in order for the physician to enroll the patient and initiate the patient-specific immunotherapy procedure. The user interface module 108a may generate UI screens to enable the physician to enter the patient's identifying information (e.g., full name, date of birth), demographics (e.g., gender), and healthcare provider information (e.g., physician name, hospital name).

The user interface module 108a may also provide a UI element for entry of a healthcare-provider-specific or hospital-specific user identifier (e.g., medical record number, hospital patient ID). FIGS. 3A and 3B are exemplary screenshots generated by the user interface module 108a that enable enrollment of new patients into the system; FIG. 3A depicts the patient enrollment data entry screen, and FIG. 3B depicts a patient information review and confirmation screen.

[0131] Turning back to FIG. 2, the client computing device 102a generates a request to create transfected T cells for a patient, and the server computing device 106 receives (202) the request. As described above, the physician at client computing device 102a interacts with the user interface module 108a to enroll the patient by providing the necessary patient information. Once the user interface module 108a receives confirmation from the client computing device 102a that the patient information has been fully entered and is accurate, the user interface module 108a stores the data in database 110. The user interface module 108a also generates (204) a patient-specific identifier that will be used as part of the sample tracking and chain-of-custody / chain-of-identity process described below. In one embodiment, the patient-specific identifier comprises a patient identity element (e.g., a patient ID number), a sales order identifier, and a cell order lot number. For example, the user interface module 108a may generate the patient-specific identifier by mapping the patient identity element, sales order number, and cell order lot number into a database table that is indexed with an identifier (e.g., a nine-digit numeric code) that uniquely identifies the patient, sales order, and cell lot combination.

[0132] Next, the physician at client computing device 102a interacts with the user interface module 108a to schedule an appointment to obtain the biological material from the patient and, due to the time sensitivity of providing the altered biological material back to the patient quickly, confirming that the manufacturing facility has availability to process the

biological material shortly after the material is obtained. The user interface module 108a requests confirmation of the material extraction site (e.g., site name, address, contact information) for drop-off of an extraction kit (e.g., leukapheresis kit) and confirmation of the altered material delivery and treatment site (e.g., site name, address, contact information) for delivery of the material (e.g., transfected T cells) from the manufacturing facility. FIGS. 4A-4D are exemplary screenshots generated by the user interface module 108a that enable confirmation of these sites and scheduling of the appointment; FIG. 4A depicts the drop-off site confirmation screen, FIG. 4B depicts the material delivery site confirmation screen; FIG. 4C depicts the screen to open the appointment scheduler; and FIG. 4D depicts the appointment scheduler. In some embodiments, the user interface module 108a communicates with a remote computing device of the manufacturing facility, in conjunction with the database 110, to coordinate scheduling of the biological material modification to ensure the most efficient processing schedule so that the modified material is returned quickly back to the patient.

[0133] Turning back to FIG. 2, once the cell order process is complete as described above, a process 206 is initiated to perform the biological material extraction procedure at the extraction site, ship the extracted material to the manufacturing facility for modification, and send the modified material back to a delivery site for infusion back into the patient's bloodstream. First, the patient arrives at the material extraction site and a procedure (e.g., a leukapheresis procedure) is performed (206a) on a sample of the patient's blood to collect T cells from the sample. When the procedure is performed, a client computing device (e.g., device 102b) at the extraction site communicates with the event tracking module 108b of server computing device 106 to transmit a tracking event to the module 108b that corresponds to performance of the procedure. For example, a clinician at client computing device 102b may submit the tracking event by entering information into a user interface. In another

example, the client computing device 102b may automatically transmit the tracking event to the module 108b (e.g., via API) when information about the procedure is captured by the client computing device 102b (e.g., scanning a barcode).

[0134] The tracking event may comprise the patient-specific identifier, a timestamp, an event ID (e.g., that indicates a material extraction procedure was performed), and other information relevant to the process (e.g., cell order lot number, sales order number, site location, etc.). The event tracking module 108b stores the tracking event in database 110 based upon the information received from the client computing device 102b. Because this is the first step in the biological material extraction and modification process, the event tracking module 108b notifies the chain of custody module 108c of receipt of the tracking event. The chain of custody module 108c generates a chain of custody data structure (e.g., in database 110) that incorporates the tracking event (and each subsequent tracking event described herein) in an ordered sequence that enables the patient, the physician, the manufacturer, and other parties to understand the precise status of the biological material and to ensure that the biological material is accounted for at all times in avoidance of loss or mishandling. In an example, the chain of custody data structure may be a linked list that connects each of the tracking events together in a sequential manner according to, e.g., timestamp of the tracking event.

[0135] Next, the collected T cells are transferred (206b) to a container (e.g., a tube, vial, or other type of biological material carrier) and another tracking event is captured and transmitted to the event tracking module 108b for integration into the chain of custody data structure described above. Then, the container is labeled (206c) with the patient-specific identifier, and another tracking event is captured and transmitted to the event tracking module 108b for communication with the chain of custody module 108c to integrate into the chain of custody data structure. For example, the container that houses the collected T cells is labeled

with a barcode comprising the patient-specific identifier, which is then scanned at the extraction site—indicating that the collected T cells are ready for shipment to the manufacturing facility. Upon scanning the barcode, the client computing device 102b generates the tracking event and transmits the event to the event tracking module 108b.

[0136] Then, the extraction site transmits (206d) the collected T cells to the manufacturing facility, which performs the procedure to generate the transfected T cells. Both when the collected T cells are shipped to the manufacturing facility and when the collected T cells are received at the manufacturing facility, one or more of the devices used to record the shipment and receipt of the T cells communicate with the event tracking module 108b to transmit a tracking event associated with the particular activity for communication with the chain of custody module 108c to integrate into the chain of custody. In this way, the chain of custody module 108c automatically and continuously updates the chain of custody data structure with the latest information, and that information is reflected in one or more screens generated by the user interface module 108a.

[0137] The manufacturing facility then creates (206e) transfected T cells from the collected T cells using a cell modification technique, and a client computing device (e.g., device 102c) generates one or more tracking events based upon the particular cell modification technique being used. For example, a cell modification technique may comprise several phases—such as (i) quality assurance of the collected T cells prior to modification, (ii) modification of the T cells; (ii) release testing of the transfected T cells, and (iv) finalization of the transfected T cells for shipment back to the infusion site. For each of these phases, the client computing device 102c captures a tracking event and transmits the tracking event to the event tracking module 108b for integration by the chain of custody module 108c into the chain of custody data structure.

[0138] Once the transfected T cells are shipped, the infusion site receives (206f) the transfected T cells and a client computing device (e.g., device 102d) generates a tracking event for transmission to the event tracking module 108b for integration by the chain of custody module 108c into the chain of custody data structure. For example, the client computing device 102d may scan a barcode associated with the shipment and/or the transfected T cells to automatically generate the tracking event and transmit the event to the server computing device 106.

[0139] After receipt, the transfected T cells are infused (206g) into the patient's bloodstream, thereby completing the process. At the same time, the client computing device 102d generates a tracking event and transmits the event to the event tracking module 108b for integration by the chain of custody module 108c into the chain of custody data structure.

[0140] FIGS. 5A and 5B are exemplary screenshots generated by the user interface module 108a to enable the client computing devices 102a-102d to view the chain of custody associated with a particular patient, biological material, and cell modification process. As shown in FIG. 5A, the chain of custody of the biological material during the leukapheresis process (including the steps of scheduling the procedure, completing the procedure, and having the extracted T cells ready for shipment) is captured in a timeline at the top of the screen, where each step of the leukapheresis process is associated with a point on the timeline, and the chain of custody of the biological material during the delivery process (e.g., T cells shipped from extraction site, T cells delivered to manufacturing facility) is captured in a timeline at the bottom of the screen. When the event tracking module 108b and chain of custody module 108c record a tracking event as described above, the user interface module 108a traverses the chain of custody data structure to graphically represent the current status of the chain of custody on screen.

[0141] As shown in FIG. 5B, the chain of custody of the biological material during the manufacturing process (including QA, manufacturing, release testing, and finalizing for shipment) is shown in a timeline at the top of the screen, and the chain of custody of the biological material during the final product delivery process (including shipment and delivery to the infusion site) is shown in the middle of the screen. In addition, the treatment details, including the treatment date, are displayed at the bottom of the screen. Also, the chain of custody is constantly associated with the specific patient—thereby ensuring a complete chain of identity between the patient and the biological material during all phases of manufacturing.

[0142] The above-described techniques may be implemented in digital and/or analog electronic circuitry, or in computer hardware, firmware, software, or in combinations of them. The implementation may be as a computer program product, i.e., a computer program tangibly embodied in a machine-readable storage device, for execution by, or to control the operation of, a data processing apparatus, e.g., a programmable processor, a computer, and/or multiple computers. A computer program may be written in any form of computer or programming language, including source code, compiled code, interpreted code and/or machine code, and the computer program may be deployed in any form, including as a stand-alone program or as a subroutine, element, or other unit suitable for use in a computing environment. A computer program may be deployed to be executed on one computer or on multiple computers at one or more sites. The computer program may be deployed in a cloud computing environment (e.g., Amazon® AWS, Microsoft® Azure, IBM®).

[0143] Method steps may be performed by one or more processors executing a computer program to perform functions of the invention by operating on input data and/or generating output data. Method steps may also be performed by, and an apparatus may be implemented as, special purpose logic circuitry, e.g., a FPGA (field programmable gate array), a FPAA (field-programmable analog array), a CPLD (complex programmable logic

device), a PSoC (Programmable System-on-Chip), ASIP (application-specific instruction-set processor), or an ASIC (application-specific integrated circuit), or the like. Subroutines may refer to portions of the stored computer program and/or the processor, and/or the special circuitry that implement one or more functions.

[0144] Processors suitable for the execution of a computer program include, by way of example, special purpose microprocessors specifically programmed with instructions executable to perform the methods described herein. Generally, a processor receives instructions and data from a read-only memory or a random access memory or both. The essential elements of a computer are a processor for executing instructions and one or more memory devices for storing instructions and/or data. Memory devices, such as a cache, may be used to temporarily store data. Memory devices may also be used for long-term data storage. Generally, a computer also includes, or is operatively coupled to receive data from or transfer data to, or both, one or more mass storage devices for storing data, e.g., magnetic, magneto-optical disks, or optical disks. A computer may also be operatively coupled to a communications network in order to receive instructions and/or data from the network and/or to transfer instructions and/or data to the network. Computer-readable storage mediums suitable for embodying computer program instructions and data include all forms of volatile and non-volatile memory, including by way of example semiconductor memory devices, e.g., DRAM, SRAM, EPROM, EEPROM, and flash memory devices; magnetic disks, e.g., internal hard disks or removable disks; magneto-optical disks; and optical disks, e.g., CD, DVD, HD-DVD, and Blu-ray disks. The processor and the memory may be supplemented by and/or incorporated in special purpose logic circuitry.

[0145] To provide for interaction with a user, the above described techniques may be implemented on a computing device in communication with a display device, e.g., a CRT (cathode ray tube), plasma, or LCD (liquid crystal display) monitor, a mobile device display

or screen, a holographic device and/or projector, for displaying information to the user and a keyboard and a pointing device, e.g., a mouse, a trackball, a touchpad, or a motion sensor, by which the user may provide input to the computer (e.g., interact with a user interface element). Other kinds of devices may be used to provide for interaction with a user as well; for example, feedback provided to the user may be any form of sensory feedback, e.g., visual feedback, auditory feedback, or tactile feedback; and input from the user may be received in any form, including acoustic, speech, and/or tactile input.

[0146] The above-described techniques may be implemented in a distributed computing system that includes a back-end component. The back-end component may, for example, be a data server, a middleware component, and/or an application server. The above described techniques may be implemented in a distributed computing system that includes a front-end component. The front-end component may, for example, be a client computer having a graphical user interface, a Web browser through which a user may interact with an example implementation, and/or other graphical user interfaces for a transmitting device. The above described techniques may be implemented in a distributed computing system that includes any combination of such back-end, middleware, or front-end components.

[0147] The components of the computing system may be interconnected by transmission medium, which may include any form or medium of digital or analog data communication (e.g., a communication network). Transmission medium may include one or more packet-based networks and/or one or more circuit-based networks in any configuration. Packet-based networks may include, for example, the Internet, a carrier internet protocol (IP) network (e.g., local area network (LAN), wide area network (WAN), campus area network (CAN), metropolitan area network (MAN), home area network (HAN)), a private IP network, an IP private branch exchange (IPBX), a wireless network (e.g., radio access network (RAN), Bluetooth, near field communications (NFC) network, Wi-Fi, WiMAX, general packet radio

service (GPRS) network, HiperLAN), and/or other packet-based networks. Circuit-based networks may include, for example, the public switched telephone network (PSTN), a legacy private branch exchange (PBX), a wireless network (e.g., RAN, code-division multiple access (CDMA) network, time division multiple access (TDMA) network, global system for mobile communications (GSM) network), and/or other circuit-based networks.

[0148] Information transfer over transmission medium may be based on one or more communication protocols. Communication protocols may include, for example, Ethernet protocol, Internet Protocol (IP), Voice over IP (VOIP), a Peer-to-Peer (P2P) protocol, Hypertext Transfer Protocol (HTTP), Session Initiation Protocol (SIP), H.323, Media Gateway Control Protocol (MGCP), Signaling System #7 (SS7), a Global System for Mobile Communications (GSM) protocol, a Push-to-Talk (PTT) protocol, a PTT over Cellular (POC) protocol, Universal Mobile Telecommunications System (UMTS), 3GPP Long Term Evolution (LTE) and/or other communication protocols.

[0149] Devices of the computing system may include, for example, a computer, a computer with a browser device, a telephone, an IP phone, a mobile device (e.g., cellular phone, personal digital assistant (PDA) device, smart phone, tablet, laptop computer, electronic mail device), and/or other communication devices. The browser device includes, for example, a computer (e.g., desktop computer and/or laptop computer) with a World Wide Web browser (e.g., Chrome™ from Google, Inc., Microsoft® Internet Explorer® available from Microsoft Corporation, and/or Mozilla® Firefox available from Mozilla Corporation). Mobile computing device include, for example, a Blackberry® from Research in Motion, an iPhone® from Apple Corporation, and/or an Android™-based device. IP phones include, for example, a Cisco® Unified IP Phone 7985G and/or a Cisco® Unified Wireless Phone 7920 available from Cisco Systems, Inc.

Additional Definitions

[0150] The terms “polypeptide” or “protein” refer to a macromolecule having the amino acid sequence of a protein, including deletions from, additions to, and/or substitutions of one or more amino acids of the native sequence, and preferably no more than 8 amino acid substitutions therein. Preferably, the polypeptides or proteins are isolated as defined herein. The term “polypeptide fragment” refers to an isolated polypeptide that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion as compared with the full-length native protein. Such fragments may also contain modified amino acids as compared with the native protein. Useful polypeptide fragments include immunologically functional fragments of antigen binding molecules. Useful fragments include but are not limited to one or more CDR regions, variable domains of a heavy and/or light chain, a portion of other portions of an antibody chain, and the like.

[0151] The term “antibody” refers to an intact immunoglobulin of any isotype, or a fragment thereof that may compete with the intact antibody for specific binding to the target antigen / molecule, and includes, for instance, chimeric, humanized, fully human, and bispecific antibodies. An “antibody” is a species of an antigen binding molecule as defined herein. An intact antibody will generally comprise at least two full-length heavy chains and two full-length light chains, but in some instances may include fewer chains such as antibodies naturally occurring in camelids which may comprise only heavy chains. Antibodies may be derived solely from a single source, or may be chimeric, that is, different portions of the antibody may be derived from two different antibodies as described further below. The antigen binding molecules, antibodies, or binding fragments may be produced in hybridomas, by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies. Unless otherwise indicated, the term “antibody” includes, in addition to antibodies comprising two full-length heavy chains and two full-length light chains, derivatives, variants, fragments, and muteins thereof, examples of which are described below.

Furthermore, unless explicitly excluded, antibodies include monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as “antibody mimetics”), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions (sometimes referred to herein as “antibody conjugates”) and fragments thereof, respectively.

[0152] The variable regions typically exhibit the same general structure of relatively conserved framework regions (FR) joined by the 3 hypervariable regions (*i.e.*, “CDRs”). The CDRs from the two chains of each pair typically are aligned by the framework regions, which may enable binding to a specific epitope. From N-terminal to C-terminal, both light and heavy chain variable regions typically comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. By convention, CDR regions in the heavy chain are typically referred to as HC CDR1, CDR2, and CDR3. The CDR regions in the light chain are typically referred to as LC CDR1, CDR2, and CDR3. The assignment of amino acids to each domain is typically in accordance with the definitions of Kabat, Chothia, or the AbM definition.

[0153] The term “Kabat numbering” and like terms are recognized in the art and refer to a system of numbering amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen-binding portion thereof. In certain aspects, the CDRs of an antibody may be determined according to the Kabat numbering system (*see, e.g.*, Kabat EA & Wu TT (1971) Ann NY Acad Sci 190: 382-391 and Kabat EA *et al.*, (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). Using the Kabat numbering system, CDRs within an antibody heavy chain molecule are typically present at amino acid positions 31 to 35, which optionally may include one or two additional amino acids, following 35 (referred to in the Kabat numbering scheme as 35A and 35B) (CDR1), amino acid positions 50 to 65 (CDR2), and amino acid positions 95 to 102 (CDR3). Using the Kabat numbering system,

CDRs within an antibody light chain molecule are typically present at amino acid positions 24 to 34 (CDR1), amino acid positions 50 to 56 (CDR2), and amino acid positions 89 to 97 (CDR3). In a specific embodiment, the CDRs of the antibodies described herein have been determined according to the Kabat numbering scheme.

[0154] In certain aspects, the CDRs of an antibody may be determined according to the Chothia numbering scheme, which refers to the location of immunoglobulin structural loops (*see, e.g.*, Chothia C & Lesk AM, (1987), J Mol Biol 196: 901-917; Al-Lazikani B *et al.*, (1997) J Mol Biol 273: 927-948; Chothia C *et al.*, (1992) J Mol Biol 227: 799-817; Tramontano A *et al.*, (1990) J Mol Biol 215(1): 175-82; and U.S. Patent No. 7,709,226). Typically, when using the Kabat numbering convention, the Chothia CDR-H1 loop is present at heavy chain amino acids 26 to 32, 33, or 34, the Chothia CDR-H2 loop is present at heavy chain amino acids 52 to 56, and the Chothia CDR-H3 loop is present at heavy chain amino acids 95 to 102, while the Chothia CDR-L1 loop is present at light chain amino acids 24 to 34, the Chothia CDR-L2 loop is present at light chain amino acids 50 to 56, and the Chothia CDR-L3 loop is present at light chain amino acids 89 to 97. The end of the Chothia CDR-HI loop when numbered using the Kabat numbering convention varies between H32 and H34 depending on the length of the loop (this is because the Kabat numbering scheme places the insertions at H35A and H35B; if neither 35A nor 35B is present, the loop ends at 32; if only 35A is present, the loop ends at 33; if both 35A and 35B are present, the loop ends at 34).

[0155] In a specific embodiment, the CDRs of the antibodies described herein have been determined according to the Chothia numbering scheme.

[0156] A number of definitions of the CDRs are commonly in use: Kabat numbering, Chothia numbering, AbM numbering, or contact numbering. The AbM definition is a compromise between the two used by Oxford Molecular's AbM antibody modelling software. The contact definition is based on an analysis of the available complex crystal structures.

Table 2: CDR Numbering

Loop	Kabat	AbM	Chothia	Contact
L1	L24--L34	L24--L34	L24--L34	L30--L36
L2	L50--L56	L50--L56	L50--L56	L46--L55
L3	L89--L97	L89--L97	L89--L97	L89--L96
H1	H31--H35B (Kabat Numbering)	H26--H35B	H26--H32..34	H30--H35B
H1	H31--H35 (Chothia Numbering)	H26--H35	H26--H32	H30--H35
H2	H50--H65	H50--H58	H52--H56	H47--H58
H3	H95--H102	H95--H102	H95--H102	H93--H101

[0157] As used herein, the term “heavy chain” when used in reference to an antibody may refer to any distinct type, *e.g.*, alpha (α), delta (δ), epsilon (ϵ), gamma (γ) and mu (μ), based on the amino acid sequence of the constant domain, which give rise to IgA, IgD, IgE, IgG and IgM classes of antibodies, respectively, including subclasses of IgG, *e.g.*, IgG₁, IgG₂, IgG₃ and IgG₄.

[0158] As used herein, the term “light chain” when used in reference to an antibody may refer to any distinct type, *e.g.*, kappa (κ) or lambda (λ) based on the amino acid sequence of the constant domains. Light chain amino acid sequences are well known in the art. In specific embodiments, the light chain is a human light chain.

[0159] The term “variable region” or “variable domain” refers to a portion of the light and/or heavy chains of an antibody, typically including approximately the amino-terminal 120 to 130 amino acids in the heavy chain and about 100 to 110 amino terminal amino acids in the light chain. The variable region of an antibody typically determines specificity of a particular antibody for its target.

[0160] Variability is not evenly distributed throughout the variable domains of antibodies or antigen binding molecules; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These subdomains are called “hypervariable regions” or “complementarity determining regions” (CDRs) as further described herein. The more conserved (*i.e.*, non-hypervariable) portions of the variable domains are called the “framework” regions (FRM or FR) and provide a scaffold for the six CDRs in three dimensional space to form an antigen-binding surface. The variable domains of naturally occurring heavy and light chains each comprise four FRM regions (FR1, FR2, FR3, and FR4), largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.*, described further herein).

[0161] Typically, CDRs form a loop structure that may be classified as a canonical structure. The term “canonical structure” refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure may be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as

within the conserved framework (i.e., outside of the loop). Assignment to a particular canonical class may therefore be made based on the presence of these key amino acid residues.

[0162] The term “canonical structure” may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.*, herein). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations may also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering may be described by the numbering system of Chothia *et al.* and/or revealed by other techniques, for example, crystallography and two- or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (*e.g.*, based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.* (herein) and their implications for construing canonical aspects of antibody structure, are described in the literature. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, eds. Harlow *et al.*, 1988.

[0163] The CDR3 of the light chain and, particularly, the CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. In vitro selection schemes in which CDR3 alone is varied may be used to vary the binding properties of an

antibody or determine which residues contribute to the binding of an antigen. Hence, CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, may be as short as two amino acid residues or greater than 26 amino acids.

[0164] As used herein, the terms “constant region” and “constant domain” are interchangeable and have a meaning common in the art. The constant region is an antibody portion, *e.g.*, a carboxyl terminal portion of a light and/or heavy chain which is not directly involved in binding of an antibody to antigen but which may exhibit various effector functions, such as interaction with the Fc receptor. The constant region of an immunoglobulin molecule generally has a more conserved amino acid sequence relative to an immunoglobulin variable domain.

[0165] An “Fc” region comprises two heavy chain fragments comprising the CH1 and CH2 domains of an antibody. The two heavy chain fragments are held together by two or more disulfide bonds and by hydrophobic interactions of the CH3 domains.

[0166] A “Fab fragment” comprises one light chain and the CH1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule. A “Fab” fragment” comprises one light chain and a portion of one heavy chain that contains the VH domain and the CH1 domain and also the region between the CH1 and CH2 domains, such that an interchain disulfide bond may be formed between the two heavy chains of two Fab' fragments to form an F(ab')₂ molecule. An “F(ab')₂ fragment” contains two light chains and two heavy chains containing a portion of the constant region between the CH1 and CH2 domains, such that an interchain disulfide bond is formed between the two heavy chains. An F(ab')₂ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

[0167] The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0168] A “bivalent antigen binding molecule” comprises two antigen binding sites. In some instances, the two binding sites have the same antigen specificities. Bivalent antigen binding molecules may be bispecific. A “multispecific antigen binding molecule” is one that targets more than one antigen or epitope. A “bispecific,” “dual-specific” or “bifunctional” antigen binding molecule is a hybrid antigen binding molecule or antibody, respectively, having two different antigen binding sites. The two binding sites of a bispecific antigen binding molecule will bind to two different epitopes, which may reside on the same or different protein targets.

[0169] “Binding affinity” generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen). Unless indicated otherwise, as used herein, “binding affinity” refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen). The affinity of a molecule X for its partner Y may generally be represented by the dissociation constant (K_D). Affinity may be measured and/or expressed in a number of ways known in the art, including, but not limited to, equilibrium dissociation constant (K_D), and equilibrium association constant (K_A). The K_D is calculated from the quotient of k_{off}/k_{on} , whereas K_A is calculated from the quotient of k_{on}/k_{off} . k_{on} refers to the association rate constant of, *e.g.*, an antibody to an antigen, and k_{off} refers to the dissociation of, *e.g.*, an antibody to an antigen. The k_{on} and k_{off} may be determined by techniques known to one of ordinary skill in the art, such as BIAcore[®] or KinExA.

[0170] The term “neutralizing” refers to an antigen binding molecule, scFv, or antibody, respectively, that binds to a ligand and prevents or reduces the biological effect of that ligand. This may be done, for example, by directly blocking a binding site on the ligand or by binding to the ligand and altering the ligand's ability to bind through indirect means (such as structural or energetic alterations in the ligand). In some embodiments, the term

may also denote an antigen binding molecule that prevents the protein to which it is bound from performing a biological function.

[0171] The term “compete” when used in the context of antigen binding molecules that compete for the same epitope means competition between antigen binding molecules as determined by an assay in which the antigen binding molecule (*e.g.*, antibody or immunologically functional fragment thereof) being tested prevents or inhibits (*e.g.*, reduces) specific binding of a reference antigen binding molecule to an antigen. Numerous types of competitive binding assays may be used to determine if one antigen binding molecule competes with another, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (Stahli *et al.*, 1983, *Methods in Enzymology* 9:242-253); solid phase direct biotin-avidin EIA (Kirkland *et al.*, 1986, *J. Immunol.* 137:3614-3619), solid phase direct labeled assay, solid phase direct labeled sandwich assay (Harlow and Lane, 1988, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press); solid phase direct label RIA using 1-125 label (Morel *et al.*, 1988, *Molec. Immunol.* 25:7-15); solid phase direct biotin-avidin EIA (Cheung, *et al.*, 1990, *Virology* 176:546-552); and direct labeled RIA (Moldenhauer *et al.*, 1990, *Scand. J. Immunol.* 32:77-82).

[0172] As used herein, the term “epitope” refers to a localized region of an antigen to which an antibody may specifically bind. An epitope may be, for example, contiguous amino acids of a polypeptide (linear or contiguous epitope) or an epitope may, for example, come together from two or more non-contiguous regions of a polypeptide or polypeptides (conformational, non-linear, discontinuous, or non-contiguous epitope). In certain embodiments, the epitope to which an antibody binds may be determined by, *e.g.*, NMR spectroscopy, X-ray diffraction crystallography studies, ELISA assays, hydrogen/deuterium exchange coupled with mass spectrometry (*e.g.*, liquid chromatography electrospray mass

spectrometry), array-based oligo-peptide scanning assays, and/or mutagenesis mapping (*e.g.*, site-directed mutagenesis mapping). For X-ray crystallography, crystallization may be accomplished using any of the known methods in the art (*e.g.*, Giegé R. *et al.*, (1994) *Acta Crystallogr D Biol Crystallogr* 50(Pt 4): 339-350; McPherson A (1990) *Eur J Biochem* 189: 1-23; Chayen NE (1997) *Structure* 5: 1269-1274; McPherson A (1976) *J Biol Chem* 251: 6300-6303). Antibody:antigen crystals may be studied using well known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; see *e.g.* *Meth Enzymol* (1985) volumes 114 & 115, eds Wyckoff HW *et al.*,; U.S. 2004/0014194), and BUSTER (Bricogne G (1993) *Acta Crystallogr D Biol Crystallogr* 49(Pt 1): 37-60; Bricogne G (1997) *Meth Enzymol* 276A: 361-423, ed Carter CW; Roversi P *et al.*, (2000) *Acta Crystallogr D Biol Crystallogr* 56(Pt 10): 1316-1323). Mutagenesis mapping studies may be accomplished using any method known to one of skill in the art. *See, e.g.*, Champe M *et al.*, (1995) *J Biol Chem* 270: 1388-1394 and Cunningham BC & Wells JA (1989) *Science* 244: 1081-1085 for a description of mutagenesis techniques, including alanine scanning mutagenesis techniques.

[0173] The term “genetically engineered” or “engineered” refers to a method of modifying the genome of a cell, including, but not limited to, deleting a coding or non-coding region or a portion thereof or inserting a coding region or a portion thereof. In some embodiments, the cell that is modified is a lymphocyte, *e.g.*, a T cell, which may either be obtained from a patient or a donor. The cell may be modified to express an exogenous construct, such as, *e.g.*, a chimeric antigen receptor (CAR) or a T cell receptor (TCR), which is incorporated into the cell's genome.

[0174] An “immune response” refers to the action of a cell of the immune system (for example, T lymphocytes, B lymphocytes, natural killer (NK) cells, macrophages, eosinophils, mast cells, dendritic cells and neutrophils) and soluble macromolecules produced by any of

these cells or the liver (including Abs, cytokines, and complement) that results in selective targeting, binding to, damage to, destruction of, and/or elimination from a vertebrate's body of invading pathogens, cells or tissues infected with pathogens, cancerous or other abnormal cells, or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues.

[0175] The term “immunotherapy” refers to the treatment of a subject afflicted with, or at risk of contracting or suffering a recurrence of, a disease by a method comprising inducing, enhancing, suppressing or otherwise modifying an immune response. Examples of immunotherapy include, but are not limited to, T cell therapies. T cell therapy may include adoptive T cell therapy, tumor-infiltrating lymphocyte (TIL) immunotherapy, autologous cell therapy, engineered autologous cell therapy (eACT), and allogeneic T cell transplantation. However, one of skill in the art would recognize that the conditioning methods disclosed herein would enhance the effectiveness of any transplanted T cell therapy. Examples of T cell therapies are described in U.S. Patent Publication Nos. 2014/0154228 and 2002/0006409, U.S. Patent No. 5,728,388, and International Publication No. WO 2008/081035.

[0176] The T cells of the immunotherapy may come from any source known in the art. For example, T cells may be differentiated *in vitro* from a hematopoietic stem cell population, or T cells may be obtained from a subject. T cells may be obtained from, *e.g.*, peripheral blood mononuclear cells (PBMCs), bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In addition, the T cells may be derived from one or more T cell lines available in the art. T cells may also be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as FICOLL™ separation and/or apheresis. Additional methods of isolating T cells for a T cell therapy are disclosed in U.S.

Patent Publication No. 2013/0287748, which is herein incorporated by references in its entirety.

[0177] The term “engineered Autologous Cell Therapy,” which may be abbreviated as “eACT™,” also known as adoptive cell transfer, is a process by which a patient's own T cells are collected and subsequently genetically altered to recognize and target one or more antigens expressed on the cell surface of one or more specific tumor cells or malignancies. T cells may be engineered to express, for example, chimeric antigen receptors (CAR) or T cell receptor (TCR). CAR positive (+) T cells are engineered to express an extracellular single chain variable fragment (scFv) with specificity for a particular tumor antigen linked to an intracellular signaling part comprising at least one costimulatory domain and at least one activating domain. The costimulatory domain may be derived from (or correspond to), *e.g.*, CD28, and the activating domain may be derived from (or correspond to) *e.g.*, CD3-zeta. In certain embodiments, the CAR is designed to have two, three, four, or more costimulatory domains.

[0178] The term “autologous” refers to any material derived from the same individual to which it is later to be re-introduced. For example, the engineered autologous cell therapy (eACT™) method described herein involves collection of lymphocytes from a patient, which are then engineered to express, *e.g.*, a CAR construct, and then administered back to the same patient.

[0179] The term “allogeneic” refers to any material derived from one individual which is then introduced to another individual of the same species, *e.g.*, allogeneic T cell transplantation.

[0180] Standard techniques may be used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (*e.g.*, electroporation, lipofection). Enzymatic reactions and purification techniques may be performed according to

manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures may be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. See, *e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)), which is incorporated herein by reference for any purpose.

[0181] Comprise, include, and/or plural forms of each are open ended and include the listed parts and may include additional parts that are not listed. And/or is open ended and includes one or more of the listed parts and combinations of the listed parts.

[0182] It will be understood that descriptions herein are exemplary and explanatory only and are not restrictive of the invention as claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise.

[0183] All documents, or portions of documents, cited in this application, including but not limited to patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose. As utilized in accordance with the present disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

[0184] In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including”, as well as other forms, such as “includes” and “included”, is not limiting. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one subunit unless specifically stated otherwise.

[0185] The citation of a reference herein should not be construed as an acknowledgement that such reference is prior art to the present invention. To the extent that

any of the definitions or terms provided in the references incorporated by reference differ from the terms and discussion provided herein, the present terms and definitions control.

[0186] One skilled in the art will realize the subject matter may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting of the subject matter described herein.

[0187] The following sequences will further exemplify the invention:

[0188] CD28T DNA Extracellular, transmembrane, intracellular

CTTGATAATGAAAAGTCAAACGGAACAATCATTACGTGAAGGGC
AAGCACCTCTGTCCGTCACCCCTTGTTCCCTGGTCCATCCAAGCCATT
CTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGC
TCGTCACCGTGGCTTTTATAATCTTCTGGGTAGATCCAAAAGAAG
CCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCT
GGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGC (SEQ ID NO. 1)

[0189] CD28T Extracellular, transmembrane, intracellular AA

LDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVWLVVVGGVLACYSLLV
TVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY
RS (SEQ ID NO. 2)

[0190] CD28T DNA - Extracellular

CTTGATAATGAAAAGTCAAACGGAACAATCATTACGTGAAGGGC
AAGCACCTCTGTCCGTCACCCCTTGTTCCCTGGTCCATCCAAGCCA
(SEQ ID NO. 3)

[0191] CD28T AA - Extracellular

LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP (SEQ ID NO. 4)

[0192] CD28 DNA Transmembrane Domain

TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCT
GCTCGTCACCGTGGCTTTTATAATCTTCTGGGT (SEQ ID NO. 5)

[0193] CD28 AA Transmembrane Domain

- [0194] FWVLVVVGGV LACYSLLVTV AFHFWV (SEQ ID NO. 6)
CD28 DNA Intracellular Domain
AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACG
CACCACCTAGAGATTTGCTGCCTATCGGAGC (SEQ ID NO. 7)
- [0195] CD28 AA Intracellular Domain
RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS (SEQ ID NO. 8)
- [0196] CD3 zeta DNA
AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAG
AGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGG
GTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATG
AGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCA
TGAAAGGAGAGCGGAGAAGGGGAAAAGGGGCACGACGGTTTGTAC
CAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACA
TGCAAGCCCTGCCACCTAGG (SEQ ID NO. 9)
- [0197] CD3 zeta AA
RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMG
GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG
LSTATKDTYDALHMQALPPR (SEQ ID NO. 10)
- [0198] CD28 DNA
ATTGAGGTGATGTATCCACCGCCTTACCTGGATAACGAAAAGAGTA
ACGGTACCATCATTACGTGAAAGGTAAACACCTGTGTCCTTCTCC
CCTCTTCCCCGGGCCATCAAAGCCC (SEQ ID NO. 11)
- [0199] CD28 AA
IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKP (SEQ ID NO. 12)
- [0200] CD8 DNA extracellular & transmembrane domain
GCTGCAGCATTGAGCAACTCAATAATGTATTTTAGTCACTTTGTAC
CAGTGTTCTTGCCGGCTAAGCCTACTACCACACCCGCTCCACGGCC

- ACCTACCCCAGCTCCTACCATCGCTTCACAGCCTCTGTCCCTGCGCC
CAGAGGCTTGCCGACCGGCCGCAGGGGGCGCTGTTCATAACCAGAG
GACTGGATTTCGCCTGCGATATCTATATCTGGGCACCCCTGGCCGG
AACCTGCGGCGTACTCCTGCTGTCCCTGGTCATCACGCTCTATTGTA
ATCACAGGAAC (SEQ ID NO. 13)
- [0201] CD8 AA extracellular & transmembrane Domain
- AAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEAC
RPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRN
(SEQ ID NO. 14)
- [0202] Clone 24C1 HC DNA
- CAGGTGCAGCTGCAGGAATCCGGACCGGGGCTGGTGAAGCCCAGC
GAGACTCTGAGTCTCACGTGTACAGTTTCTGGAGGTAGCATTAGCT
CCTACTATTGGTCATGGATAAAGGCAGCCCCCGGGAAGGGATTGG
AATGGATCGGCTATATTTACTACAGTGGGAGCACCAATTACAACCC
CTCACTGAAGTCTAGAGTTACAATCAGCGTTGACACCTCAAAGAAT
CAGTTCAGTTTGAAATTGTCTAGCGTCACAGCAGCTGATACAGCCG
TCTATTATTGTGTTTCTCTGGTCTATTGCGGTGGGGATTGTTACAGT
GGCTTTGACTATTGGGGGCAGGGTACTCTGGTTACAGTTTCTTCC
(SEQ ID NO. 15)
- [0203] Clone 24C1 HC AA (CDRs Underlined)
- QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
Y
IYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVSLV
YCGGDCYSGFDYWGQGTLVTVSS (SEQ ID NO. 16)
- [0204] Clone 24C1 HC AA CDR1: GGSISSY (SEQ ID NO. 17)
- [0205] Clone 24C1 HC AA CDR2: YYS GS (SEQ ID NO. 18)
- [0206] Clone 24C1 HC AA CDR3: LVYCGGDCYS GFDY (SEQ ID NO. 19)
- [0207] Clone 24C1 LC DNA
- GACATCCAGTTGACACAGAGCCCGAGTTCCTTGTCCGCCTCCGTCG
GGGATAGAGTGTCAATTACCTGTCAGGCCTCTCAGGATATTAATAA
CTTTCTGAATTGGTATCAGCAAAAGCCCGGAAAGGCACCCAAGCTG

TTGATTTACGACGCCAGTAACCTGGAGACAGGCGTGCCCTCCCGGT
TTAGTGGTAGCGGAAGCGGTACGGATTTTACCTTTACTATCAGCTC
TCTCCAACCCGAAGACATTGCAACCTACTATTGTCAACAATATGGA
AACCTGCCTTTTACATTTGGCGGCGGCACCAAGGTGGAGATTAAGC
GG (SEQ ID NO. 20)

[0208] Clone 24C1 LC AA (CDRs Underlined)

DIQLTQSPSSLSASVGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIY
DASNLETGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQQYGNLPFTFG
GGTKVEIKR (SEQ ID NO. 21)

[0209] Clone 24C1 LC CDR1 AA: QASQDINNFLN (SEQ ID NO. 22)

[0210] Clone 24C1 LC CDR2 AA: DASNLET (SEQ ID NO. 23)

[0211] Clone 24C1 LC CDR3 AA: QQYGNLPFT (SEQ ID NO. 24)

[0212] Clone 24C1 CD28T CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAACCTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTCCAACCTGCAAGAAAGCGGACCCGG
ACTGGTGAAGCCTTCTGAGACACTTAGTCTGACGTGCACGGTCAGT
GGCGGCTCCATCTCCTCCTATTATTGGTCATGGATACGACAACCCC
CAGGTAAGGGCCTGGAATGGATTGGCTATATCTACTATTCAGGAAG
CACGAACTACAATCCCAGCCTGAAGTCCCGAGTGACAATTTTCAGTA
GATACCAGTAAAAACCAGTTCAGTCTTAAACTGTCAAGCGTGACAG
CTGCCGACACCGCTGTGTATTACTGCGTCTCACTGGTGTATTGTGG
AGGGGATTGTTATAGCGGGTTCGATTATTGGGGACAGGGAACCCTG
GTGACTGTATCTTCCGGCGGCGGCGGCTCAGGGGGTGGCGGTAGTG
GCGGTGGGGGTTCGATATTCAACTGACACAATCCCCCAGCTCACT
CAGCGCCAGCGTGGGGGACAGGGTTAGCTTTACCTGTCAAGCCTCT
CAGGATATAAATAACTTTCTGAACTGGTATCAACAGAAGCCTGGGA
AGGCGCCCAAACCTCCTGATCTATGATGCGTCCAACCTGGAAACTGG
CGTGCCTTCACGCTTTAGCGGCTCTGGCAGTGGTACAGACTTCACT
TTTACCATCTCTTCACTTCAGCCGGAGGACATCGCCACATATTACTG
TCAACAGTACGGAACTTGCCCTTTACTTTTGGAGGCGGCACCAAA
GTTGAAATCAAAAGGGCCGCTGCCCTGGATAACGAAAAGAGCAAT
GGGACTATAATACATGTAAAGGAAAACACCTGTGTCCATCTCCCC

TGTTCCCTGGACCGTCAAAGCCATTTTGGGTGCTCGTGGTTGTCGGT
GGCGTTCTCGCCTGTTATAGCTTGCTGGTGACAGTAGCCTTCATTAT
CTTTTGGGTGAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTAC
ATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACC
AGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGCAGGGT
GAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAG
AACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTG
CAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA
GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGG
ACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAA
GCCCTGCCACCTAGGTAA (SEQ ID NO. 25)

[0213] Clone 24C1 CD28T CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **bold**)

MALPVTALLLPLALLHAARPQVQLQESGPLVKPSETLSLTCTVSG
GSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRVTISVDTSK
NQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWGGQGLTVTS
SGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTQCASQDINNF
LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFITISLQPE
DIATYYCQQYGNLPFTFGGGTKVEIKRAAALDNEKSNGTIIHVKGKHL
CPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS
DYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQ
GQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE
LQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA
LHMQUALPPR (SEQ ID NO. 26)

[0214] Clone 24C1 CD28T CD3 zeta CAR DNA Heavy & Light Chains

CAGGTCCAACCTGCAAGAAAGCGGACCCGGACTGGTGAAGCCTTCT
GAGACACTTAGTCTGACGTGCACGGTCAGTGGCGGCTCCATCTCCT
CCTATTATTGGTCATGGATACGACAACCCCCAGGTAAGGGCCTGGA
ATGGATTGGCTATATCTACTATTTCAGGAAGCACGAACACTACAATCCC
AGCCTGAAGTCCCGAGTGACAATTTTCAGTAGATACCAGTAAAAAC
CAGTTCAGTCTTAAACTGTCAAGCGTGACAGCTGCCGACACCGCTG

TGTATTACTGCGTCTCACTGGTGTATTGTGGAGGGGATTGTTATAGC
GGGTTCGATTATTGGGGACAGGGAACCCTGGTGACTGTATCTTCCG
GCGGCGGCGGCTCAGGGGGTGGCGGTAGTGGCGGTGGGGGTTCG
ATATTCAACTGACACAATCCCCCAGCTCACTCAGCGCCAGCGTGGG
GGACAGGGTTAGCTTTACCTGTCAAGCCTCTCAGGATATAAATAAC
TTTCTGAACTGGTATCAACAGAAGCCTGGGAAGGCGCCCAAACCTCC
TGATCTATGATGCGTCCAACCTGGAAACTGGCGTGCCTTCACGCTT
TAGCGGCTCTGGCAGTGGTACAGACTTCACTTTTACCATCTCTTCAC
TTCAGCCGGAGGACATCGCCACATATTACTGTCAACAGTACGGAAA
CTTGCCCTTTACTTTTGGAGGCGGCACCAAAGTTGAAATCAAAAGG
GCCGCTGCCCTGGATAACGAAAAGAGCAATGGGACTATAATACAT
GTAAAGGAAAACACCTGTGTCCATCTCCCCTGTTCCCTGGACCGT
CAAAGCCATTTTGGGTGCTCGTGGTTGTCTGGTGGCGTTCTCGCCTGT
TATAGCTTGCTGGTGACAGTAGCCTTCATTATCTTTTGGGTGAGATC
CAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCA
CGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCAC
CTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATC
TGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAA
CGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAA
AAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGA
TGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAA
GGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTA
CGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAG
G (SEQ ID NO. 27)

[0215]

Clone 24C1 CD28T CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
YIYYSGSTNYPNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCVSL
VYCGGDCYSGFDYWQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQS
PSSLSASVGDVRSFTCQASQDINNFLNWYQQKPGKAPKLLIYDASNLE
TGVPSRFSGSGSGTDFFTISSLQPEDATYYCQQYGNLPFTFGGGTKV
EIKRAAALDNEKSNGTIIHVKGKHLCPSPFLPGPSKPFVVLVVVGGVL
ACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAP

[0216]

PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK
RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG
KGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 28)

Clone 24C1 CD28 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTGCAGCTGCAGGAATCCGGACCGGG
GCTGGTGAAGCCCAGCGAGACTCTGAGTCTCACGTGTACAGTTTCT
GGAGGTAGCATTAGCTCCTACTATTGGTCATGGATAAGGCAGCCCC
CCGGGAAGGGATTGGAATGGATCGGCTATATTTACTACAGTGGGA
GCACCAATTACAACCCCTCACTGAAGTCTAGAGTTACAATCAGCGT
TGACACCTCAAAGAATCAGTTCAGTTTGAAATTGTCTAGCGTCACA
GCAGCTGATACAGCCGTCTATTATTGTGTTTCTCTGGTCTATTGCGG
TGGGGATTGTTACAGTGGCTTTGACTATTGGGGGCAGGGTACTCTG
GTTACAGTTTCTTCCGGGGGGGGAGGCTCTGGGGGCGGAGGCTCA
GGTGGTGGAGGCAGCGACATCCAGTTGACACAGAGCCCGAGTTCC
TTGTCCGCCTCCGTCGGGGATAGAGTGTCATTTACCTGTCAGGCCT
CTCAGGATATTAATAACTTTCTGAATTGGTATCAGCAAAAGCCCGG
AAAGGCACCCAAGCTGTTGATTTACGACGCCAGTAACCTGGAGAC
AGGCGTGCCCTCCCGGTTTAGTGGTAGCGGAAGCGGTACGGATTTT
ACCTTTACTATCAGCTCTCTCCAACCCGAAGACATTGCAACCTACT
ATTGTCAACAATATGGAAACCTGCCTTTTACATTTGGCGGCGGCAC
CAAGGTGGAGATTAAGCGGGCGGCAGCTATTGAGGTGATGTATCC
ACCGCCTTACCTGGATAACGAAAAGAGTAACGGTACCATCATTAC
GTGAAAGGTAAACACCTGTGTCCTTCTCCCCCTCTCCCCGGGCCAT
CAAAGCCCTTCTGGGTTCTTGTGGTCGTGGGAGGCGTGCTTGCTTG
TTATTCTCTGCTCGTTACCGTGGCGTTTATCATTTTTTTGGGTTAGATC
CAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCA
CGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCAC
CTAGAGATTTCTGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATC
TGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAA
CGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAA
AAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGA

TGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAA
GGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTA
CGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAG
GTAA (SEQ ID NO. 29)

[0217]

Clone 24C1 CD28 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLHAARPQVQLQESGPGLVKPSSETLSLTCTVSG
GSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTISVDTSK
NQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWGGQGLTVTS
SGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTCQASQDINNF
LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFITISLQPE
DIATYYCQQYGNLPFTFGGGTKVEIKRAAAIEVMYPPPYLDNEKSNGT
IIHVKGKHLCPSPFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVR
SKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRS
ADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK
NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK
DTYDALHMQALPPR (SEQ ID NO. 30)

[0218]

Clone 24C1 CD28 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGCTGCAGGAATCCGGACCGGGGCTGGTGAAGCCCAGC
GAGACTCTGAGTCTCACGTGTACAGTTTCTGGAGGTAGCATTAGCT
CCTACTATTGGTCATGGATAAGGCAGCCCCCGGGAAGGGATTGG
AATGGATCGGCTATATTTACTACAGTGGGAGCACCAATTACAACCC
CTCACTGAAGTCTAGAGTTACAATCAGCGTTGACACCTCAAAGAAT
CAGTTCAGTTTGAAATTGTCTAGCGTCACAGCAGCTGATACAGCCG
TCTATTATTGTGTTTCTCTGGTCTATTGCGGTGGGGATTGTTACAGT
GGCTTTGACTATTGGGGGCAGGGTACTCTGGTTACAGTTTCTTCCG
GGGGGGGAGGCTCTGGGGGCGGAGGCTCAGGTGGTGGAGGCAGCG
ACATCCAGTTGACACAGAGCCCGAGTTCCTTGTCCGCCTCCGTCGG
GGATAGAGTGTCATTTACCTGTCAGGCCTCTCAGGATATTAATAAC
TTTCTGAATTGGTATCAGCAAAGCCCGGAAAGGCACCCAAGCTGT
TGATTTACGACGCCAGTAACCTGGAGACAGGCGTGCCCTCCCGGTT
TAGTGGTAGCGGAAGCGGTACGGATTTTACCTTTACTATCAGCTCT
CTCCAACCCGAAGACATTGCAACCTACTATTGTCAACAATATGGAA

ACCTGCCTTTTACATTTGGCGGGCGGCACCAAGGTGGAGATTAAGCG
GGCGGCAGCTATTGAGGTGATGTATCCACCGCCTTACCTGGATAAC
GAAAAGAGTAACGGTACCATCATTACGTGAAAGGTAAACACCTG
TGTCCTTCTCCCCCTCTTCCCCGGGCCATCAAAGCCCTTCTGGGTTCT
TGTGGTCGTGGGAGGCGTGCTTGCTTGTTATTCTCTGCTCGTTACCG
TGGCGTTTATCATTTTTTGGGTTAGATCCAAAAGAAGCCGCCTGCT
CCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCT
ATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTA
TCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACG
CAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCC
TGAGATGGGTGGCAAACCAAGACGAAAAAACCCCAAGGAGGGTCT
CTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGA
AATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACG
GTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGC
TCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 31)

[0219] Clone 24C1 CD28 CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
YIYYSGSTNYPNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVSL
VYCGGDCYSGFDYWQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQS
PSSLSASVGDVRSFTCQASQDINNFLNWYQQKPGKAPKLLIYDASNLE
TGVPSRFSGSGSGTDFTFTISLQPEDATYYCQQYGNLPFTFGGGTKV
EIKRAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVW
LVVVGGVLACYSLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTR
KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
KGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR (SEQ ID NO.
32)

[0220] Clone 24C1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAACCTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTGCAATTGCAAGAGTCCGGCCCCGG
ACTCGTTAAACCCAGTGAGACGCTTAGCCTGACCTGTACCGTCTCA
GGGGGCAGCATCTCCTCTTATTACTGGAGCTGGATCAGGCAGCCTC

CAGGAAAAGGCCTTGAATGGATTGGGTACATCTACTACTCTGGCTC
 AACAAATTATAATCCATCCCTGAAGTCCCGCGTGACTATCTCTGTG
 GACACCAGCAAGAATCAGTTTTTCACTGAAGTTGTCTAGTGTTACCG
 CGGCCGACACCGCCGTATACTACTGTGTGTCTCTTGTGTACTGTGG
 CGGCGACTGCTATTCCGGGTTGCGACTACTGGGGCCAAGGGACTCTG
 GTAACCGTGTCTCAGGCGGCGGGCAGGAGGAGGCGGCAGT
 GGAGGTGGCGGCTCCGACATCCAGCTGACACAATCACCATCTTCCC
 TTTCAGCTTCAGTCGGGGACAGAGTGTCTTCACATGCCAGGCCAG
 CCAGGATATCAATAACTTCCTGAACTGGTACCAACAGAAACCCGG
 AAAGGCTCCAAAGCTCCTGATCTATGATGCTTCCAACCTGGAGACC
 GCGGTGCCCTCCAGGTTCACTGGTTCAGGATCAGGCACTGACTTTA
 CGTTCACCATATCCAGTCTTCAGCCCGAAGACATTGCAACCTATTA
 CTGCCAACAATACGGGAACCTTCCCTTTACATTCGGAGGCGGCACC
 AAGGTGGAAATCAAAAGGGCTGCAGCATTGAGCAACTCAATAATG
 TATTTTAGTCACTTTGTACCAGTGTCTTGCCGGCTAAGCCTACTAC
 CACACCCGCTCCACGGCCACCTACCCAGCTCCTACCATCGCTTCA
 CAGCCTCTGTCCCTGCGCCCAGAGGCTTGCCGACCGGCCGCAGGGG
 GCGCTGTTCCATACCAGAGGACTGGATTTGCGCTGCGATATCTATAT
 CTGGGCACCCCTGGCCGGAACCTGCGGCGTACTCCTGCTGTCCCTG
 GTCATCACGCTCTATTGTAATCACAGGAACAGATCCAAAAGAAGCC
 GCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGG
 CCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
 GCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCAC
 CAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACC
 TGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGAC
 GGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCAAG
 AGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCT
 ATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGG
 CACGACGGTTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTT
 ATGACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID
 NO. 33)

[0221]

Clone 24C1 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal peptide in **bold**)

MALPVTALLPLALLHAARPQVQLQESGPGLVKPSSETLSLTCTVSG
 GSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTISVDTSK
 NQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWGGTLVTVS
 SGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTCQASQDINNF
 LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFITISLQPE
 DIATYYCQQYGNLPFTFGGGTKVEIKRAAALSNSIMYFSHFVPVFLPA
 KPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYI
 WAPLAGTCGVLLLSLVITLYCNHRNRSKRSRLHSDYMNMTPRRPGP
 TRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR
 REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
 GMKGERRRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID
 NO. 34)

[0222]

Clone 24C1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAATTGCAAGAGTCCGGCCCCGGACTCGTTAAACCCAGTG
 AGACGCTTAGCCTGACCTGTACCGTCTCAGGGGGCAGCATCTCCTC
 TTATTACTGGAGCTGGATCAGGCAGCCTCCAGGAAAAGGCCTTGAA
 TGGATTGGGTACATCTACTACTCTGGCTCAACAAATTATAATCCAT
 CCCTGAAGTCCCGCGTGACTATCTCTGTGGACACCAGCAAGAATCA
 GTTTTCACTGAAGTTGTCTAGTGTTACCGCGGCCGACACCGCCGTA
 TACTACTGTGTGTCTCTTGTGTACTGTGGCGGCGACTGCTATTCCGG
 GTTCGACTACTGGGGCCAAGGGACTCTGGTAACCGTGTCTCAGGC
 GGCGGCGGGTCAGGAGGAGGCGGCAGTGGAGGTGGCGGCTCCGAC
 ATCCAGCTGACACAATCACCATCTTCCCTTTCAGCTTCAGTCGGGG
 ACAGAGTGTCTTCACATGCCAGGCCAGCCAGGATATCAATAACTT
 CCTGAACTGGTACCAACAGAAACCCGGAAAGGCTCAAAGCTCCT
 GATCTATGATGCTTCCAACCTGGAGACCGGCGTGCCCTCCAGGTTC
 AGTGGTTCAGGATCAGGCACTGACTTTACGTTCACCATATCCAGTC
 TTCAGCCCGAAGACATTGCAACCTATTACTGCCAACAATACGGGAA
 CCTTCCCTTTACATTCGGAGGCGGCACCAAGGTGGAAATCAAAAGG
 GCTGCAGCATTGAGCAACTCAATAATGTATTTTAGTCACTTTGTAC
 CAGTGTCTTGCCGGCTAAGCCTACTACCACACCCGCTCCACGGCC
 ACCTACCCAGCTCCTACCATCGCTTCACAGCCTCTGTCCCTGCGCC
 CAGAGGCTTGCCGACCGGCCGCAGGGGGCGCTGTTCATACCAGAG

GACTGGATTTCGCCTGCGATATCTATATCTGGGCACCCCTGGCCGG
AACCTGCGGCGTACTCCTGCTGTCCCTGGTCATCACGCTCTATTGTA
ATCACAGGAACAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATT
ACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACT
ACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGCAG
GGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGC
CAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAG
TATGACGTTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGT
GGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATG
AAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCA
GGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG
CAAGCCCTGCCACCTAGG (SEQ ID NO. 35)

[0223]

Clone 24C1 CD8 CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
YIYYSGSTNYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCVSL
VYCGGDCYSGFDYWQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQS
PSSLSASVGDVRSFTCQASQDINNFLNWYQQKPGKAPKLLIYDASNLE
TGVPSRFSGSGSGTDFTFITISLQPEDATYYCQYGNLPFTFGGGTKV
EIKRAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRP
EACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCNHR
NRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFS
RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR
KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT
K DTYDALHMQALPPR (SEQ ID NO. 36)

[0224]

Clone 24C1 CD28T CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAACCTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGGATATCCAGCTCACGCAATCCCCCTCAAGC
TTGAGTGCCTCCGTGGGCGACCGGGTGTCTTCACATGTCAGGCAA
GCCAAGACATAAATAATTCCTGAATTGGTACCAACAAAAACCCG
GCAAGGCTCCCAAACCTCCTGATTTATGATGCCTCCAATCTGGAGAC
CGGGGTCCCTTCTAGATTCAGCGGAAGTGGCAGCGGCACAGACTTT
ACATTTACTATCTCTTCTCTGCAACCAGAGGACATCGCCACATACT

ATTGCCAGCAATACGGCAATCTGCCCTTCACCTTCGGAGGCGGAAC
CAAGGTAGAAATTAAAAGGGGCGGTGGAGGCTCCGGAGGGGGGG
GCTCTGGCGGAGGGGGGCTCCCAAGTACAATTGCAGGAGTCAGGGC
CTGGACTCGTGAAGCCTTCAGAACTTTGTCACTGACATGTACAGT
GTCCGGCGGAAGCATTTCAGTTACTATTGGTCCTGGATTAGACAG
CCACCCGGCAAAGGACTGGAATGGATTGGATATATCTACTACTCTG
GATCTACAAACTATAATCCCAGCCTCAAATCCAGGGTCACTATTAG
TGTGGATACATCAAAGAATCAGTTCTCCTTGAAGCTGAGCTCAGTC
ACTGCTGCCGACACCGCAGTGTACTATTGTGTGAGCCTGGTCTACT
GCGGCGGAGATTGCTACAGCGGTTTCGATTACTGGGGCCAGGGCA
CCCTGGTTACCGTTAGTTCCGCGGCTGCTCTTGATAACGAGAAGTC
CAACGGTACGATTATCCACGTTAAGGGTAAGCACCTTTGCCCTAGC
CCGCTGTTCCCAGGCCCCAGTAAGCCCTTTTGGGTCCTCGTTGTGGT
AGGTGGGGTACTCGCCTGCTACTCCCTGCTCGTCACTGTTCGATTC
ATCATCTTCTGGGTCAGATCCAAAAGAAGCCGCCTGCTCCATAGCG
ATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACA
CTACCAGCCTTACGCACCACCTAGAGATTTGCTGCCTATCGGAGC
AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAG
AGTATGACGTTTTTGACAAGCGCAGAGGACGGGACCCTGAGATGG
GTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATG
AGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCA
TGAAAGGAGAGCGGAGAAGGGGAAAAGGGGCACGACGGTTTGTAC
CAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACA
TGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 37)

[0225]

Clone 24C1 CD28T CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLPLALLHAARPDIQLTQSPSSLSASVGDRVSTFCQAS
QDINNFLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGDTFTI
SSLQPEDIATYYCQQYGNLPFTFGGGTKVEIKRGGGSGGGGSGGGGS
QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
YIYYSGSTNYPNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCVSL
VYCGGDCYSGFDYWQGTLVTVSSAAALDNEKSNGTIIHVKGKHLCP

SPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSD
YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQG
QNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA
LHMQUALPPR (SEQ ID NO. 38)

[0226]

Clone 24C1 CD28T CD3 zeta CAR DNA Heavy & Light Chains

GATATCCAGCTCACGCAATCCCCCTCAAGCTTGAGTGCCTCCGTGG
GCGACCGGGTGTCTTCACATGTCAGGCAAGCCAAGACATAAATA
ATTTCTGAATTGGTACCAACAAAAACCCGGCAAGGCTCCCAA
CCTGATTTATGATGCCTCCAATCTGGAGACCGGGGTCCCTTCTAGA
TTCAGCGGAAGTGGCAGCGGCACAGACTTTACATTTACTATCTCTT
CTCTGCAACCAGAGGACATCGCCACATACTATTGCCAGCAATACGG
CAATCTGCCCTTCACCTTCGGAGGCGGAACCAAGGTAGAAATTA
AGGGGCGGTGGAGGCTCCGGAGGGGGGGGCTCTGGCGGAGGGGG
CTCCCAAGTACAATTGCAGGAGTCAGGGCCTGGACTCGTGAAGCCT
TCAGAACTTTGTCACTGACATGTACAGTGTCCGGCGGAAGCATTT
CCAGTTACTATTGGTCCTGGATTAGACAGCCACCCGGCAAAGGACT
GGAATGGATTGGATATATCTACTACTCTGGATCTACAACTATAAT
CCCAGCCTCAAATCCAGGGTCACTATTAGTGTGGATACATCAAAGA
ATCAGTTCTCCTTGAAGCTGAGCTCAGTCACTGCTGCCGACACCGC
AGTGTACTATTGTGTGAGCCTGGTCTACTGCGGCGGAGATTGCTAC
AGCGGTTTCGATTACTGGGGCCAGGGCACCCCTGGTTACCGTTAGTT
CCGCGGCTGCTCTTGATAACGAGAAGTCCAACGGTACGATTATCCA
CGTTAAGGGTAAGCACCTTTGCCCTAGCCCGCTGTTCCCAGGCCCC
AGTAAGCCCTTTTGGGTCCTCGTTGTGGTAGGTGGGGTACTCGCCT
GCTACTCCCTGCTCGTCACTGTCGCATTCATCATCTTCTGGGTCAGA
TCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTC
CACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACC
ACCTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGA
TCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTAT
AACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACG
AAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAA

GATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAG
AAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGC
TACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCT
AGG (SEQ ID NO. 39)

[0227]

Clone 24C1 CD28T CD3 zeta CAR AA Heavy & Light Chains

DIQLTQSPSSLSASVGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIY
DASNLETGVPSRFSGSGSGTDFTFTISLQPEDATYYCQQYGNLPFTFG
GGTKVEIKRGGGGSGGGGSGGGGSQVQLQESGPGLVKPSSETLSLTCT
VSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTISVD
TSKNQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWGGTLV
TVSSAAALDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVGGVL
ACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAP
PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK
RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG
KGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 40)

[0228]

Clone 24C1 CD28 CD3 zeta CAR DNA AA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGGATATCCAGCTGACCCAGTCTCCATCCTCT
TTGAGTGCTCCGTGGGTGACCGCGTCTCTTTCACTTGCCAAGCCA
GCCAAGACATCAACAACCTTTCTGAATTGGTACCAGCAGAAACCAG
GCAAAGCACCAAAGCTCCTCATCTACGACGCCTCCAACCTGGAAAC
CGGGGTGCCCAGCAGGTTTAGCGGGAGCGGTTCTGGCACGGATTTT
ACGTTACCATCTCCTCTCTGCAGCCCGAGGATATAGCTACTTATTA
CTGTCAGCAGTACGGGAATCTGCCATTTACTTTTGGGGGTGGAAC
AAGGTGGAAATCAAAAGGGGCGGCGGGGGAAGCGGGGGCGGGGG
CTCAGGTGGCGGAGGGAGCCAGGTGCAACTCCAGGAAAGTGGCCC
AGGATTGGTGAAGCCCAGCGAGACCCTTTCCCTTACTTGTACTGTT
AGCGGAGGCAGCATAAGCAGCTACTATTGGTCCTGGATCAGACAG
CCACCAGGGAAAGGGCTTGAATGGATTGGCTACATTTACTATTCCG
GGTCCACCAACTACAACCCATCCCTCAAGTCCCAGCTGACAATTTT
CGTCGACACAAGCAAGAACCAGTTCTCCCTGAAACTTAGTAGCGTC
ACTGCTGCAGATACAGCAGTGTACTATTGTGTCAGCCTTGTCTACT
GTGGCGGCGACTGCTACAGTGGCTTTGATTACTGGGGACAGGGCAC

GCTCGTGACAGTGTCCAGCGCTGCGGCTATCGAGGTAATGTATCCG
 CCACCGTATCTGGACAACGAGAAGTCTAATGGGACAATCATTACG
 TGAAGGGGAAGCACCTGTGTCCATCCCCCTGTTTCCGGGTCCCAG
 TAAACCCTTCTGGGTGCTTGTGTCTGTTGGCGGGGTGCTGGCCTGCT
 ATTCCCTGCTGGTGACCGTCGCGTTTATTATTTTCTGGGTAGATCC
 AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCAC
 GCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACC
 TAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
 GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC
 GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAG
 CGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAA
 AAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGAT
 GGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAG
 GGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
 GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG
 TAA (SEQ ID NO. 41)

[0229] Clone 24C1 CD28 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLPLALLHARPDIQLTQSPSSLSASVGDRVSF~~TCQAS~~
 QDINNFLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGDFTFTI
 SSLQPEDIATYYCQQYGNLPFTFGGGTKVEIKRGGGSGGGGSGGGGS
 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
 YIYYSGSTNYNPSLKS~~RV~~TISVDTSKNQFSLKLSSVTAADTAVYYCVSL
 VYCGGDCYSGFDYWQGTLVTVSSAAIEVMYPPPYLDNEKSNGTII
 HVKGKHLCPSP~~LP~~PGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVRS
 KRSRL~~LH~~SDYMNMT~~PR~~PGPTRKHYPYAPPRDFAAYRSRVKFSRSA
 DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP
 QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT
 YDALHMQALPPR (SEQ ID NO. 42)

[0230] Clone 24C1 CD28 CD3 zeta CAR DNA Heavy & Light Chains

GATATCCAGCTGACCCAGTCTCCATCCTCTTTGAGTGCCTCCGTGG
 GTGACCGCGTCTCTTTCACTTGCCAAGCCAGCCAAGACATCAACAA
 CTTTCTGAATTGGTACCAGCAGAAACCAGGCAAAGCACCAAAGCT

CCTCATCTACGACGCCTCCAACCTGGAAACCGGGGTGCCCAGCAGG
TTAGCGGGAGCGGTTCTGGCACGGATTTTACGTTACCATCTCCTC
TCTGCAGCCCGAGGATATAGCTACTTATTACTGTCAGCAGTACGGG
AATCTGCCATTTACTTTTGGGGGTGGAACTAAGGTGGAAATCAAAA
GGGGCGGCGGGGGAAGCGGGGGCGGGGGCTCAGGTGGCGGAGGG
AGCCAGGTGCAACTCCAGGAAAGTGGCCCAGGATTGGTGAAGCCC
AGCGAGACCCTTTCCTTACTTGTACTGTTAGCGGAGGCAGCATAA
GCAGCTACTATTGGTCCTGGATCAGACAGCCACCAGGGAAAGGGC
TTGAATGGATTGGCTACATTTACTATTCCGGGTCCACCAACTACAA
CCCATCCCTCAAGTCCCGCGTGACAATTTCCGTCGACACAAGCAAG
AACCAGTTCTCCCTGAACTTAGTAGCGTCACTGCTGCAGATACAG
CAGTGTACTATTGTGTCAGCCTTGTCTACTGTGGCGGCGACTGCTA
CAGTGGCTTTGATTACTGGGGACAGGGCACGCTCGTGACAGTGTCC
AGCGCTGCGGCTATCGAGGTAATGTATCCGCCACCGTATCTGGACA
ACGAGAAGTCTAATGGGACAATCATTACGTGAAGGGGAAGCACC
TGTGTCCATCCCCCTGTTTCCGGGTCCCAGTAAACCCTTCTGGGTG
CTTGTTGTCGTTGGCGGGGTGCTGGCCTGCTATTCCCTGCTGGTGAC
CGTCGCGTTTATTATTTTCTGGGTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCCGCCCTGGCCCCA
CAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCTGCTGC
CTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGA
CGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGAC
CCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTG
AAATAGGCATGAAAGGAGAGCGGAGAAAGGGGAAAAGGGCACGAC
GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACG
CTCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 43)

[0231]

Clone 24C1 CD28 CD3 zeta CAR AA Heavy & Light Chains

DIQLTQSPSSLSASVGDRVSFTCQASQDINNFLNWFYQQKPGKAPKLLIY
DASNLETGVPSRFSGSGSGTDFTFTISLQPEDATYYCQQYGNLPFTFG
GGTKVEIKRGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCT
VSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTVISVD

TSKNQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWQGTLV
TVSSAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPFVW
LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTR
KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
44)

[0232]

Clone 24C1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCCGGACATTCAATTGACCCAGTCCCCTAGCAGT
CTCTCAGCAAGTGTGGGAGATAGGGTGTTCATTACCTGTCAGGCTT
CACAGGACATCAACAACCTTCCTCAATTGGTATCAGCAGAAGCCAG
GGAAGGCACCAAAGCTGCTCATATATGACGCTTCAAACCTTGAAAC
CGGAGTACCTAGCCGCTTCAGCGGAAGCGGATCAGGGACTGACTT
CACTTTTACCATCTCTTCACTGCAGCCCGAAGACATCGCCACATAC
TACTGCCAGCAGTACGGAAACTTGCCTTTTACATTTGGGGGCGGCA
CCAAAGTGGAGATTAAGCGAGGGGGAGGCGGCTCAGGAGGCGGTG
GCTCCGGAGGCGGGGGTTCAGGTCCAGCTCCAGGAATCCGGCC
CAGGTCTGGTTAAGCCCAGTGAAACTTTGTCCCTCACGTGTACTGT
GAGCGGTGGTTCAATCTCCTCATACTATTGGTCTTGGATACGGCAA
CCTCCTGGAAAGGGCCTCGAGTGGATCGGCTATATCTACTATAGTG
GCTCCACTAATTACAACCCTTCCCTCAAGTCCAGAGTCACCATTTCC
GTGGACACATCTAAGAACCAGTTCAGTCTGAAGTTGTCCAGCGTTA
CAGCCGCAGACACAGCCGTTTATTACTGTGTGTCTCTTGTTTACTGC
GGGGGAGACTGTTATAGCGGCTTCGATTACTGGGGCCAGGGCACCT
TGGTCACAGTCTCTTCCGCGGCCGCCCTCTCTAACAGTATTATGTAC
TTTTCTCATTTTGTACCCGTGTTCCCTCCCGCTAAGCCAACTACTAC
CCCGGCCCCACGGCCGCCTACCCCTGCACCCACAATAGCCAGTCAG
CCTTTGAGCCTGAGACCTGAGGCTTGTCGGCCGGCTGCTGGGGGTG
CAGTGCACACACGAGGTCTTGATTTTGCTTGCGACATATACATCTG
GGCCCCCTCTGGCCGGGACCTGTGGGGTGCTGCTTCTGAGCTTGGTC
ATCACGCTCTATTGCAACCATCGCAACAGATCCAAAAGAAGCCGCC
TGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCC

CACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGCT
 GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAG
 CGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGG
 GACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGG
 ACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGG
 GTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
 TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACG
 ACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGA
 CGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 45)

[0233]

Clone 24C1 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLPLALLHAARPDIQLTQSPSSLSASVGDRVSFTCQAS
 QDINNFLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFI
 SSLQPEDIATYYCQQYGNLPFTFGGGTKVEIKRGGGSGGGGSGGGGS
 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIG
 YIYYSGSTNYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCVSL
 VYCGGDCYSGFDYWQGTLVTVSSAAALSNSIMYFSHFVPVFLPAKP
 TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW
 APLAGTCGVLLLSLVITLYCNHRNRSKRSRLHSDYMNMTPRRPGPTR
 KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
 EYDVLDKRRGRDPENGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
 KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
 46)

[0234]

Clone 24C1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

GACATTCAATTGACCCAGTCCCCTAGCAGTCTCTCAGCAAGTGTGG
 GAGATAGGGTGTCAATTCACCTGTCAGGCTTCACAGGACATCAACAA
 CTTCTCAATTGGTATCAGCAGAAGCCAGGGAAGGCACCAAAGCT
 GCTCATATATGACGCTTCAAACCTTGAAACCGGAGTACCTAGCCGC
 TTCAGCGGAAGCGGATCAGGGACTGACTTCACTTTTACCATCTCTT
 CACTGCAGCCCGAAGACATCGCCACATACTACTGCCAGCAGTACG
 GAAACTTGCCCTTTTACATTTGGGGGCGGCACCAAAGTGGAGATTAA
 GCGAGGGGGAGGCGGCTCAGGAGGCGGTGGCTCCGGAGGCGGGG
 GTTCCCAGGTCCAGCTCCAGGAATCCGGCCCAGGTCTGGTTAAGCC

CAGTGAAACTTTGTCCCTCACGTGTACTGTGAGCGGTGGTTCAATC
 TCCTCATACTATTGGTCTTGGATACGGCAACCTCCTGGAAAGGGCC
 TCGAGTGGATCGGCTATATCTACTATAGTGGCTCCACTAATTACAA
 CCCTTCCCTCAAGTCCAGAGTCACCATTTCGTGGACACATCTAAG
 AACCAGTTCAGTCTGAAGTTGTCCAGCGTTACAGCCGCAGACACAG
 CCGTTTATTACTGTGTGTCTCTTGTTTACTGCGGGGGAGACTGTTAT
 AGCGGCTTCGATTACTGGGGCCAGGGCACCTTGGTCACAGTCTCTT
 CCGCGGCCGCCCTCTCTAACAGTATTATGTACTTTTCTCATTTTGTA
 CCCGTGTTCTTCCCGCTAAGCCAACTACTACCCCGGCCCCACGGC
 CGCCTACCCCTGCACCCACAATAGCCAGTCAGCCTTTGAGCCTGAG
 ACCTGAGGCTTGTCGGCCGGCTGCTGGGGGTGCAGTGCACACACG
 AGGTCTTGATTTTGCTTGCGACATATACATCTGGGCCCTCTGGCCG
 GGACCTGTGGGGTGCTGCTTCTGAGCTTGGTCATCACGCTCTATTG
 CAACCATCGCAACAGATCCAAAAGAAGCCGCCTGCTCCATAGCGA
 TTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACAC
 TACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCA
 GGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGG
 CCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
 GTATGACGTTTTTGACAAGCGCAGAGGACGGGACCCTGAGATGGG
 TGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGA
 GCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCAT
 GAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACC
 AGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACAT
 GCAAGCCCTGCCACCTAGG (SEQ ID NO. 47)

[0235]

Clone 24C1 CD8 CD3 zeta CAR AA Heavy & Light Chains

DIQLTQSPSSLSASVGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIY
 DASNLETGVPSRFSGSGSGTDFTFTISLQPEDATYYCQQYGNLPFTFG
 GGTKVEIKRGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCT
 VSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTISVD
 TSKNQFSLKLSSVTADTAVYYCVSLVYCGGDCYSGFDYWQGTLVT
 VSSAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPE
 ACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRN
 RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSR

- SADAPAYQQGQNQLYNELNLGREEYDVLDKRRGRDPEMGGKPRRKN
PQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGHDGLYQGLSTATK
DTYDALHMQA LPPR (SEQ ID NO. 48)
- [0236] Clone 24C8 Heavy Chain (HC) DNA
- CAGGTACAGCTGCAGGAATCTGGGCCCCGGAAGTGTCAAGCCAAGT
CAGACACTTTCTCTTACATGTACCGTGAGCGGCGGAAGTATAAGCA
GTGGAGGCTTTTACTGGTCTTGATACGGCAGCACCCAGGCAAAGG
CTTGGAGTGGATTGGATACATTCATCATTAGGATCTACACACTAT
AATCCATCCCTTAAGTCCCGGGTCACCATTAGCATTGATACGTCTA
AGAATCTGTTCAGTCTCAGGCTGTCTCCGTCAGTGTGCGGACAC
AGCCGTGTACTACTGCGCCTCCTTGGTTTACTGCGGAGGCGACTGT
TATAGCGGCTTTGATTATTGGGGGCAGGGGACCCTCGTAACCGTGA
GCTCT (SEQ ID NO. 49)
- [0237] Clone 24C8 AA HC (CDRs in Underline)
- QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGFYWSWIRQHPGKGLE
WIGYIHHSGSTHYNPSLKSRTVISIDTSKNLFSRLSSVTAADTAVYYC
ASLVYCGGDCYSGFDYWGQGTLLVTVSS (SEQ ID NO. 50)
- [0238] Clone 24C8 HC CDR1 AA: GGSISSGGF (SEQ ID NO. 51)
- [0239] Clone 24C8 HC CDR2 AA: HHSGS (SEQ ID NO. 52)
- [0240] Clone 24C8 HC CDR3 AA: LVYCGGDCYS GFDY (SEQ ID NO. 53)
- [0241] Clone 24C8 Light Chain (LC) DNA
- GATATCCAGCTCACTCAAAGCCCCTCTAGTCTCTCTGCCTCAGTGG
GGGATCGGGTCAGTTTTACTTGTCAAGCTTCACAGGATATCAACAA
CTTCCTTAATTGGTATCAGCAGAAGCCAGGAAAAGCACCCAAGCTG
CTCATCTATGATGCCTCAAATTTGGAGACGGGTGTTCCAGTCGAT
TCTCTGGGTCAGGGTCCGGGACCGACTTTACGTTTACGATCTCCTCT
CTGCAGCCCGAAGACATCGCCACATACTATTGTCAACAGTACGGCA
ACTTGCCTTTCACATTTGGGGGCGGGACTAAGGTTGAAATCAAGAG
G (SEQ ID NO. 54)
- [0242] Clone 24C8 LC AA (CDRs in Underline)

DIQLTQSPSSLSASVGDRVSFTCQASQDINNFLN WYQQKPGKAPKLLIY
DASNLETGVPSRFSGSGSGTDFTFITSSSLQPEDIATYYCQQYGNLPFTFG
 GGTKVEIKR (SEQ ID NO. 55)

[0243] Clone 24C8 LC CDR1 AA: QASQDINNFLN (SEQ ID NO. 56)

[0244] Clone 24C8 LC CDR2 AA: DASNLET (SEQ ID NO. 57)

[0245] Clone 24C8 LC CDR3 AA: QQYGNLPFT (SEQ ID NO. 58)

[0246] Clone 24C8 CD28T CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
 GCACGCCGCACGCCCGCAGGTACAGCTGCAGGAATCTGGGCCCCG
 ACTTGTCAAGCCAAGTCAGACACTTTCTCTTACATGTACCGTGAGC
 GGCGGAAGTATAAGCAGTGGAGGCTTTTACTGGTCTTGGATACGGC
 AGCACCCAGGCAAAGGCTTGGAGTGGATTGGATACATTCATCATTC
 AGGATCTACACACTATAATCCATCCCTTAAGTCCCGGGTCACCAT
 AGCATTGATACGTCTAAGAATCTGTTCAGTCTCAGGCTGTCCTCCG
 TCACTGCTGCCGACACAGCCGTGTACTACTGCGCCTCCTTGGTTTAC
 TGCGGAGGCGACTGTTATAGCGGCTTTGATTATTGGGGGCAGGGGA
 CCCTCGTAACCGTGAGCTCTGGAGGGGGGTGGGAGCGGGGGAGGAG
 GTTCAGGGGGGGGGCGGCTCCGATATCCAGCTCACTCAAAGCCCCTC
 TAGTCTCTCTGCCTCAGTGGGGGATCGGGTCAGTTTTACTTGTCAA
 GCTTCACAGGATATCAACAACCTTCCTTAATTGGTATCAGCAGAAGC
 CAGGAAAAGCACCCAAGCTGCTCATCTATGATGCCTCAAATTTGGA
 GACGGGTGTTCCAGTCGATTCTCTGGGTCAGGGTCCGGGACCGAC
 TTTACGTTTACGATCTCCTCTCTGCAGCCCGAAGACATCGCCACAT
 ACTATTGTCAACAGTACGGCAACTTGCCCTTTCACATTTGGGGGCGG
 GACTAAGGTTGAAATCAAGAGGGCCGCTGCACTGGACAATGAGAA
 GTCCAACGGCACCATCATCCACGTGAAGGGCAAGCACCTGTGCCCT
 AGTCCTCTGTTCCCAGGCCCATCCAAACCTTTTTGGGTTCTTGTTGT
 GGTCGGGGGGGGTGCTGGCCTGCTATTCTCTGCTGGTACGGTGGCC
 TTCATAATTTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATA
 GCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAA
 ACACTACCAGCCTTACGCACCACCTAGAGATTTGCTGCCTATCGG
 AGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGC

AGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGG
AAGAGTATGACGTTTTTGGACAAGCGCAGAGGACGGGACCCTGAGA
TGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATA
ATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAG
GCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTG
TACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 59)

[0247] Clone 24C8 CD28T CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQTLSTCTVSG
GSISSGGFYWSWIRQHPGKGLEWIGYIHHSSTHYNPSLKSRTISIDTS
KNLFSRLSSVTAADTAVYYCASLVYCGGDCYSGFDYWQGTLVTV
SSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTTCQASQDINNF
LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFITISLQPE
DIATYYCQQYGNLPFTFGGGTKVEIKRAAALDNEKSNGTIIHVKGKHL
CPSPLFPGSPKFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLS
DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQ
GQNQLYNELNLGRREEYDVLDRRRGRDPEMGGKPRRKNPQEGLYNE
LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM
QALPPR (SEQ ID NO. 60)

[0248] Clone 24C8 CD28T CD3 zeta CAR DNA Heavy & Light Chains

CAGGTACAGCTGCAGGAATCTGGGCCCCGACTTGTCAAGCCAAGT
CAGACACTTTCTCTTACATGTACCGTGAGCGGCGGAAGTATAAGCA
GTGGAGGCTTTTACTGGTCTTGGATACGGCAGCACCCAGGCAAAGG
CTTGGAGTGGATTGGATACATTCATCATTAGGATCTACACACTAT
AATCCATCCCTTAAGTCCCGGGTCACCATTAGCATTGATACGTCTA
AGAATCTGTTCAGTCTCAGGCTGTCTCCGTCAGTGTGCCGACAC
AGCCGTGTACTACTGCGCCTCCTTGGTTTACTGCGGAGGGCGACTGT
TATAGCGGCTTTGATTATTGGGGGCAGGGGACCCTCGTAACCGTGA
GCTCTGGAGGGGGTGGGAGCGGGGGAGGAGGTTTCAGGGGGGGGC
GGCTCCGATATCCAGCTCACTCAAAGCCCCTCTAGTCTCTCTGCCTC
AGTGGGGGATCGGGTCAGTTTTACTTGTCAAGCTTCACAGGATATC
AACAACTTCCTTAATTGGTATCAGCAGAAGCCAGGAAAAGCACCC

AAGCTGCTCATCTATGATGCCTCAAATTTGGAGACGGGTGTTCCCA
 GTCGATTCTCTGGGTCAGGGTCCGGGACCGACTTTACGTTTACGAT
 CTCCTCTCTGCAGCCCGAAGACATCGCCACATACTATTGTCAACAG
 TACGGCAACTTGCCTTTCACATTTGGGGGCGGGACTAAGGTTGAAA
 TCAAGAGGGGCCGCTGCACTGGACAATGAGAAGTCCAACGGCACCA
 TCATCCACGTGAAGGGCAAGCACCTGTGCCCTAGTCCTCTGTTCCC
 AGGCCCATCCAAACCTTTTTGGGTTCTTGTTGTGGTCGGGGGGGTG
 CTGGCCTGCTATTCTCTGCTGGTCACGGTGGCCTTCATAATTTCTG
 GGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
 ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTT
 ACGCACCACTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTT
 TTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCA
 ACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGT
 TTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACC
 AAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAA
 GGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGA
 GCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAG
 CACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTG
 CCACCTAGG (SEQ ID NO. 61)

[0249]

Clone 24C8 CD28T CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGFYWSWIRQHPGKGLE
 WIGYIHHSGSTHYNPSLKSRTVISIDTSKNLFSRLSSVTAADTAVYYC
 ASLVYCGGDCYSGFDYWQGTLVTVSSGGGGSGGGGSGGGGSDIQL
 TQSPSSLSASVGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIYDAS
 NLETGVPSRFSGSGSGTDFTFITSSLPEDIATYYCQQYGNLPFTFGGGT
 KVEIKRAAALDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVWLVVVGG
 VLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPY
 APPRDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL
 KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR
 GKGHDLGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 62)

[0250]

Clone 24C8 CD28 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
 GCACGCCGCACGCCCGCAGGTGCAGCTGCAGGAAAGCGGTCCGGG

ACTTGTCAAGCCGTCCCAAACGCTGAGTCTGACGTGTACTGTCTCT
GGTGGCTCTATTTCTTCCGGGGGCTTTTATTGGTCTTGGATCAGACA
ACACCCTGGCAAAGGGCTGGAGTGGATAGGGTATATTCACCACTCT
GGGTCCACTCACTACAACCCATCATTGAAATCCAGAGTGACTATCT
CAATCGACACATCCAAGAACCTTTTCAGCCTGAGGTTGTCATCAGT
TACCGCCGCTGACACCGCGGTGTATTATTGCGCCTCTCTCGTGTACT
GCGGTGGCGATTGTTATAGTGGCTTTGACTACTGGGGGCAGGGGAC
ATTGGTTACCGTTTCAAGTGGAGGCGGTGGGTCTGGCGGGGGCGGT
AGCGGAGGTGGGGGGAGCGACATACAGCTTACGCAGAGCCCCCTCC
AGCCTTTCAGCCTCCGTGGGGGATAGGGTGTCTTTACCTGCCAGG
CTTCCCAGGACATAAAACAACCTTCCTCAATTGGTATCAGCAAAAGCC
CGGGAAAGCACCAAAGCTGCTCATCTACGATGCCAGCAACCTGGA
AACCGGAGTGCCGTCTCGCTTCTCTGGAAGTGGCAGTGGGACCGAT
TTCACTTTTACAATCTCAAGTTTGCAGCCAGAAGACATTGCAACAT
ACTACTGTCAACAGTACGGCAATCTCCCCTTTACATTTGGGGGGGG
AACTAAAGTGGAGATTAAGCGCGCTGCAGCCATTGAAGTTATGTAT
CCGCCCCCGTATCTGGATAACGAGAAATCTAATGGTACCATAATAC
ATGTGAAGGGGAAGCACCTCTGTCCATCACCGCTGTTCCCCGGCCC
TTCAAAACCTTTCTGGGTACTCGTTGTCGTGGGTGGAGTTCTGGCCT
GCTATAGTCTGCTGGTGACCGTGGCGTTTATCATCTTCTGGGTAAG
ATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACT
CCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCAC
CACCTAGAGATTTCTGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAG
ATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTA
TAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGA
CAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACG
AAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAA
GATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAG
AAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGC
TACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCT
AGGTAA (SEQ ID NO. 63)

[0251]

Clone 24C8 CD28 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQTLSTCTVSG
 GSISGGFYWSWIRQHPGKGLEWIGYIHHSGSTHYNPSLKSRTVISIDTS
 KNLFSLRLSSVTAADTAVYYCASLVYCGGDCYSGFDYWGGQTLVTV
 SSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTCQASQDINNF
 LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFITISLQPE
 DIATYYCQQYGNLPFTFGGGTKVEIKRAAAIEVMYPPPYLDNEKSNGT
 IHHVKGKHLCPSPLPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVR
 SKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRS
 ADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRK
 NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK
 DTYDALHMQALPPR (SEQ ID NO. 64)

[0252]

Clone 24C8 CD28 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGCTGCAGGAAAGCGGTCCGGGACTTGTCAAGCCGTCC
 CAAACGCTGAGTCTGACGTGTACTGTCTCTGGTGGCTCTATTTCTTC
 CGGGGGCTTTTATTGGTCTTGGATCAGACAACACCCTGGCAAAGGG
 CTGGAGTGGATAGGGTATATTCACCACTCTGGGTCCACTCACTACA
 ACCCATCATTGAAATCCAGAGTGACTATCTCAATCGACACATCCAA
 GAACCTTTTCAGCCTGAGGTTGTCATCAGTTACCGCCGCTGACACC
 GCGGTGTATTATTGCGCCTCTCTCGTGTACTGCGGTGGCGATTGTTA
 TAGTGGCTTTGACTACTGGGGGCAGGGGACATTGGTTACCGTTTCA
 AGTGGAGGCGGTGGGTCTGGCGGGGGCGGTAGCGGAGGTGGGGGG
 AGCGACATACAGCTTACGCAGAGCCCCTCCAGCCTTTCAGCCTCCG
 TGGGGGATAGGGTGTCTTTACCTGCCAGGCTTCCCAGGACATAAA
 CAACTTCCTCAATTGGTATCAGCAAAAGCCCGGGAAAGCACCAAA
 GCTGCTCATCTACGATGCCAGCAACCTGGAAACCGGAGTGCCGTCT
 CGCTTCTCTGGAAGTGGCAGTGGGACCGATTTCACTTTTACAATCT
 CAAGTTTGCAGCCAGAAGACATTGCAACATACTACTGTCAACAGTA
 CGGCAATCTCCCCTTTACATTTGGGGGGGGAACTAAAGTGGAGATT
 AAGCGCGCTGCAGCCATTGAAGTTATGTATCCGCCCCCGTATCTGG
 ATAACGAGAAATCTAATGGTACCATAATACATGTGAAGGGGAAGC
 ACCTCTGTCCATCACCGCTGTTCCCCGGCCCTTCAAAACCTTTCTGG
 GTACTCGTTGTCGTGGGTGGAGTTCTGGCCTGCTATAGTCTGCTGGT
 GACCGTGGCGTTTATCATCTTCTGGGTAAGATCCAAAAGAAGCCGC

CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCC
CCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGC
TGCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGG
GACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATT
CTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCAC
GACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATG
ACGCTCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 65)

[0253] Clone 24C8 CD28 CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGFYWSWIRQHPGKGLE
WIGYIHHSGSTHYNPSLKSRTISIDTSKNLFSRLSSVTAADTAVYYC
ASLVYCGGDCYSGFDYWGGQTLVTVSSGGGGSGGGGSGGGGSDIQL
TQSPSSLSASVGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIYDAS
NLETGVPSRFSGSGSGTDFTFITSSLPEDIATYYCQQYGNLPFTFGGGT
KVEIKRAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPF
WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPG
PTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG
RREEYDVLDKRRGRDPENMGKPRRKNPQEGLYNELQKDKMAEAYSE
IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID
NO. 66)

[0254] Clone 24C8 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTGCAGTTGCAGGAAAGCGGGCCTGG
CCTTGTGAAACCAAGCCAGACACTGAGCCTGACATGCACTGTGTCC
GGCGGGTCCATATCTTCCGGGGGTTTTTATTGGTCCTGGATACGCC
AGCATCCCGGGAAAGGACTTGAATGGATTGGATATATCCACCATTC
CGGAAGCACCCACTACAATCCAAGCCTTAAATCCCGGGTGACAATC
TCCATCGACACCTCAAAGAATCTTTTTTCCCTGCGGTTGTCTTCAGT
AACTGCCGCCGATACCGCTGTGTACTACTGTGCCAGCCTCGTCTAT
TGCGGCGGAGATTGTTATTCTGGGTTCGATTATTGGGGTCAAGGCA
CACTGGTAACTGTCAGCAGCGGAGGCGGCGGTTCCGGGGGCGGGG

GCAGTGGAGGGGGCGGATCTGACATTCAGCTTACGCAGTCCCCATC
TTCACCTAGCGCCAGCGTTGGCGATCGGGTCAGCTTCACGTGTCAA
GCAAGTCAGGATATCAACAACCTTTCTTAACTGGTACCAGCAGAAGC
CAGGCAAGGCACCCAAGTTGCTGATTTACGATGCTTCTAACCTCGA
GACGGGAGTGCCTAGCCGCTTCTCCGGGAGCGGCAGCGGCACAGA
CTTTACCTTTACGATTTCCAGTCTGCAGCCAGAGGATATAGCAACT
TATTACTGTCAGCAGTATGGCAACCTCCCTTTTACCTTCGGTGGTGG
CACAAAGGTCGAGATTAAAAGAGCCGCAGCGTTGTCCAACCTCCAT
AATGTATTTTTCTCATTTTGTGCCCGTCTTTCTGCCTGCCAAACCTA
CCACCACCCCCGCCCCACGACCACCTACTCCAGCCCCCACCATCGC
CTCCCAGCCCCTCAGCCTGAGGCCAGAGGCTTGTCGCCCTGCTGCG
GGGGGCGCTGTCCATACCAGAGGACTCGACTTCGCCTGCGATATTT
ATATATGGGCCCCCCTCGCCGGCACCTGCGGAGTCTTGCTCCTGAG
CCTTGTGATCACGCTTTATTGTAACCATCGGAATAGATCCAAAAGA
AGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCC
CTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAG
ATTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGA
TGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCT
CAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAG
AGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGA
AGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAA
AGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGA
TACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA
(SEQ ID NO. 67)

[0255] Clone 24C8 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQTLSTCTVSG
GSISSGGFYWSWIRQHPGKGLEWIGYIHHSGSTHYNPSLKS RVTISIDTS
KNLFSRLSSVTAADTAVYYCASLVYCGGDCYSGFDYWQGTLVTV
SSGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSFTCQASQDINN
LNWYQQKPGKAPKLLIYDASNLETGVPRFSGSGSGTDFTFTISSLQPED
IATYYCQYGNLPFTFGGGTKVEIKRAAALSNSIMYFSHFVPVFLPAKPT

[0256]

TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA
PLAGTCGVLLLSLVITLYCNHRNRSKRSRLLHSDYMNMTPRRPGPTRK
HYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE
YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK
GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 68)

Clone 24C8 CD8 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGTTGCAGGAAAGCGGGCCTGGCCTTGTGAAACCAAGC
CAGACACTGAGCCTGACATGCACTGTGTCCGGCGGGTCCATATCTT
CCGGGGGTTTTTATTGGTCCTGGATACGCCAGCATCCCGGGAAAGG
ACTTGAATGGATTGGATATATCCACCATTCCGGAAGCACCCACTAC
AATCCAAGCCTTAAATCCCGGGTGACAATCTCCATCGACACCTCAA
AGAATCTTTTTTCCCTGCGGTTGTCTTCAGTAACTGCCGCCGATACC
GCTGTGTACTACTGTGCCAGCCTCGTCTATTGCGGCGGAGATTGTT
ATTCTGGGTTTCGATTATTGGGGTCAAGGCACACTGGTAACTGTCAG
CAGCGGAGGCGGGCGGTTCCGGGGGCGGGGGCAGTGGAGGGGGCG
GATCTGACATTCAGCTTACGCAGTCCCCATCTTCACTTAGCGCCAG
CGTTGGCGATCGGGTCAGCTTCACGTGTCAAGCAAGTCAGGATATC
AACAACTTTCTTAACTGGTACCAGCAGAAGCCAGGCAAGGCACCC
AAGTTGCTGATTTACGATGCTTCTAACCTCGAGACGGGAGTGCCTA
GCCGCTTCTCCGGGAGCGGCAGCGGCACAGACTTTACCTTTACGAT
TTCCAGTCTGCAGCCAGAGGATATAGCAACTTATTACTGTCAGCAG
TATGGCAACCTCCCTTTTACCTTCGGTGGTGGCACAAAGGTCGAGA
TTAAAAGAGCCGCAGCGTTGTCCAACCTCCATAATGTATTTTTCTCAT
TTTGTGCCCCGTCTTTCTGCCTGCCAAACCTACCACCACCCCCGCCCC
ACGACCACCTACTCCAGCCCCCACCATCGCCTCCCAGCCCCTCAGC
CTGAGGCCAGAGGCTTGTCGCCCTGCTGCGGGGGGCGCTGTCCATA
CCAGAGGACTCGACTTCGCCTGCGATATTTATATATGGGCCCCCCT
CGCCGGCACCTGCGGAGTCTTGCTCCTGAGCCTTGTGATCACGCTT
TATTGTAACCATCGGAATAGATCCAAAAGAAGCCGCCTGCTCCATA
GCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAA
ACACTACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGG
AGCAGGGTGAAGTTTTTCCAGATCTGCAGATGCACCAGCGTATCAGC
AGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGG

AAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGA
TGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATA
ATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAG
GCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTG
TACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 69)

[0257] Clone 24C8 CD8 CD3 zeta CAR AA Heavy & Light Chains

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGFYWSWIRQHPGKGLE
WIGYIHHSGSTHYNPSLKSRTISIDTSKNLFSRLSSVTAADTAVYYC
ASLVYCGGDCYSGFDYWGGQTLVTVSSGGGGSGGGGSGGGGSDIQL
TQSPSSLSASVGDVRSFTCQASQDINNFLNWYQQKPGKAPKLLIYDAS
NLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYGNLPFTFGGGT
KVEIKRAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLS
LRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYC
NHRNRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV
KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPENGGK
PRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS
TA TKDITYDALHM QALPPR (SEQ ID NO. 70)

[0258] Clone 20C5.1 HC DNA

CAGGTCCAACCTGGTGCAGTCCGGAGCCGAAGTCAAGAAACCAGGT
GCCTCCGTAAAGTGAGTTGCAAAGTCTCTGGATACACTCTGACCG
AGCTCTCTATGCACTGGGTCCGGCAGGCCCCCGGCAAGGGATTGGA
ATGGATGGGCGGGTTCGATCCTGAGGACGGAGAGACTATCTACGC
TCAAAAATTCCAGGGACGAGTGACTGTGACCGAAGACACTAGTAC
CGACACTGCCTACATGGAACCTTCCTCTCTGCGATCAGAAGATACC
GCAGTGTACTACTGTGCTACTGAATCTAGGGGCATTGGATGGCCCT
ACTTCGATTACTGGGGTCAGGGAACCTCTGGTGACTGTCTCCAGC
(SEQ ID NO. 71)

[0259] Clone 20C5.1 AA HC (CDRs in Underline)

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTEL^{SMHWVRQAPGKGLE}
WMGGFDPEDGETIYAQKFQGRVTVTEDTSTDTAYMELSSLRSED^{TAV}
YYCATESRGIGWPYFDYWGQGTLVTVSS (SEQ ID NO. 72)

[0260] Clone 20C5.1 HC AA CDR1: GYTLTEL (SEQ ID NO. 73)

- [0261] Clone 20C5.1 HC AA CDR2: DPEDGE (SEQ ID NO. 74)
- [0262] Clone 20C5.1 HC AA CDR3: ESRGIGWPYFDY (SEQ ID NO. 75)
- [0263] Clone 20C5.1 LC DNA
- GATATTCAGATGACTCAATCTCCTTCTTCTCTGTCCGCTTCCGTGGG
CGATAGAGTGACCATTACTTGTAGGGCGTCCCAGTCAATCTCCAGT
TATTTGAATTGGTATCAGCAGAAGCCCGGGAAAGCACCTAAGCTGT
TGATCAGCGGGGCTTCTAGCCTGAAGAGTGGGGTACCTTCACGGTT
CAGCGGAAGCGGAAGCGGAACCGATTTCACCCTGACTATCAGCAG
CCTGCCACCTGAGGACTTTGCAACTTACTACTGCCAACAGTCATAC
AGCACTCCGATCACTTTTCGGCCAGGGCACCCGGCTCGAAATCAAGC
GC (SEQ ID NO. 76)
- [0264] Clone 20C5.1 AA LC (CDRs in Underline)
- DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIS
GASSLKSGVPSRFSSGSGSGTDFLTISLPPEDFATYYCQQSYSTPITFG
QGTRLEIKR (SEQ ID NO. 77)
- [0265] Clone 20C5.1 AA LC CDR1: RASQSISSYLN (SEQ ID NO. 78)
- [0266] Clone 20C5.1 AA LC CDR2: GASSLK (SEQ ID NO. 79)
- [0267] Clone 20C5.1 AA LC CDR3: QQSYSTPIT (SEQ ID NO. 80)
- [0268] Clone 20C5.1 CD28T CD3 zeta CAR DNA Heavy & Light Chains
- ATGGCACTCCCCGTAAGTCTGCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTCCAAGTGGTGCAGTCCGGAGCCGA
AGTCAAGAAACCAGGTGCCTCCGTAAAGTGAGTTGCAAAGTCTCT
GGATACTCTGACCGAGCTCTCTATGCACTGGGTCCGGCAGGCCC
CCGGCAAGGGATTGGAATGGATGGGCGGGTTCGATCCTGAGGACG
GAGAGACTATCTACGCTCAAAAATTCCAGGGACGAGTGACTGTGA
CCGAAGACACTAGTACCGACACTGCCTACATGGAACCTTCCTCTCT
GCGATCAGAAGATAACCGCAGTGTACTACTGTGCTACTGAATCTAGG
GGCATTGGATGGCCCTACTTCGATTACTGGGGTCAGGGAACTCTGG
TGACTGTCTCCAGCGGTGGAGGTGGCAGCGGTGGTGGCGGAAGCG
GGGGGGGCGGCTCTGATATTCAGATGACTCAATCTCCTTCTTCTCT
GTCCGCTTCCGTGGGCGATAGAGTGACCATTACTTGTAGGGCGTCC

CAGTCAATCTCCAGTTATTTGAATTGGTATCAGCAGAAGCCCGGGA
 AAGCACCTAAGCTGTTGATCAGCGGGGCTTCTAGCCTGAAGAGTGG
 GGTACCTTCACGGTTCAGCGGAAGCGGAAGCGGAACCGATTTCAC
 CCTGACTATCAGCAGCCTGCCACCTGAGGACTTTGCAACTTACTAC
 TGCCAACAGTCATACAGCACTCCGATCACTTTCGGCCAGGGCACCC
 GGCTCGAAATCAAGCGCGCTGCTGCTTTGGACAATGAGAAGTCAA
 ACGGCACCATCATACATGTTAAAGGTAAACATCTGTGTCCCTCCCC
 GCTGTTCCCCGGCCCTTCCAAACCGTTCTGGGTCTGGTGGTGGTTCG
 GAGGCGTACTCGCTTGCTATAGTCTGCTGGTAACTGTCGCCTTCATC
 ATCTTTTGGGTGAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATT
 ACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACT
 ACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGCAG
 GGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGC
 CAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAG
 TATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGT
 GGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
 CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATG
 AAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCA
 GGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG
 CAAGCCCCTGCCACCTAGGTAA (SEQ ID NO. 81)

[0269]

Clone 20C5.1 CD28T CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKVS
 GYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTVT
 EDTSTDTAYMELSSLRSEDNAVYYCATESRGIGWPYFDYWGGTTLVT
 VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISS
 YLNWYQQKPGKAPKLLISGASSLKSGVPSRFSGSGSGTDFLTISLPPPE
 DFATYYCQQSYSTPITFGQGTRLEIKRAAALDNEKSNGTIIHVKGKHLCD
 PSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSD
 YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQG
 QNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
 QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ
 ALPPR (SEQ ID NO. 82)

[0270]

Clone 20C5.1 CD28T CD3 zeta CAR DNA Heavy & Light Chains

CAGGTCCAACCTGGTGCAGTCCGGAGCCGAAGTCAAGAAACCAGGT
GCCTCCGTTAAAGTGAGTTGCAAAGTCTCTGGATACTCTGACCG
AGCTCTCTATGCACTGGGTCCGGCAGGCCCGGCAAGGGATTGGA
ATGGATGGGCGGGTTCGATCCTGAGGACGGAGAGACTATCTACGC
TCAAAAATTCCAGGGACGAGTGACTGTGACCGAAGACACTAGTAC
CGACACTGCCTACATGGAACCTTTCCTCTCTGCGATCAGAAGATACC
GCAGTGTACTACTGTGCTACTGAATCTAGGGGCATTGGATGGCCCT
ACTTCGATTACTGGGGTCAGGGAACCTCTGGTGACTGTCTCCAGCGG
TGGAGGTGGCAGCGGTGGTGGCGGAAGCGGGGGGGGCGGCTCTGA
TATTCAGATGACTCAATCTCCTTCTTCTCTGTCCGCTTCCGTGGGCG
ATAGAGTGACCATTACTTGTAGGGCGTCCCAGTCAATCTCCAGTTA
TTTGAATTGGTATCAGCAGAAGCCCGGGAAAGCACCTAAGCTGTTG
ATCAGCGGGGCTTCTAGCCTGAAGAGTGGGGTACCTTCACGGTTCA
GCGGAAGCGGAAGCGGAACCGATTTCACCCTGACTATCAGCAGCC
TGCCACCTGAGGACTTTGCAACTTACTACTGCCAACAGTCATACAG
CACTCCGATCACTTTCGGCCAGGGCACCCGGCTCGAAATCAAGCGC
GCTGCTGCTTTGGACAATGAGAAAGTCAAACGGCACCATCATACATG
TTAAAGGTAAACATCTGTGTCCCTCCCCGCTGTTCCCCGGCCCTTCC
AAACCGTTCTGGGTTCTGGTGGTGGTCGGAGGCGTACTCGCTTGCT
ATAGTCTGCTGGTAACTGTCGCCTTCATCATCTTTTGGGTGAGATCC
AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCAC
GCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACC
TAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC
GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAG
CGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAA
AAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGAT
GGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAG
GGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG
(SEQ ID NO. 83)

[0271]

Clone 20C5.1 CD28T CD3 zeta CAR AA Heavy & Light Chains

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLE
WMGGFDPEDGETIYAQKFQGRVTVTEDTSTDYAYMELSSLRSEDYAV
YYCATESRGIGWPYFDYWGGQGLVTVSSGGGGSGGGGSGGGGSDIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLISGAS
SLKSGVPSRFSGSGSGTDFTLTISSLPPEDFATYYCQQSYSTPITFGQGT
RLEIKRAAALDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVVGG
VLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPY
APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL
KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR
GKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 84)

[0272]

Clone 20C5.1 CD28 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTGCAGCTTGTGCAGAGCGGGGCCGA
GGTGAAGAAGCCCGGGGCCAGCGTCAAAGTGTCTGTAAAGGTCAG
CGGTTACACCCTCACCGAGCTGAGCATGCACTGGGTACGGCAGGCT
CCCGGCAAAGGTCTTGAGTGGATGGGTGGATTTGATCCAGAAGAT
GGAGAGACTATCTACGCCCAGAAGTTCCAGGGCCGGGTACCGTA
ACAGAAGACACCTCAACTGACACCGCTTACATGGAGCTGAGTTCAC
TGCGGTCCGAGGACACGGCCGTGTATTATTGTGCCACCGAGAGCCG
CGGAATCGGATGGCCTTACTTCGACTACTGGGGACAGGGTACACTT
GTTACAGTATCATCCGGGGGTGGCGGCTCTGGTGGGGGCGGCTCCG
GAGGGGGTGGATCAGATATCCAAATGACTCAAAGTCCAAGTTCCT
GTCTGCCTCAGTCGGAGATAGAGTCACCATAACCTGCAGGGCAAGT
CAGTCCATCTCCTCCTATCTGAACTGGTACCAACAGAAACCTGGAA
AGGCGCCTAAGCTCCTGATCTCCGGAGCCTCATCTTTGAAATCCGG
TGTCCCATCTCGCTTCAGTGGCTCTGGAAGCGGTACAGATTTTACTT
TGACCATTAGCAGCCTCCACCGGAAGACTTTGCTACATATTACTG
CCAGCAGTCTTACTCAACCCCAATCACCTTCGGGCAAGGCACCAGA
CTCGAAATAAAAAGAGCAGCTGCTATCGAGGTTATGTACCCACCGC
CGTACTTGGATAACGAAAAAAGCAATGGGACCATCATTCATGTGA
AGGGTAAGCACCTTTGCCCTAGCCCACTGTTTCCTGGCCCGAGTAA
ACCTTTTGGGTACTTGTGGTCGTCGGCGGCGTGCTGGCCTGCTACT
CACTCCTGGTTACCGTCGCATTCATCATCTTTTGGGTGAGATCCAAA

AGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCC
 GCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAG
 AGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
 GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAG
 CTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGC
 AGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAA
 CCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGC
 TGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGG
 AAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAA
 GGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA
 (SEQ ID NO. 85)

[0273]

Clone 20C5.1 CD28 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in Bold)

MALPVTALLPLALLHAARPQVQLVQSGAEVKKPGASVKVSCKVS
 GYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTVT
 EDTSTDTAYMELSSLRSEDVAVYYCATESRGIGWPYFDYWGGQTLVT
 VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISS
 YLNWYQQKPGKAPKLLISGASSLKSGVPSRFSGSGSGTDFLTISLPP
 DFATYYCQQSYSTPITFGQGTRLEIKRAAAIEVMYPPPYLDNEKSNGTII
 HVKGKHLCPSPFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRS
 KRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSA
 DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP
 QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST
 ATKDITYDALHMQALPPR (SEQ ID NO. 86)

[0274]

Clone 20C5.1 CD28 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGCTTGTGCAGAGCGGGGCCGAGGTGAAGAAGCCCGGG
 GCCAGCGTCAAAGTGTCCTGTAAGGTCAGCGGTTACACCCTCACCG
 AGCTGAGCATGCACTGGGTACGGCAGGCTCCCGGCAAAGGTCTTG
 AGTGGATGGGTGGATTTGATCCAGAAGATGGAGAGACTATCTACG
 CCCAGAAGTTCCAGGGCCGGGTCACCGTAACAGAAGACACCTCAA
 CTGACACCGCTTACATGGAGCTGAGTTCACTGCGGTCCGAGGACAC
 GGCCGTGTATTATTGTGCCACCGAGAGCCGCGGAATCGGATGGCCT
 TACTTCGACTACTGGGGACAGGGTACACTTGTTACAGTATCATCCG

GGGGTGGCGGCTCTGGTGGGGGCGGCTCCGGAGGGGGTGGATCAG
 ATATCCAAATGACTCAAAGTCCAAGTTCCCTGTCTGCCTCAGTCGG
 AGATAGAGTCACCATAACCTGCAGGGCAAGTCAGTCCATCTCCTCC
 TATCTGAACTGGTACCAACAGAAACCTGGAAAGGCGCCTAAGCTC
 CTGATCTCCGGAGCCTCATCTTTGAAATCCGGTGTCCCATCTCGCTT
 CAGTGGCTCTGGAAGCGGTACAGATTTTACTTTGACCATTAGCAGC
 CTCCCACCGGAAGACTTTGCTACATATTACTGCCAGCAGTCTTACT
 CAACCCCAATCACCTTCGGGCAAGGCACCAGACTCGAAATAAAAA
 GAGCAGCTGCTATCGAGGTTATGTACCCACCGCCGTACTTGGATAA
 CGAAAAAAGCAATGGGACCATCATTATGTGAAGGGTAAGCACCT
 TTGCCCTAGCCCCTGTTCCTGGCCCGAGTAAACCCTTTTGGGTAC
 TTGTGGTCGTCGGCGGCGTGTCTGGCCTGCTACTCACTCCTGGTTACC
 GTCGCATTCATCATCTTTTGGGTGAGATCCAAAAGAAGCCGCCTGC
 TCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCAC
 AAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCC
 TATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGT
 ATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGAC
 GCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACC
 CTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTC
 TCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGA
 AATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACG
 GTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGC
 TCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 87)

[0275]

Clone 20C5.1 CD28 CD3 zeta CAR AA Heavy & Light Chains

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLE
 WMGGFDPEDGETIYAQKFQGRVTVTEDTSTDATYMESSLRSEDATV
 YYCATESRGIGWPYFDYWGGTLVTVSSGGGGSGGGGSGGGGSDIQ
 MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGAPKLLISGAS
 SLKSGVPSRFSGSGSGTDFLTISLPPEDFATYYCQQSYSTPITFGQGT
 RLEIKRAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPGPSKPF
 WVLVVVGGLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPG
 PTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG
 RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE

IGMKGERRRGK GHDGLYQGLSTATKDTYDALHM QALPPR (SEQ ID NO. 88)

[0276]

Clone 20C5.1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTA ACTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCCG CAGGTGCAGTTGGTGCAAAGCGGCGCAGA
AGTTAAGAAACCTGGGGCGTCAGTTAAGGTGTCTTGCAAAGTATCT
GGCTATAACCCTCACTGAGCTGTCCATGCATTGGGTAAGGCAGGCTC
CTGGAAAGGGGCTCGAATGGATGGGAGGATTTGACCCTGAAGACG
GAGAGACCATCTACGCCCAGAAATTCCAGGGTAGAGTAACAGTGA
CTGAGGACACTAGCACTGACACAGCGTACATGGAGCTGAGTTCTCT
GAGAAGTGAGGACACAGCCGTTTACTACTGCGCTACCGAGTCCAG
AGGTATTGGCTGGCCATACTTCGACTATTGGGGTCAGGGCACCCCTG
GTTACAGTGAGTTCAGGAGGCGGGGGCTCTGGGGGGGGCGGTTCC
GGAGGGGGGGGGCTCAGATATACAGATGACGCAGAGTCCATCAAGT
CTCTCAGCCAGCGTGGGAGATCGCGTGACTATTACTTGCCGCGCCA
GCCAGAGTATTAGCTCCTATCTGAATTGGTACCAGCAAAAGCCCCG
GAAGGCCCTAAGCTTCTGATTTCTGGCGCCTCCTCTTTGAAGTCA
GGTGTGCCAAGCAGATTTAGCGGGTCTGGAAGTGGCACTGACTTTA
CACTTACTATCTCCAGCCTGCCCCCAGAGGATTTTGCCACATATTAC
TGTCAGCAAAGCTACTCTACTCCAATCACTTTCGGCCAGGGCACAA
GATTGGAGATTAAGAGGGCTGCCGCACTTTCAAATTCCATCATGTA
TTTCAGCCATTTTGTGCCTGTTTTTCTTCCGGCCAAACCTACAACCA
CTCCCGCCCCACGCCCACCTACTCCCGCCCCTACCATTGCCTCCCAG
CCTCTGTCTCTTAGACCTGAGGCTTG TAGACCTGCTGCCGGCGGAG
CCGTGCACACTCGCGGTCTGGACTTCGCCTGCGACATCTATATCTG
GGCCCCCTCTGGCCGGCACCTGCGGGCGTTCTCCTTCTCTCACTCGTAA
TCACACTCTATTGCAATCACAGGAACAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCC
ACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTGCTG
CCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGC
GTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGG
ACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGA
CCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGG

[0277]

TCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCT
GAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGA
CGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGAC
GCTCTCCACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 89)

Clone 20C5.1 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKVS
GYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTVT
EDTSTD TAYMELSSLRSEDTAVYYCATESRGIGWPYFDYWGGQTLVT
VSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISS
YLNWYQQKPGKAPKLLISGASSLKSGVPSRFSGSGSGTDFTLTISSLPPE
DFATYYCQQSYSTPITFGQGTRLEIKRAAALSNSIMYFSHFVPVFLPAK
PTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW
APLAGTCGVLLLSLVITLYCNHRNRSKRSRLHSDYMNMTPRRPGPTR
KHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
90)

[0278]

Clone 20C5.1 CD8 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGTTGGTGCAAAGCGGCGCAGAAGTTAAGAAACCTGGG
GCGTCAGTTAAGGTGTCTTGCAAAGTATCTGGCTATACCCTCACTG
AGCTGTCCATGCATTGGGTAAGGCAGGCTCCTGGAAAGGGGCTCG
AATGGATGGGAGGATTTGACCCTGAAGACGGAGAGACCATCTACG
CCCAGAAATTCCAGGGTAGAGTAACAGTGACTGAGGACACTAGCA
CTGACACAGCGTACATGGAGCTGAGTTCTCTGAGAAGTGAGGACA
CAGCCGTTTACTACTGCGCTACCGAGTCCAGAGGTATTGGCTGGCC
ATACTTCGACTATTGGGGTCAGGGCACCCCTGGTTACAGTGAGTTCA
GGAGGCGGGGGCTCTGGGGGGGGCGGTTCCGGAGGGGGGGGCTCA
GATATACAGATGACGCAGAGTCCATCAAGTCTCTCAGCCAGCGTGG
GAGATCGCGTGACTATTACTTGCCGCGCCAGCCAGAGTATTAGCTC
CTATCTGAATTGGTACCAGCAAAAGCCCGGGAAGGCCCTAAGCTT
CTGATTTCTGGCGCCTCCTCTTTGAAGTCAGGTGTGCCAAGCAGAT
TTAGCGGGTCTGGAAGTGGCACTGACTTTACACTTACTATCTCCAG

CCTGCCCCCAGAGGATTTTGCCACATATTACTGTCAGCAAAGCTAC
TCTACTCCAATCACTTTCGGCCAGGGCACAAGATTGGAGATTAAGA
GGGCTGCCGCACTTTCAAATTCCATCATGTATTTAGCCATTTTGTG
CCTGTTTTTCTTCCGGCCAAACCTACAACCACTCCCGCCCCACGCCC
ACCTACTCCCGCCCCCTACCATTGCCTCCCAGCCTCTGTCTCTTAGAC
CTGAGGCTTGTAGACCTGCTGCCGGCGGAGCCGTGCACACTCGCGG
TCTGGACTTCGCCTGCGACATCTATATCTGGGCCCCTCTGGCCGGC
ACCTGCGGGCGTTCTCCTTCTCTCACTCGTAATCACACTCTATTGCAA
TCACAGGAACAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTA
CATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGCAGGG
TGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCA
GAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTA
TGACGTTTTTGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGG
CAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCT
GCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAA
AGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGG
GACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCA
AGCCCTGCCACCTAGG (SEQ ID NO. 91)

[0279]

Clone 20C5.1 CD8 CD3 zeta CAR AA Heavy & Light Chains

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLE
WMGGFDPEDGETIYAQKFQGRVTVTEDTSTDYAYMELSSLRSEDYAV
YYCATESRGIGWPYFDYWQGTLVTVSSGGGGSGGGGSGGGGSDIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLISGAS
SLKSGVPSRFSGSGSGTDFTLTISSLPPEDFATYYCQQSYSTPITFGQGT
RLEIKRAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSL
RPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCN
HRNRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVK
FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPENGGKP
RRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST
ATKDTYDALHMQALPPR (SEQ ID NO. 92)

[0280]

Clone 20C5.2 HC DNA

CAGGTCCAGTTGGTCGAAAGTGGCGGTGGTGTAGTGCAGCCGGGC
CGCAGTTTGAGGCTTTCCTGTGCGGCTTCAGGCTTTACTTTTTCCAG
CTATGGAATGCACTGGGTGCGGCAGGCCCGGCAAAGGACTTGA
GTGGGTGGCCGTCATTTCTTATGACGGATCAGATAAGTACTACGTG
GACAGCGTCAAGGGCAGATTCACCATCTCTAGGGACAACAGTAAA
AATAGACTCTACCTCCAGATGAATAGCCTCAGAGCTGAAGACACG
GCCGTCTACTATTGTGCTCGGGAGCGGTATAGTGGCAGAGACTACT
GGGGGCAGGGCACACTCGTTACAGTGAGTAGC (SEQ ID NO. 93)

[0281] Clone 20C5.2 AA HC (CDRs in Underline)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
WVAVISYDGSDKYYVDSVKGRFTISRDNLSKNRLYLQMNSLRAEDTAV
YYCARERYSGRDYWGQGTLVTVSS (SEQ ID NO. 94)

[0282] Clone 20C5.2 HC AA CDR1: GFTFSSY (SEQ ID NO. 95)

[0283] Clone 20C5.2 HC AA CDR2: SYDGSD (SEQ ID NO. 96)

[0284] Clone 20C5.2 HC AA CDR3: ERYSGRDY (SEQ ID NO. 97)

[0285] Clone 20C5.2 LC DNA

GAGATTGTTATGACCCAGAGTCCTGCGACCCTCTCAGTCAGCCCCG
GGGAGCGCGCAACTTTGTCTTGCAGAGCTAGTCAGTCCGTGTCCTC
TCTTCTGACATGGTACCAGCAAAAGCCCGGGCAGGCTCCGCGCCTT
TTGATCTTTGGGGCTTCAACAAGAGCCACTGGGATTCCCGCACGAT
TCTCTGGCTCCGGGAGCGGTACTGGTTTCACCCTGACGATTAGCAG
TCTCCAGAGCGAGGACTTCGCCGTATACTACTGCCAGCAGTACGAT
ACGTGGCCATTCACTTTTGGACCAGGGACTAAAGTGGATTTTAAGC
GC (SEQ ID NO. 98)

[0286] Clone 20C5.2 AA LC (CDRs in Underline)

EIVMTQSPATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLIF
GASTRATGIPARFSGSGSGTGFTLTISLQSEDFAVYYCQQYDTWPFT
GPGTKVDFKR (SEQ ID NO. 99)

[0287] Clone 20C5.2 AA LC CDR1: RASQSVSSLLT (SEQ ID NO. 100)

[0288] Clone 20C5.2 AA LC CDR2: GASTRAT (SEQ ID NO. 101)

[0289] Clone 20C5.2 AA LC CDR3: QQYDTWPFT (SEQ ID NO. 102)

[0290]

Clone 20C5.2 CD28T CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTCCAGTTGGTCGAAAGTGGCGGTGG
TGTAGTGCAGCCGGGCCGCAGTTTGAGGCTTTCCTGTGCGGCTTCA
GGCTTTACTTTTTCCAGCTATGGAATGCACTGGGTGCGGCAGGCCC
CCGGCAAAGGACTTGAGTGGGTGGCCGTCATTTCTTATGACGGATC
AGATAAGTACTACGTGGACAGCGTCAAGGGCAGATTCACCATCTCT
AGGGACAACAGTAAAAATAGACTCTACCTCCAGATGAATAGCCTC
AGAGCTGAAGACACGGCCGTCTACTATTGTGCTCGGGAGCGGTATA
GTGGCAGAGACTACTGGGGGCAGGGCACACTCGTTACAGTGAGTA
GCGGCGGAGGAGGGAGTGGGGGCGGTGGCTCCGGTGGAGGAGGTT
CTGAGATTGTTATGACCCAGAGTCCTGCGACCCTCTCAGTCAGCCC
CGGGGAGCGCGCAACTTTGTCTTGCAGAGCTAGTCAGTCCGTGTCC
TCTCTTCTGACATGGTACCAGCAAAAGCCCCGGGCAGGCTCCGCGCC
TTTTGATCTTTGGGGCTTCAACAAGAGCCACTGGGATTCCCGCACG
ATTCTCTGGCTCCGGGAGCGGTACTGGTTTCACCCTGACGATTAGC
AGTCTCCAGAGCGAGGACTTCGCCGTATACTACTGCCAGCAGTACG
ATACGTGGCCATTCACTTTTGGACCAGGGACTAAAGTGGATTTTAA
GCGCGCCGCCGCTCTCGATAACGAAAAGTCAAATGGCACCATAAT
CCACGTCAAAGGCAAGCACCTGTGCCCTTCCCCGCTCTTCCCCGGA
CCCAGTAAACCATTTTGGGTGCTGGTTGTTGTGGGGGGCGTGCTGG
CCTGCTATAGCCTTTTGGTCACTGTAGCCTTCATTATTTTTTGGGTC
AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACG
CACCACCTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTC
CAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACT
GTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTT
GGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAA
GACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGG
ATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGC
GGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCA
CTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCC
ACCTAGGTAA (SEQ ID NO. 103)

[0291] Clone 20C5.2 CD28T CD3 zeta CAR AA Heavy & Light Chains
(Signal Peptide in **Bold**)
MALPVTALLLPLALLLHAARPQVQLVESGGGVVQPGRSLRLSCAAS
GFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGRFTISR
DNSKNRLYLQMNSLRAEDTAVYYCARERYSGRDYWGQGT**LVTVSSG**
GGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLSCRASQSVSSLLT
WYQKPGQAPRL**LIFGA****STRATGIPARFSGSGSGTGFTLTISSLQSE****DFA**
VYYCQ**QYDTWPFTFGPGTKVDFKRAAALDNEKSNGTIIHVKGKHLCP**
SPLFPGPSKPF**WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSD**
YMNMT**PRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQG**
QNQLYNELNLGRREEYDVL**DKRRGRDPEMGGKPRRKNPQEGLYNEL**
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK
DTYDALHMQALPPR (SEQ ID NO. 104)

[0292] Clone 20C5.2 CD28T CD3 zeta CAR DNA Heavy & Light Chains
CAGGTCCAGTTGGTCGAAAGTGGCGGTGGTGTAGTGCAGCCGGGC
CGCAGTTTGAGGCTTTCCTGTGCGGCTTCAGGCTTTACTTTTTCCAG
CTATGGAATGCACTGGGTGCGGCAGGCCCCCGGCAAAGGACTTGA
GTGGGTGGCCGTCATTTCTTATGACGGATCAGATAAGTACTACGTG
GACAGCGTCAAGGGCAGATTCACCATCTCTAGGGACAACAGTAAA
AATAGACTCTACCTCCAGATGAATAGCCTCAGAGCTGAAGACACG
GCCGTCTACTATTGTGCTCGGGAGCGGTATAGTGGCAGAGACTACT
GGGGGCAGGGCACACTCGTTACAGTGAGTAGCGGCGGAGGAGGGA
GTGGGGGCGGTGGCTCCGGTGGAGGAGGTTCTGAGATTGTTATGAC
CCAGAGTCCTGCGACCCTCTCAGTCAGCCCCGGGGAGCGCGCAACT
TTGTCTTGCAGAGCTAGTCAGTCCGTGTCCTCTCTTCTGACATGGTA
CCAGCAAAAGCCCGGGCAGGCTCCGCGCCTTTTGATCTTTGGGGCT
TCAACAAGAGCCACTGGGATTCCCGCACGATTCTCTGGCTCCGGGA
GCGGTACTGGTTTCACCCTGACGATTAGCAGTCTCCAGAGCGAGGA
CTTCGCCGTATACTACTGCCAGCAGTACGATACGTGGCCATTCACT
TTTGGAACAGGGACTAAAGTGGATTTTAAGCGCGCCGCCGCTCTCG
ATAACGAAAAGTCAAATGGCACCATAATCCACGTCAAAGGCAAGC
ACCTGTGCCCTTCCCCGCTCTTCCCCGGACCCAGTAAACCATTTTGG
GTGCTGGTTGTTGTGGGGGGCGTGCTGGCCTGCTATAGCCTTTTGGT

CACTGTAGCCTTCATTATTTTTTTGGGTCAGATCCAAAAGAAGCCGC
 CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCC
 CCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGC
 TGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
 GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
 GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGG
 GACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
 GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATT
 CTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCAC
 GACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATG
 ACGCTCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 105)

[0293]

Clone 20C5.2 CD28T CD3 zeta CAR AA Heavy & Light Chains

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
 WVAVISYDGS DKYYVDSVKGRFTISRDN SKNRLYLQMNSLRAEDTAV
 YYCARERYSGRDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIVMTQS
 PATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLLIFGA STRAT
 GIPARFSGSGSGTGFTLTIS SLQSEDFAVYYCQQYDTWPFTFGPGTKVD
 FKRAAALDNEKSNGTIIHVKGKHLCP SPLFPGPSKPFWVLVVVGGLA
 CYSLLVTVAFIIFWVR SKRSRLLHSDYMNMTPRRPGPTRKH YQPYAPP
 RDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKR
 RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK
 GHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 106)

[0294]

Clone 20C5.2 CD28 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTA ACTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
 GCACGCCGCACGCCCGCAGGTGCAGCTCGTGGAGTCTGGCGGCGG
 CGTGGTCCAGCCCCGGCCGGTCCCTGCGCCTGTCCTGCGCCGCCAGC
 GGGTTTACTTTTTCTCCTACGGCATGCACTGGGTGCGCCAGGCTCC
 CGGCAAGGGCCTCGAGTGGGTCGCCGTGATCTCATACGATGGGTCA
 GACAAATACTATGTCGATTCTGT TAAAGGGCGGTTTACCATTTC AA
 GAGATAACTCTAAGAATAGGCTGTATTTGCAGATGAACAGCCTGA
 GGGCTGAAGATAACGCAGTGTACTATTGCGCTAGGGAGCGGTATA
 GTGGCCGCGATTACTGGGGACAGGGTACACTGGTGACCGTGAGCT
 CTGGGGGTGGCGGAAGCGGGGGTGGCGGAAGCGGCGGAGGGGGT

AGTGAAATTGTGATGACCCAGTCTCCGGCTACACTTTTCAGTCTCCC
 CTGGGGAGAGAGCTACACTGTCATGCAGAGCGTCCCAGTCCGTCTC
 TTCTCTCCTTACCTGGTATCAGCAGAAGCCCGGCCAGGCTCCTCGA
 CTGCTGATCTTCGGTGCCTCCACAAGGGCGACCGGGATTCCAGCCC
 GCTTCTCAGGTTCTGGGAGCGGAACTGGTTTCACTTTGACAATCAG
 TTCACTGCAGTCAGAGGATTTGCGCCGTGTACTACTGCCAGCAATAC
 GACACATGGCCATTCACTTTTCGGACCCGGTACCAAAGTCGATTTCA
 AGAGAGCCGCGGCCATCGAGGTTATGTACCCACCACCATATCTGGA
 CAATGAAAAAAGCAATGGAACCATTATCCATGTGAAGGGTAAACA
 CCTCTGCCCTAGCCCACTTTTCCCTGGCCCATCAAAGCCCTTCTGGG
 TCTTGGTGGTCGTGGGGGGTGTGCTGGCCTGTTACAGCCTTCTGGT
 GACGGTTGCTTTCATTATCTTCTGGGTTAGATCCAAAAGAAGCCGC
 CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCC
 CCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGC
 TGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
 GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
 GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGG
 GACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
 GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATT
 CTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCAC
 GACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATG
 ACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO.
 107)

[0295] Clone 20C5.2 CD28 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLPLALLHAARPQVQLVESGGGVVQPGRSLRLSCAAS
 GFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGRFTISR
 DNSKNRLYLQMNSLRAEDTAVYYCARERYSGRDYWGQGTLLTVSSG
 GGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLSCRASQSVSSLLT
 WYQQKPGQAPRLLIFGASTRATGIPARFSGSGSGTGFTLTISSLQSEDF
 VYYCQYDTPFTFGPGTKVDFKRAAAIEVMYPPPYLDNEKSNGTIIH
 VKGKHLCPSPFLPGPSKPFVWLTVVGGVLACYSLLVTVAFIIFWVRSK
 RSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSAD

[0296]

APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY
DALHMQALPPR (SEQ ID NO. 108)

Clone 20C5.2 CD28 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGCTCGTGGAGTCTGGCGGCGGCGTGGTCCAGCCCGGC
CGGTCCCTGCGCCTGTCCTGCGCCGCCAGCGGGTTTACTTTTTCTC
CTACGGCATGCACTGGGTGCGCCAGGCTCCCGGCAAGGGCCTCGA
GTGGGTCGCCGTGATCTCATACGATGGGTGAGACAAATACTATGTC
GATTCTGTAAAGGGCGGTTTACCATTTCAGAGATAACTCTAAGA
ATAGGCTGTATTTGCAGATGAACAGCCTGAGGGCTGAAGATACCG
CAGTGTACTATTGCGCTAGGGAGCGGTATAGTGGCCGCGATTACTG
GGGACAGGGTACACTGGTGACCGTGAGCTCTGGGGGTGGCGGAAG
CGGGGGTGGCGGAAGCGGCGGAGGGGGTAGTGAAATTGTGATGAC
CCAGTCTCCGGCTACACTTTTCACTCTCCCTGGGGAGAGAGCTACA
CTGTCATGCAGAGCGTCCCAGTCCGTCTCTTCTCTCCTTACCTGGTA
TCAGCAGAAGCCCGGCCAGGCTCCTCGACTGCTGATCTTCGGTGCC
TCCACAAGGGCGACCGGGATTCCAGCCCGCTTCTCAGGTTCTGGGA
GCGGAAGTGGTTTCACTTTGACAATCAGTTCAGTGCAGTCAGAGGA
TTTCGCCGTGTACTACTGCCAGCAATACGACACATGGCCATTCACT
TTCGGACCCGGTACCAAAGTCGATTTCAAGAGAGCCGCGGCCATCG
AGGTTATGTACCCACCACCATATCTGGACAATGAAAAAGCAATG
GAACCATTATCCATGTGAAGGGTAAACACCTCTGCCCTAGCCCACT
TTTCCCTGGCCCATCAAAGCCCTTCTGGGTCTTGGTGGTTCGTGGGG
GGTGTGCTGGCCTGTTACAGCCTTCTGGTGACGGTTGCTTTCATTAT
CTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTAC
ATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACC
AGCCTTACGCACCACCTAGAGATTTGCTGCCTATCGGAGCAGGGT
GAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAG
AACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCAAGGAGGGTCTCTATAATGAGCTG
CAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA
GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGG

[0297]

ACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAA
GCCCTGCCACCTAGG (SEQ ID NO. 109)

Clone 20C5.2 CD28 CD3 zeta CAR AA Heavy & Light Chains

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
WVAVISYDGSDKYYVDSVKGRFTISRDN SKNRLYLQMNSLRAEDTAV
YYCARERYSGRDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQS
PATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLLIFGASTRAT
GIPARFSGSGSGTGFSLTISSLSQSEDAVYYCQQYDTWPFTFGPGTKVD
FKRAAAIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPGPSKPFWVL
VVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTR
KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
EYDVLDKRRGRDPENGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
110)

[0298]

Clone 20C5.2 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCTGCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGCAGGTGCAGTTGGTTGAATCAGGAGGGGG
TGTGGTGCAACCCGGTCGGTCACTGCGCCTCAGTTGTGCTGCTTCC
GGGTTTACTTTCAGCTCATATGGGATGCACTGGGTACGGCAGGCTC
CAGGTAAAGGCTTGGAATGGGTGGCGGTGATCAGCTATGACGGCT
CTGACAAATATTATGTGGACTCCGTGAAAGGCAGATTCACCATCAG
TCGAGACAACTCAAAGAATAGACTCTACTTGCAGATGAATAGCCTC
CGGGCCGAAGATACTGCAGTCTATTATTGCGCCCGGGAGCGCTACA
GTGGAAGAGACTATTGGGGGCAAGGAAGTCTTGTCACAGTCTCATC
TGGCGGCGGCGGCAGCGGTGGGGGCGGATCTGGCGGGGGCGGCAG
CGAAATCGTTATGACTCAGAGTCCTGCCACACTGAGCGTTAGCCCT
GGTGAGAGAGCAACACTTAGCTGCAGAGCTAGTCAGAGTGTTTCC
AGTCTTTTGACATGGTACCAACAGAAGCCCGGTCAAGCTCCACGAC
TGCTCATCTTCGGTGCATCCACCCGCGCAACCGGGATAACCGCCCG
GTTTTCCGGTTCTGGAAGTGGCACAGGATTACGCTCACCATTCTT
CTCTGCAGTCTGAAGACTTTGCCGTGTATTACTGCCAGCAGTACGA
TACCTGGCCCTTTACCTTTGGCCCAGGTACTAAAGTGGATTTTAAA
CGAGCTGCTGCACTTTCCAATAGTATTATGTACTTTTCACATTTTGT

GCCCGTGTTCTCCTGCCTGCGAAGCCTACGACAACCCCAGCCCCTAGG
CCGCCCACACCGGGCCCCAACTATTGCCTCCCAGCCATTGTCTCTGA
GACCCGAAGCTTGCAGACCTGCTGCTGGAGGCGCCGTTACACCCCG
AGGATTGGATTTCGCATGTGACATTTACATCTGGGGCCCCTTTGGCC
GGAACCTGCGGTGTGCTGCTGCTGCTCACTCGTGATTACACTTTACT
GCAACCACCGAAACAGATCCAAAAGAAGCCGCCTGCTCCATAGCG
ATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACA
CTACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGC
AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAG
AGTATGACGTTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGG
GTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATG
AGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCA
TGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTAC
CAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACA
TGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 111)

[0299] Clone 20C5.2 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal peptide in **Bold**)

MALPVTALLPLALLHAARPQVQLVESGGGVVQPGRSLRLSCAAS
GFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGRFTISR
DNSKNRLYLQMNSLRAEDTAVYYCARERYSGRDYWGGLTVTVSSGG
GGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLSCRASQSVSSLLTW
YQQKPGQAPRLLIFGASTRATGIPARFSGSGSGTGFTLTISSLQSEDFAV
YYCQQYDTPFTFGPGTKVDFKRAAALSNSIMYFSHFVPVFLPAKPTT
TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP
LAGTCGVLLLSLVITLYCNHRNRSKRSRLLHSDYMNMTPRRPGPTRK
HYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE
YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK
GERRRGKGHGGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
112)

[0300] Clone 20C5.2 CD8 CD3 zeta CAR DNA Heavy & Light Chains

CAGGTGCAGTTGGTTGAATCAGGAGGGGGTGTGGTGCAACCCGGT
CGGTCCTGCGCCTCAGTTGTGCTGCTTCCGGGTTTACTTTCAGCTC

ATATGGGATGCACTGGGTACGGCAGGCTCCAGGTAAAGGCTTGGA
ATGGGTGGCGGTGATCAGCTATGACGGCTCTGACAAATATTATGTG
GACTCCGTGAAAGGCAGATTCACCATCAGTCGAGACAACTCAAAG
AATAGACTCTACTTGCAGATGAATAGCCTCCGGGCCGAAGATACTG
CAGTCTATTATTGCGCCCGGGAGCGCTACAGTGGAAGAGACTATTG
GGGGCAAGGAACTCTTGTCACAGTCTCATCTGGCGGGCGGCGGCAG
CGGTGGGGGGCGGATCTGGCGGGGGGCGGCAGCGAAATCGTTATGAC
TCAGAGTCCTGCCACACTGAGCGTTAGCCCTGGTGAGAGAGCAAC
ACTTAGCTGCAGAGCTAGTCAGAGTGTTTCCAGTCTTTTGACATGG
TACCAACAGAAGCCCGGTCAAGCTCCACGACTGCTCATCTTCGGTG
CATCCACCCGCGCAACCGGGATACCCGCCCGGTTTTCCGGTTCTGG
AAGTGGCACAGGATTCACGCTCACCATTTCTTCTCTGCAGTCTGAA
GACTTTGCCGTGTATTACTGCCAGCAGTACGATACCTGGCCCTTTA
CCTTTGGCCCAGGTACTAAAGTGGATTTTAAACGAGCTGCTGCACT
TTCCAATAGTATTATGTACTTTTCACATTTTGTGCCCGTGTTCCTGC
CTGCGAAGCCTACGACAACCCCAGCCCCTAGGCCGCCACACCGG
CCCCAACTATTGCCTCCCAGCCATTGTCTCTGAGACCCGAAGCTTG
CAGACCTGCTGCTGGAGGCGCCGTTACACCCGAGGATTGGATTTC
GCATGTGACATTTACATCTGGGCCCTTTGGCCGGAACCTGCGGTG
TGCTGCTGCTGTCACCTCGTGATTACACTTTACTGCAACCACCGAAA
CAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACG
CACCACCTAGAGATTTGCTGCCTATCGGAGCAGGGTGAAGTTTTC
CAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACT
GTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTT
GGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAA
GACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGG
ATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGC
GGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCA
CTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCC
ACCTAGG (SEQ ID NO. 113)

[0301]

Clone 20C5.2 CD8 CD3 zeta CAR AA Heavy & Light Chains

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
WVAVISYDGSDKYVDSVKGRFTISRDN SKNRLYLQMNSLRAEDTAV
YYCARERYSGRDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIVMTQS
PATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLLIFGA STRAT
GIPARFSGSGGTGFTLTISSLQSEDAVYYCQQYDTWPFTFGPGTKVD
FKRAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRP
EACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHR
NRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFS
RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRR
KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT
KDTYDALHMQALPPR (SEQ ID NO. 114)

[0302]

Clone 20C5.2 CD28T CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTA ACTGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGGAGATTGTGATGACCCAGTCCCCTGCTACC
CTGTCCGTCAGTCCGGGCGAGAGAGCCACCTTGTCATGCCGGGCCA
GCCAGTCCGTCAGCAGTCTCCTGACTTGGTATCAGCAAAAACCAGG
GCAGGCACCGCGGCTTTTGATTTTGGTGCAAGCACACGCGCCACT
GGCATTCCAGCTAGGTTTTCTGGAAGTGGATCTGGGACAGGCTTCA
CTCTGACAATCAGTAGCCTGCAGAGTGAGGACTTTGCTGTTTACTA
CTGTCAACAGTACGACACCTGGCCATTACATTCCGGGCCCGGCACC
AAGGTCGACTTCAAGAGGGGCGGTGGAGGTT CAGGTGGTGGCGGG
TCAGGCGGCGGTGGGTCTCAGGTTCAACTGGTGGAATCAGGTGGC
GGCGTTGTCCAACCGGGGCGATCACTTCGACTTTCCTGTGCTGCCT
CAGGCTTTACTTTTTCATCCTATGGGATGCACTGGGTTCGGCAGGCT
CCCGGAAAAGGACTCGAGTGGGTTGCAGTGATCTCTTACGATGGCT
CAGACAAGTATTATGTGGACTCAGTCAAGGGGAGATTCACAATAA
GCCGAGACAACTCCAAAAACCGGCTTTATCTCCAGATGAACAGCCT
TAGAGCGGAAGATAACCGCGGTATACTACTGTGCCCCGCGAGAGGTA
TTCCGGCAGAGACTACTGGGGACAGGGCACACTGGTCACCGTGAG
TTCTGCCGCAGCGCTCGATAACGAAAAGAGCAACGGAACCATTAT
CCACGTTAAGGGCAAGCACCTGTGCCCCAGTCCCCTCTTCCCAGGA
CCATCTAAACCTTCTGGGTTCTGGTAGTAGTTGGAGGGGTCTTTG
CATGTTACTCCCTTTTGGTCACCGTCGCCTTCATTATTTTCTGGGTG

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACG
CACCACCTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTC
CAGATCTGCAGATGCACCAGCGTATCAGCAGGGGCCAGAACCAACT
GTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTT
GGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAA
GACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGG
ATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGC
GGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCA
CTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCC
ACCTAGGTAA (SEQ ID NO. 115)

[0303]

Clone 20C5.2 CD28T CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLPLALLHAARPEIVMTQSPATLSVSPGERATLSCRAS
QSVSSLLTWYQQKPGQAPRLIFGASTRATGIPARFSGSGSGTGFTLTIS
SLQSEDFAVYYCQQYDTWPFTFGPGTKVDFKRGGGSGGGSGGGG
SQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
WVAVISYDGSDKYYVDSVKGRFTISRDN SKNRLYLQMNSLR AEDTAV
YYCARERYSGRDYWGQGLVTVSSAAALDNEKSNGTIIHVKGKHLCP
SPLFPGPSKPFWVLVVVGGVLACYSLVTVAFIIFWVR SKRSRL LHS
YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQG
QNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ
ALPPR (SEQ ID NO. 116)

[0304]

Clone 20C5.2 CD28T CD3 zeta CAR DNA Heavy & Light Chains

GAGATTGTGATGACCCAGTCCCCTGCTACCCTGTCCGTCAGTCCGG
GCGAGAGAGCCACCTTGTCATGCCGGGCCAGCCAGTCCGTCAGCA
GTCTCCTGACTTGGTATCAGCAAAAACCAGGGCAGGCACCGCGGCT
TTTGATTTTTTGGTGCAAGCACACGCGCCACTGGCATTCCAGCTAGG
TTTTCTGGAAGTGGATCTGGGACAGGCTTCACTCTGACAATCAGTA
GCCTGCAGAGTGAGGACTTTGCTGTTTACTACTGTCAACAGTACGA
CACCTGGCCATTACATTCGGGCCCGGCACCAAGGTCGACTTCAAG
AGGGGCGGTGGAGGTT CAGGTGGTGGCGGGTCAGGCGGCGGTGGG

TCTCAGGTTCAACTGGTGAATCAGGTGGCGGCGTTGTCCAACCGG
GGCGATCACTTCGACTTTCCTGTGCTGCCTCAGGCTTTACTTTTTCA
TCCTATGGGATGCACTGGGTTCGGCAGGCTCCCGGAAAAGGACTCG
AGTGGGTTGCAGTGATCTCTTACGATGGCTCAGACAAGTATTATGT
GGA CT CAGTCAAGGGGAGATT CACAATAAGCCGAGACA ACTCCAA
AAACCGGCTTTATCTCCAGATGAACAGCCTTAGAGCGGAAGATACC
GCGGTATACTACTGTGCCCCGCGAGAGGTATTCCGGCAGAGACTACT
GGGGACAGGGCACACTGGTCACCGTGAGTTCTGCCGCAGCGCTCG
ATAACGAAAAGAGCAACGGAACCAT TATCCACGTTAAGGGCAAGC
ACCTGTGCCCCAGTCCCCCTCTTCCCAGGACCATCTAAACCCTTCTGG
GTTCTGGTAGTAGTTGGAGGGGTCCTTGCATGTTACTCCCTTTTGGT
CACCGTCGCCTTCATTATTTTCTGGGTGAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCC
CCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGC
TGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGG
GACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATT
CTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCAC
GACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATG
ACGCTCTCCACATGCAAGCCCTGCCACCTAGG (SEQ ID NO. 117)

[0305]

Clone 20C5.2 CD28T CD3 zeta CAR AA Heavy & Light Chains

EIVMTQSPATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLIF
GASTRATGIPARFSGSGSGTGFTLTISLQSEDFAVYYCQQYDTPFTF
GPGTKVDFKRGSGSGSGSGSGSQVQLVESGGGVVQPGRSLRLS
CAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGR
FTISRDNSKNRLYLQMNSLRAEDTAVYYCARERYSGRDYWGQGLV
TVSSAAALDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVGGVL
ACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAP
PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK
RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG
KGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO. 118)

[0306]

Clone 20C5.2 CD28 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAC TGCTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCGGAGATCGTCATGACACAGAGTCCAGCTAC
CCTGAGCGTGTCCCCTGGAGAGAGAGCCACCCTGTCCTGTAGGGCT
AGTCAGAGTGTGTCCAGCCTCCTCACCTGGTATCAACAGAAGCCTG
GTCAAGCTCCCCGGCTGCTTATCTTCGGGGCCAGCACGCGAGCCAC
AGGCATCCCGGCCAGATTCTCTGGCTCTGGCAGTGGCACCGGGTTC
ACTCTCACGATCTCATCCCTGCAGTCAGAGGATTTTCGCTGTGTATTA
CTGTCAGCAGTACGATACATGGCCCTTCACCTTCGGCCCGGGCACA
AAAGTAGATTTCAAGCGCGGCGGGCGGGGGTAGTGGGGGCGGGGGA
TCAGGAGGAGGGGGGCTCCCAAGTACAGCTGGTTGAGAGCGGCGGC
GGGGTGGTTCAGCCCGGGCGCAGCCTCAGGCTGAGTTGCGCAGCA
TCAGGATTCACATTCAGTTCTTATGGAATGCATTGGGTCAGACAGG
CTCCCGGGAAGGGCCTTGAATGGGTGGCAGTCATTAGCTACGACG
GAAGCGATAAGTACTATGTGGACTCAGTTAAAGGGAGATTTACTAT
CAGCCGCGACAATTCCAAAAACAGATTGTATTTGCAGATGAACTCC
CTCAGGGCGGAGGACACTGCTGTATATTACTGCGCACGAGAGAGA
TACTCCGGCCGAGACTATTGGGGCCAAGGAACATTGGTAACTGTGA
GCTCCGCCGCAGCTATTGAGGTCATGTACCCCCACCTTATCTCGA
TAATGAGAAGAGTAATGGGACTATAATTACGTAAAGGGCAAACA
CCTGTGCCCTTCCCCGCTGTTTCCAGGTCCAAGTAAGCCGTTCTGGG
TCCTGGTTGTGGTGGGAGGGGTGCTGGCCTGCTATTCTCTGTTGGTT
ACCGTGGCCTTTATCATTTTCTGGGTGAGATCCAAAAGAAGCCGCC
TGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCC
CACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCTGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAG
CGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGG
GACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGG
ACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGG
GTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACG
ACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGA
CGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 119)

[0307] Clone 20C5.2 CD28 CD3 zeta CAR AA Heavy & Light Chains
(Signal Peptide in **Bold**)
MALPVTALLLPLALLLHAARPEIVMTQSPATLSVSPGERATLSCRAS
 QSVSSLLTWYQQKPGQAPRLIFGASTRATGIPARFSGSGSGTGFTLTIS
 SLQSEDFAVYYCQQYDTWPFTFGPGTKVDFKRGGGGSGGGGSGGGG
 SQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
 WVAVISYDGSDKYYVDSVKGRFTISRDNLSKNRLYLQMNSLRAEDTAV
 YYCARERYSGRDYWGQGLVTVSSAAIEVMYPPPYLDNEKSNGTII
 HVKGKHLCPSPFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRS
 KRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSA
 DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNP
 QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD
 TYDALHMQALPPR (SEQ ID NO. 120)

[0308] Clone 20C5.2 CD28 CD3 zeta CAR DNA Heavy & Light Chains
 GAGATCGTCATGACACAGAGTCCAGCTACCCTGAGCGTGTCCCCTG
 GAGAGAGAGCCACCCTGTCCTGTAGGGCTAGTCAGAGTGTGTCCA
 GCCTCCTCACCTGGTATCAACAGAAGCCTGGTCAAGCTCCCCGGCT
 GCTTATCTTCGGGGCCAGCACGCGAGCCACAGGCATCCCGGCCAG
 ATTCTCTGGCTCTGGCAGTGGCACCGGGTTCCTCTCACGATCTCAT
 CCCTGCAGTCAGAGGATTTCTGCTGTGTATTACTGTCAGCAGTACGA
 TACATGGCCCTTCACCTTCGGCCCCGGGCACAAAAGTAGATTTCAAG
 CGCGGCGGCGGGGGTAGTGGGGGCGGGGGATCAGGAGGAGGGGG
 CTCCCAAGTACAGCTGGTTGAGAGCGGCGGGGGTGGTTCAGCC
 CGGGCGCAGCCTCAGGCTGAGTTGCGCAGCATCAGGATTCACATTC
 AGTTCTTATGGAATGCATTGGGTCAGACAGGCTCCCGGGAAGGGCC
 TTGAATGGGTGGCAGTCATTAGCTACGACGGAAGCGATAAGTACT
 ATGTGGACTCAGTTAAAGGGAGATTTACTATCAGCCGCGACAATTC
 CAAAAACAGATTGTATTTGCAGATGAACTCCCTCAGGGCGGAGGA
 CACTGCTGTATATTACTGCGCACGAGAGAGATACTCCGGCCGAGAC
 TATTGGGGCCAAGGAACATTGGTAACTGTGAGCTCCGCCGCAGCTA
 TTGAGGTCATGTACCCCCACCTTATCTCGATAATGAGAAGAGTAA
 TGGGACTATAATTCACGTAAAGGGCAAACACCTGTGCCCTTCCCCG
 CTGTTTCCAGGTCCAAGTAAGCCGTTCTGGGTCCTGGTTGTGGTGG

GAGGGGTGCTGGCCTGCTATTCTCTGTTGGTTACCGTGGCCTTTATC
 ATTTTCTGGGTGAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATT
 ACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACT
 ACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCTATCGGAGCAG
 GGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGC
 CAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAG
 TATGACGTTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGT
 GGCAAACCAAGACGAAAAAACCCCAAGGAGGGTCTCTATAATGAG
 CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATG
 AAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCA
 GGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG
 CAAGCCCTGCCACCTAGG (SEQ ID NO. 121)

[0309] Clone 20C5.2 CD28 CD3 zeta CAR AA Heavy & Light Chains

EIVMTQSPATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLIF
 GASTRATGIPARFSGSGSGTGFSLTISLQSEDFAVYYCQQYDTPFTF
 GPGTKVDFKRGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLS
 CAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGR
 FTISRDNSKNRLYLQMNSLR AEDTAVYYCARERYSGRDYWGQGLTV
 TVSSAAAEVMPYPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVW
 LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTR
 KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
 EYDVLDKRRGRDPENGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
 KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
 122)

[0310] Clone 20C5.2 CD8 CD3 zeta CAR DNA Heavy & Light Chains

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
 GCACGCCGCACGCCCGGAAATAGTGATGACTCAGTCCCCGGCCAC
 CCTCAGCGTGTCCCCCGGGAGCGAGCGACCCTGTCATGCAGGGCT
 TCCCAGAGTGTCAGCTCCCTGCTCACTTGGTATCAGCAAAAGCCGG
 GGCAGGCTCCCCGCCTCCTCATCTTCGGGGCATCAACTAGGGCCAC
 CGGCATTCTGCAAGATTTTCCGGGTCTGGCAGCGGCACCGGCTTC
 ACCCTTACCATTAGCTCTCTGCAGTCTGAGGACTTCGCCGTTTACTA
 TTGTCAGCAGTATGATACTTGGCCCTTTACCTTCGGTCCCGGAAC

AGGTGGACTTCAAGCGCGGGGGGGGTGGATCTGGAGGTGGTGGCT
 CCGGGGGCGGTGGAAGCCAGGTCCAGTTGGTTGAGAGCGGCGGCG
 GAGTGGTGCAGCCCGGAGGTCCTTGCGGCTGAGCTGTGCAGCCTC
 CGGTTTTACTTTTTCTAGCTATGGAATGCATTGGGTAAGACAGGCTC
 CCGGAAAAGGCCTCGAGTGGGTGGCGGTCATTAGCTATGATGGAT
 CTGATAAATACTATGTGGACTCAGTTAAGGGGCGCTTCACAATCTC
 AAGAGACAATAGCAAAAATAGACTGTACCTGCAGATGAATAGTCT
 GCGCGCCGAGGACACTGCCGTGTACTACTGCGCCCGCGAGAGATA
 CAGCGGACGGGATTACTGGGGCCAGGGTACCCTCGTAACGGTGTC
 CTCCGCTGCCGCCCTTAGCAACAGCATTATGTACTTTTCTCATTTTCG
 TGCCAGTCTTTCTCCAGCAAAGCCCACCACTACCCCGGCCCCCAG
 GCCGCTACTCCTGCCCCCACTATCGCGTCTCAGCCTCTCTCCTTGC
 GGCCCGAGGCCTGCCGGCCAGCCGCAGGGGGCGCCGTACATACTC
 GGGGTTTGGATTTCGCTTGCGACATATATATTGGGCCCCCCTCGCC
 GGCACATGTGGAGTGCTGCTCCTGAGTCTCGTTATAACCCTCTATT
 GCAACCATAGAAACAGATCCAAAAGAAGCCGCCTGCTCCATAGCG
 ATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACA
 CTACCAGCCTTACGCACCACCTAGAGATTTGCTGCCTATCGGAGC
 AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
 GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAG
 AGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGG
 GTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATG
 AGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCA
 TGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTAC
 CAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACA
 TGCAAGCCCTGCCACCTAGGTAA (SEQ ID NO. 123)

[0311]

Clone 20C5.2 CD8 CD3 zeta CAR AA Heavy & Light Chains

(Signal Peptide in **Bold**)

MALPVTALLLPLALLLHAARPEIVMTQSPATLSVSPGERATLSCRAS
 QSVSSLLTWYQQKPGQAPRLLIFGASTRATGIPARFSGSGSGTGFTLTIS
 SLQSEDFAVYYCQQYDTWPFTFGPGTKVDFKRGGGGSGGGGSGGGG
 SQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLE
 WVAVISYDGSDKYYVDSVKGRFTISRDN SKNRLYLQMNSLR AEDTAV

YYCARERYSGRDYWGQGLVTVSSAAALSNSIMYFSHFVPVFLPAKP
 TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW
 APLAGTCGVLLLSLVITLYCNHRNRSKRSRLLHSDYMNMTPRRPGPTR
 KHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
 EYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM
 KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO.
 124)

[0312]

Clone 20C5.2 CD8 CD3 zeta CAR DNA Heavy & Light Chains

GAAATAGTGATGACTCAGTCCCCGGCCACCCTCAGCGTGTCCCCCG
 GGGAGCGAGCGACCCTGTCATGCAGGGCTTCCCAGAGTGTCAGCTC
 CCTGCTCACTTGGTATCAGCAAAAGCCGGGGCAGGCTCCCCGCCTC
 CTCATCTTCGGGGCATCAACTAGGGCCACCGGCATTCCTGCAAGAT
 TTTCCGGGTCTGGCAGCGGCACCGGCTTCACCCTTACCATTAGCTCT
 CTGCAGTCTGAGGACTTCGCCGTTTACTATTGTCAGCAGTATGATA
 CTTGGCCCTTTACCTTCGGTCCCGGAACTAAGGTGGACTTCAAGCG
 CGGGGGGGGTGGATCTGGAGGTGGTGGCTCCGGGGGCGGTGGAAG
 CCAGGTCCAGTTGGTTGAGAGCGGCGGCGGAGTGGTGCAGCCCGG
 GAGGTCCTTGCGGCTGAGCTGTGCAGCCTCCGGTTTTACTTTTTCTA
 GCTATGGAATGCATTGGGTAAGACAGGCTCCCGGAAAAGGCCTCG
 AGTGGGTGGCGGTCATTAGCTATGATGGATCTGATAAATACTATGT
 GGAATCAGTTAAGGGGCGCTTACAATCTCAAGAGACAATAGCAA
 AAATAGACTGTACCTGCAGATGAATAGTCTGCGCGCCGAGGACAC
 TGCCGTGTACTACTGCGCCCGCGAGAGATACAGCGGACGGGATTA
 CTGGGGCCAGGGTACCCTCGTAACGGTGTCTCCGCTGCCGCCCTT
 AGCAACAGCATTATGTACTTTTCTCATTTTCGTGCCAGTCTTTCTCCC
 AGCAAAGCCCACCACTACCCCGGCCCCCAGGCCGCCTACTCCTGCC
 CCCACTATCGCGTCTCAGCCTCTCTCCTTGCGGCCCCGAGGCCTGCC
 GGCCAGCCGCAGGGGGCGCCGTACATACTCGGGGTTTGGATTTCGC
 TTGCGACATATATATTTGGGCCCCCCTCGCCGGCACATGTGGAGTG
 CTGCTCCTGAGTCTCGTTATAACCCTCTATTGCAACCATAGAAACA
 GATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
 TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCA
 CCACCTAGAGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCA

GATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGT
ATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGG
ACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGAC
GAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATA
AGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGA
GAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTG
CTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACC
TAGG (SEQ ID NO. 125)

[0313] Clone 20C5.2 CD8 CD3 zeta CAR AA Heavy & Light Chains

EIVMTQSPATLSVSPGERATLSCRASQSVSSLLTWYQQKPGQAPRLIF
GASTRATGIPARFSGSGSGTGFTLTISLQSEDFAVYYCQQYDTPFTF
GPGTKVDFKRGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLS
CAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSDKYYVDSVKGR
FTISRDNSKNRLYLQMNSLR AEDTAVYYCARERYSGRDYWGQGLTV
TVSSAAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRP
EACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCNHR
NRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFS
RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPENGGKPRR
KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT
KDTYDALHMQALPPR (SEQ ID NO. 126)

[0314] CAR Signal Peptide DNA

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCT
GCACGCCGCACGCCCCG (SEQ ID NO. 127)

[0315] CAR Signal Peptide: MALPVTALLPLALLHAARP (SEQ ID NO. 128)

[0316] scFv G4S linker DNA

GGCGGTGGAGGCTCCGGAGGGGGGGGCTCTGGCGGAGGGGGGCTCC
(SEQ ID NO. 129)

[0317] scFv G4s linker: GGGGSGGGGSGGGGS (SEQ ID NO. 130)

[0318] scFv Whitlow linker DNA

GGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGT
ACAAAGGGG (SEQ ID NO. 131)

[0319] scFv Whitlow linker: GSTSGSGKPGSGEGSTKG (SEQ ID NO. 132)

- [0320] CD28 AA Extracellular Domain
MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFS
REFRASLHKGLDSAVEVCVVYGNYSQQQLQVYSKTGFNC DGKLGNES
VTFY LQNL YVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCP
PLFPGPSKP (SEQ ID NO. 133)
- [0321] GX₂X₃X₄X₅X₆X₇X₈X₉ (SEQ ID NO: 134)
- [0322] X₁X₂X₃X₄X₅X₆ (SEQ ID NO: 135)
- [0323] X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀X₁₁X₁₂DY (SEQ ID NO: 136)
- [0324] X₁ASQX₅X₆X₇X₈X₉LX₁₁ (SEQ ID NO: 137)
- [0325] X₁ASX₄X₅X₆X₇ (SEQ ID NO: 138)
- [0326] QQX₃X₄X₅X₆PX₈T (SEQ ID NO: 139)
- [0327] 4-1BB Nucleic Acid Sequence (intracellular domain)
AAGCGCGGCAGGAAGAAGCTCCTCTACATTTTAAAGCAGCCTTTTA
TGAGGCCCGTACAGACAACACAGGAGGAAGATGGCTGTAGCTGCA
GATTTCCCGAGGAGGAGGAAGGTGGGTGCGAGCTG (SEQ ID NO.
140)
- [0328] 4-1BB AA (intracellular domain)
KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID
NO. 141)
- [0329] OX40 AA
RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI (SEQ ID NO. 142)
- [0330] Leader Sequence AA
MALPVTALLLPLALLHAARP (SEQ ID NO: 143)
- [0331] Additional G4S linker: GGGGSGGGGSGGGGSGGGGS (SEQ ID NO. 144)
- [0332] CD3 zeta variant AA
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR (SEQ ID NO. 145)

[0333] Axi Cel (KTE-C19) DNA (SEQ ID NO. 146)

Atgcttctcctggtgacaagccttctgctctgtgagttaccacacccagcattcctcctgatcccagacatccagatgacacagactaca
tcctccctgtctgcctctctgggagacagagtcaccatcagttgcagggcaagtcaggacattagtaaataatttaaattggtatcagcaga
aaccagatggaactgttaaactcctgatctaccatacatcaagattacactcaggagtcctcatcaagggtcagtggcagtgggctctggaa
cagattattctctcaccattagcaacctggagcaagaagatattgccactacttttgccaacagggtaatacgttccgtacacgttcgg
aggggggactaagttggaaataacaggctccacctctggatccggcaagcccggatctggcgagggatccaccaagggcgaggtg
aaactgcaggagtcaggacctggcctggtggcgccctcacagagcctgtccgtcacatgcactgtctcaggggtctcattaccgact
atggtgtaagctggattcgccagcctccacgaaagggctctggagtggctgggagtaatatggggtagtgaaaccacatactataattca
gctctcaaatccagactgaccatcatcaaggacaactccaagagccaagttttctaaaaatgaacagtctgcaaactgatgacacagc
catttactactgtgccaacattattactacgggtggtagctatgctatggactactgggggtcaaggaacctcagtcaccgtctcctcagcg
gccgcaattgaagtatgtatcctcctcttacctagacaatgagaagagcaatggaaccattatccatgtgaaagggaacacctttgtc
caagtcacctatttccggaccttctaagcccttttgggtgctggtggtggtgggggagtcctggcttgctatagcttgctagtaacagtg
gcctttattattttctgggtgaggagtaagaggagcaggctcctgcacagtgactacatgaacatgactccccgccgccccgggcca
cccgcaagcattaccagccctatgccccaccacgcgacttcgcagcctatcgctccagagtgaagttcagcaggagcgcagacgcc
ccccgctaccagcagggccagaaccagctctataacgagctcaatctaggacgaagagaggagtacgatgttttgacaagagacg
tggccgggaccctgagatggggggaaagccgagaaggaagaaccctcaggaaggcctgtacaatgaactgcagaaagataagat
ggcggaggcctacagtgagattgggatgaaaggcgagcgccggagggggcaaggggcacgatggcctttaccagggtctcagtac
agccaccaagagacactacgacgcccttcacatgcaggccctgccccctcgc

[0334] Axi Cel (KTE-C19) AA (SEQ ID NO. 147)

MLLLVTSLLLCELPHPAFLLPDIQMTQTTSSLSASLGDRV TISCRASQDISKYLNWYQ
QKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPY
TFGGGTKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSL
PDYGVSWIRQPPRKGLEWLGVWGSSETTYYN SALKSRLTIKD NSKSQVFLKMNSLQ
TDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSAAAIEVMYPPPYLDNEKSNGTI
IHVKGKHLCPSP LFPGPSKPFWVLVVVGGVLACY SLLVTVAFIIFWVR SKRSRL LHSD

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YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN
LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER
RRGKGHDGLYQGLSTATKDTYDALHMQALPPR

[0335] Humanized anti-CD19 CAR DNA (SEQ ID NO. 148)

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCCGATATTCAAATGACCCAGTCCCCGTCCTCCCTGAGTGCCTCCGTCGG
TGACCGTGTTACGATTACCTGCCGTGCGAGCCAAGACATCTCTAAATACCTGAAC
TGGTATCAGCAAAAACCGGATCAGGCACCGAAACTGCTGATCAAACATACCTCA
CGTCTGCACTCGGGTGTGCCGAGCCGCTTTAGTGGTTCCGGCTCAGGTACCGATT
ACACCCTGACGATCAGCTCTCTGCAGCCGGAAGACTTTGCCACGTATTACTGCCA
GCAAGGTAATACCCTGCCGTATACGTTCCGGCCAAGGTACCAAACCTGGAAATCAA
AGGCTCGACGAGCGGCTCTGGTAAACCGGGCTCTGGTGAAGGCAGTACCAAAGG
TGAAGTGCAGCTGGTTGAAAGCGGTGGTGGTCTGGTTCAACCGGGTCGTTCCCTG
CGTCTGTCATGTACGGCGAGTGGTGTCTCCCTGCCGGACTATGGCGTGTCTGGA
TTCGTCAGCCGCCGGGTAAAGGCCTGGAATGGATTGGTGTCTCTGGGGCAGTG
AAACCACGTATTACAACCTCGGCCCTGAAAAGCCGTTTCACCATCTCTCGCGATAA
CAGTAAAAATACGCTGTACCTGCAGATGAATAGCCTGCGCGCGGAAGACACCGC
CGTTTACTACTGCGCAAAACATTACTACTACGGTGGCAGCTATGCTATGGATTAC
TGGGGTCAAGGCACGCTGGTCAACGTTTCGTCAGCCGCTGCCCTTGATAATGAAA
AGTCAAACGGAACAATCATTACGTGAAGGGCAAGCACCTCTGTCCGTCACCCCT
GTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTC
GCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAA
AAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC
CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC

AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTT
TGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAA
AACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG
CAAGCCCTGCCAcctagg

[0336] Humanized anti-CD19 CAR AA (SEQ ID NO. 149)

MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVITICRASQDISKYLNWY
QQKPDQAPKLLIKHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTL
PYTFGQGTKLEIKGSTSGSGKPGSGEGSTKGEVQLVESGGGLVQPGRSLRLSCTASG
VSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNLSALKSRFTISRDN SKNTLYLQMN
SLRAEDTAVYYCAKHYYYGGSYAMDYWGQGLTVTVSSAAALDNEKSNGTIIHVKG
KHLCPSP LFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRL LHSDYMN M
TPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE
EYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK
GHDGLYQGLSTATKDTYDALHMQALPPR

[0337] Fully human anti-CD19 CAR DNA (SEQ ID NO. 150)

Atggcctgcctgtgacagctctgctgctgccctggcctgctgctgcatgccccagacctgagatcgtgctgacccagctctccg
gcacctgtctctcagcccaggagagagagccacctgagctgcagagccagccagagcgtgtccagcagctacctggcctggtat
cagcagaagcccgacaggccccagactgctgatctacggcgccagctctagagccaccggcatccccacagattcagcggca
gcccagtgccaccgacttcacctgacctcagcagactggaacccgaggacttcgccgtgtactactgccagcagtacggcagc
agccggtcaccttcggcctggcaccaaggtggacatcaagggcagcacctccggcagcggcaagcctggctctggcgagggct
ctaccaagggccaggtgcagctggtgcagctctggcgccgaagtgaagaaacccggctctagcgtgaaggtgtcctgcaaggacag
cggcgccaccttcagcagctacccatcagctgggtgcgccaggccccaggacaggggctggaatggatggcgggcatcatcccc
atcttcggcaccaccaactacgccagcagttccagggcagagtgacctcaccgccgacgagagcaccagcaccgcctacatgg

aactgagcagcctgcggagcagggacacagccgtgtattactgtgcccgcgaggccgtggccgccgactggctggatccttgggg
acagggcaccctggtgacagtgtccagcttcgtgcccgtgttctgcccgccaaagcctaccaccaccctgcccctagacctcccacc
ccagccccaacaatcgccagccagcctctgtccctgcggcccgaagcctgtagacctgctgccggcggagccgtgcacaccagag
gcctggacttcgctgcgatatctacatctgggcccctctggccggcacctgtggcgtgctgctgctgagcctggtgatcacctgtact
gcaaccaccggaacagaagcaagcggagccggctgctgcacagcgactacatgaacatgaccccaagacggcctggccccacc
ggaagcactaccagccttacgcccctcccagagacttcgccgcctaccggtccagagtgaagttcagcagatccgccgacgcccct
gcctaccagcagggacagaaccagctgtacaacgagctgaacctgggcagacgggaagagtacgacgtgctggacaagcggaga
ggccgggaccccagatgggcggaaagcccagacggaagaaccccaggaaggcctgtataacgaactgcagaaagacaagat
ggccgaggcctacagcgagatcgccatgaagggcgagcggaggcgcggaagggccacgatggcctgtaccagggcctgagc
accgccaccaaggacacctacgacgccctgcacatgcaggccctgccccccaga

[0338] Fully human anti-CD19 CAR AA (SEQ ID NO. 151)

MALPVTALLLPLALLLHAARPEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWY
QQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSR
FTFGPGTKVDIKGSTSGSGKPGSGEGSTKGQVQLVQSGAEVKKPGSSVKVSCKDSGG
TFSSYAISWVRQAPGQGLEWMGGIIPFGTTNYAQQFQGRVTITADESTSTAYMELSS
LRSEDTAVYYCAREAVAADWLDPWGQGTLVTVSSFPVFLPAKPTTTPAPRPPTPAP
TIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNH
RNRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAY
QQGQNQLYNELNLGRREEYDVLDKRRGRDPGKPRRKNPQEGLYNELQKDKM
AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

[0339] MAGE A3/A6 TCR DNA (SEQ ID NO. 152)

atggcatgccctggcttctgtgggcactgtgatctccacctgtctgaatttagcatggctcagacagtcactcagtcctcaaccagaga
tgtctgtgcaggaggcagagaccgtgacctgagctgcacatatgacaccagtgagagtgattattatttcttggtacaagcagcctc
ccagcaggcagatgattctcgttattcgccaagaagcttataagcaacagaatgcaacagagaatcgtttctctgtgaactccagaaag
cagccaaatccttcagtcctcaagatctcagactcacagctgggggatgccgcgatgtatttctgtgctctccggagctcaggaacctac

aaatacatctttggaacaggcaccaggctgaaggtttagcaaatatccagaaccctgaacctgctgtgtaccagttaaaagatcctcgg
tctcaggacagcaccctctgcctgttcaccgactttgactcccaaatcaatgtgccgaaaaccatggaatctggaacgttcactgac
aaaactgtgctggacatgaaagctatggattccaagagcaatggggccattgcctggagcaaccagacaagcttcacctgccaagat
atcttcaaagagaccaacgccacctaccccagttcagacgttccctgtgatgccacgttgactgagaaaagctttgaaacagatatgaa
cctaaactttcaaacctgtcagttatgggactccgaatcctcctgtgaaagtagccggatttaacctgctcatgacgctgaggctgtgg
tccagtctgggccaagcgggtccggatccggagccaccaacttcagcctgtgaagcaggccggcgacgtggaggagaaccccggc
cccatgggcaccaggctcctcttctgggtggccttctgtctcctgggggcagatcacacaggagctggagtctcccagtcctccagta
acaaggctcacagagaagggaaggatgtagagctcaggtgtgatccaatttcaggtcatactgccctttactggtaccgacagagcct
ggggcagggcctggagttttaatttactccaaggcaacagtgccaccagacaaatcagggtgcccagtgatcgcttctctgcagaga
ggactgggggatccgtctccactctgacgatccagcgcacacagcaggaggactcggccgtgtatctctgtgccagcatccggaca
gggcctttttctctggaacaccatatattttgagaggggaagtgggtcactgttgtagaggacctgagaaacgtgacccccaccaag
gtctcctgtttgagccatcaaaagcagagattgcaaacaacaaaaggctaccctcgtgtgcttggccaggggcttcttcctgaccac
gtggagctgagctggtgggtgaatggcaaggaggtccacagtgggggtcagcacggaccctcaggcctacaaggagagcaattata
gctactgcctgagcagccgcctgagggtctctgtaccttctggcacaatcctcgaaccacttccgctgccaagtgcagttccatggg
ctttcagaggaggacaagtggccagaggggtcacccaaacctgtcacacagaacatcagtgacagggcctggggccgagcagact
gtggaatcacttcagcatcctatcatcaggggggttctgtctgcaaccatcctctatgagatcctactggggaaggccaccctatatgtctgt
gctggtcagtgccctggtgctgatggctatgggtcaaaagaaagaactcatga

[0340] MAGE A3/A6 TCR AA (SEQ ID NO. 153)

MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL
SCTYDTSESDYYLFWYKQPPSRQMILVIRQEAYKQQNATEN
RFSVNFQKAAKSFSCLKISDSQLGDAAMYFCALRSSGTYKYIF
GTGTRLKVLANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQI
NVPKTMESGTFITDKTVLDMKAMD SKSNGAIAWSNQTSFTC
QDIFKETNATYPSSDVPCD ATLTEKSFETDMNLNFQNL SVM
GLRILLK VAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQA

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GDVEENPGPMGTRLFWVAFCLLGADHTGAGVSQSPSNKVT
EKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SA
PDKSGLPSDRFSAERTGGSVSTLTIQRTQQEDSAVYLCASIRT
GPFFSGNTIYFGE GSWLTVVEDLRNVTPPKVSLFEPSKAEIA
NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQA
YKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEED
KWPEGSPKPVTQNISAEAWGRADCGITSASYHQGVLSATIL
YEILLGKATLYAVLV SGLVLMAMVKRKN S Stop

[0341] Anti-CLL-1 CAR DNA (SEQ ID NO. 154)

ATGGCACTCCCCGTA ACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCCGAGGTCCA ACTGCAAGAAAGCGGACCCGGACTGGTGAAGCCTTCTG
AGACACTTAGTCTGACGTGCACGGTCAGTGGCGGCTCCATCTCCTCCTATTATTG
GTCATGGATACGACAACCCCCAGGTAAGGGCCTGGAATGGATTGGCTATATCTA
CTATTCAGGAAGCACGA ACTACAATCCCAGCCTGAAGTCCCGAGTGACAATTTC
AGTAGATACCAGTAAAA ACCAGTTCAGTCTTAAACTGTCAAGCGTGACAGCTGC
CGACACCGCTGTGTATTACTGCGTCTCACTGGTGTATTGTGGAGGGGATTGTTAT
AGCGGGTTCGATTATTGGGGACAGGGAACCCTGGTGACTGTATCTTCCGGCGGC
GGCGGCTCAGGGGGTGGCGGTAGTGGCGGTGGGGGTTCGATATTCAACTGACA
CAATCCCCCAGCTCACTCAGCGCCAGCGTGGGGGACAGGGTTAGCTTTACCTGTC
AAGCCTCTCAGGATATAAATAACTTTCTGAACTGGTATCAACAGAAGCCTGGGA
AGGCGCCCAA ACTCCTGATCTATGATGCGTCCAACCTGGAAACTGGCGTGCCTTC
ACGCTTTAGCGGCTCTGGCAGTGGTACAGACTTCACTTTTACCATCTCTTCACTTC
AGCCGGAGGACATCGCCACATATTACTGTCAACAGTACGGAAACTTGCCCTTTAC
TTTTGGAGGCGGCACCAAAGTTGAAATCAAAAGGGCCGCTGCCCTGGATAACGA
AAAGAGCAATGGGACTATAATACATGTTAAAGGAAAACACCTGTGTCCATCTCC

CCTGTTCCCTGGACCGTCAAAGCCATTTTGGGTGCTCGTGGTTGTCGGTGGCGTT
CTCGCCTGTTATAGCTTGCTGGTGACAGTAGCCTTCATTATCTTTTGGGTGAGATC
CAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCT
GGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTTCGCTGCCT
ATCGGAGCCGAGTGAAATTTTCTAGATCAGCTGATGCTCCCGCCTATCAGCAGGG
ACAGAATCAACTTTACAATGAGCTGAACCTGGGTGCGAGAGAAGAGTACGACGT
TTTGGACAAACGCCGGGGCCGAGATCCTGAGATGGGGGGGAAGCCGAGAAGGA
AGAATCCTCAAGAAGGCCTGTACAACGAGCTTCAAAAAGACAAAATGGCTGAGG
CGTACTCTGAGATCGGCATGAAGGGCGAGCGGAGACGAGGCAAGGGTCACGAT
GGCTTGTATCAGGGCCTGAGTACAGCCACAAAGGACACCTATGACGCCCTCCAC
ATGCAGGCACTGCCCCCACGC

[0342] Anti-CLL-1 CAR AA (SEQ ID NO. 155)

MALPVTALLPLALLHAARPQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWI
RQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYC
VSLVYCGGDCYSGFDYWGGQTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSSLSAS
VGDRVSFTCQASQDINNFLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDF
TFTISSLQPEDATYYCQYGNLPFTFGGGTKVEIKRAAALDNEKSNGTIIHVKGKHL
CPSPLFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPR
RPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD
VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD
GLYQGLSTATKDTYDALHMQALPPR

[0343] Anti-BCMA CAR DNA (SEQ ID NO. 156)

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA
GGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCAT

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GCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGC
CGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCGTTCGAGGAGCCGCCATA
CGATTATGGAATGGACGTATGGGGCCAGGGAACAACCTGTCACCGTCTCCTCAGG
GTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGA
AATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGC
CACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAG
CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCC
ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGGTCTGGGACAGAGTTCCTCTCA
CCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCACCA
CGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCGCT
GCCCTTGATAATGAAAAGTCAAACGGAACAATCATTACGTGAAGGGCAAGCAC
CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGT
AGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCT
TCTGGGTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAG
AGATTTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGAT
AAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGG
AAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTA
TGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

[0344] Anti-BCMA CAR AA (SEQ ID NO. 157)

MALPVTALLLPLALLLHAARPQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMH
WVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAED
TAVYYCVKGPLQEPPYDYGMDVWGQGTTVTVSSGSTSGSGKPGSGEGSTKGEIVMT
QSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYSASTRATGIPARFS
GSGSGTEFTLTISSLQSEDFAVYYCQQHVVWPLTFGGGTKVEIKRAAALDNEKSNGT
IIHVKGKHLCPSP LFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVR SKRSRL LHS
DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEL
NLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

[0345] C185 E7₁₁₋₁₉ / HLA-A*02:01 Specific TCR DNA (SEQ ID NO. 158)

atgggcaccagactgtcttttatgtggccctgtgtctgtgtggaccggccacatggatgccggaattacacagagccccagacacaa
agtgaccgagacaggcaccctgtgacactgagatgccaccagaccgagaaccaccgctacatgtactggtacagacaggatccag
gccacggcctgagactgatccactacagctacggcgtgaaggacaccgacaagggcggaagtgtctgacggctacagcgtgtccag
aagcaagaccgaggatttctgtgacctggaaagcgccacaagcagccagaccagcgtgtactttgtgccatcagcggctacaa
gaacaccgaggccttttcggccaaggcaccaggctgacagtgggtggaagatctgaagaacgtgttccacctgaggtggcctgttt
gagccttctgaggccgagatcagccacacacagaaagccacactcgtgtgcttgccaccggctttatcccgatcacgtggaactgt
cttggtgggtcaacggcaaagaggtgcacagcggcgtagcacagaccctcagcctctgaaagagcagcccgctctgaacgacag
cagatactgtctgagcagcagactgagagtgtccgccaccttctggcagaacccagaaaccacttcagatgccaggtgcagttctac
ggcctgtccgagaatgacgagtggaccaggatagagccaagccagtgacacagattgtgtctgccgaagcctggggcagagccg
attgtggctttacaagcgagagctaccagcagggcgtgctgtctgccacaatcctgtatgagatcctgctgggcaaagccactctgtac
gctgtgctgggtgtctgcctgggtgctgatggccatgggtcaagaaaaggacagcagaggcagagccaagagatctggcagcggcg
ccacaaacttagcctgtgtaaacaggccggcgacgtggaagagaaccctggacatatgaagtcctgcgggtgctgctggttattct
gtggctgcagctgagctgggtttggagccagggacagcaagtgtgagatccctcagtagcagcgtgcaagaaggcgaggact
tcaccacctactgcaacagcagcacaacctgagcaacatccagtgggtacaagcagaggcctggcgggcaccctgtgtttctgatcc
agctgggtaagagcggcggaagtgaagaagcagaagcgggtgacctttcagttcggcgaggccaagaagaacagcagcctgcacatt

accgccacacagaccaccgacgtgggcacatatTTTTgcgtggcagagaaggcggcagcgagaagctggttttggcaagggcac
 caaactgaccgtgaatcccgacattcagaaccccgatccagccgtgtaccagctgagagacagcaagagcagcgacaagagcgtgt
 gtctgttcaccgacttcgactcccagaccaatgtgtcccagagcaaggactccgacgtgtacatcaccgataagaccgtgctggacat
 ggggagcatggacttcaagagcaatagcgccgtggcttgagcaacaagagcgactttgcctgcgccaacgccttcaacaacagca
 tcatccccgaggacacattcttcccaagtctgagagcagctgcgacgtgaagctgggtgaaaagagcttcgagacagacaccaacc
 tgaacttcagaacctgagcgtgatcggttcagaatcctgctgctgaaggtggccggcttcaacctgctgatgactctgagactgtggt
 ccagctgaattcggatccaagcttaggcctgctcgtttcttctgtgtccatttctattaaaggttcctttgttc

[0346] C185 E7₁₁₋₁₉ / HLA-A*02:01 Specific TCR AA (SEQ ID NO. 159)

MGTRLFFYVALCLLWTGHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMYWYR
 QDPGHGLRLIHYSYGVKDDTKGEVSDGYSVSRSKTEDFLLTLESATSSQTSVYFCAIS
 GYKNTEAFFGQGTRLTVVEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPD
 HVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHFR
 CQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEIL
 LGKATLYAVLVSALVLMAMVKRKDSRGRAKRSGSGATNFSLLKQAGDVEENPGPM
 KSLRVLLVILWLQLSWVWSQGQQVMQIPQYQHVEGEDFTTYCNSSTLSNIQWYK
 QRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGRE
 GGSEKLVFGKGTKLTVNPDIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKD
 SDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPESSCDV
 KLVEKSFETDTNLFQNLVIGFRILLKLVAGFNLLMTLRLWSS

[0347] E7₁₁₋₁₉ / HLA-A*02:01 Specific TCR DNA (SEQ ID NO. 160)

atgggacctggattgctttgtgggccctgctgtgtctgcttgagctggactgtggatgccggcgtgacacagctctccacacacctg
 atcaagaccagaggccagcaagtgacctgagatgtagccctaagagcggccacgacaccgtgtcttggtatcagcaggctcttgcc
 cagggacctcagttcatcttccagtactacgaggaagaggaacggcagcggggcaacttccctgatagattctctggccatcagttcc
 ccaactacagcagcgagctgaacgtgaacgctctgctgctggcgatagcgccctgtatctgtgtgccagttctcttggttgagaggc
 ggcagatacaacgagcagttctttggccctggcaccagactgacctgtgtggaagatctgaagaacgtgttccacctgaggtggcc

gtgtttgagccttctgaggccgagatcagccacacacagaaagccacactcgtgtgcctggccaccggctttatcccgatcacgtgg
aactgtcttggtgggtcaacggcaaagaggtgcacagcggcgtagcacagaccctcagcctctgaaagagcagcccgtctgaac
gacagcagatactgtctgagcagcagactgagagtgtccgccaccttctggcagaaccccagaaaccacttcagatgccaggtgcag
ttctacggcctgtccgagaatgacgagtggaaccaggatagagccaagccagtgcacagattgtgtctgccgaagcctggggcag
agccgattgtggctttacaagcgagagctaccagcagggcggtgtgtctgccacaatcctgtatgagatcctgtgggcaaagccact
ctgtacgctgtgctggtgtctgccctgggtgtgatggccatggtcaagagaaaggacagcagaggcagagccaagagatctggcag
cggcgccacaaacttttagcctgtgaaacaggccggcgacgtggaagagaaccctggacctatgaagtcctcggggtgtgtgtgg
ttattctgtggctgcagctgagctgggtttggagccagggacagaacatcgaccagcctaccgagatgacagccaccgaaggcgcc
atcgtgcagatcaattgcacctaccagaccagcggttcaacggcctgttctggtatcaacagcatgccggcgaggcccctaccttct
gagctataatgtgctggacggcctggaagaaaaggcgagattcagcagcttctgtccagaagcaagggttacagctacctgtgct
gaaagaactccagatgaaggacagcgcctcctacctgtgtgcctccgtggatggaaacaacagactggccttcggcaagggaacc
aggtggtggtcatccccgacattcagaaccccgatccagccgtgtaccagctgagagacagcaagagcagcgacaagagcgtgtgt
ctgttcaccgacttcgactcccagaccaatgtgtcccagagcaaggactccgacgtgtacatcaccgataagaccgtgtggacatgc
ggagcatggacttcaagagcaatagcgccgtggcttgagcaacaagagcgactttgcctgcgccaacgccttcaacaacagcatca
tccccgaggacacattcttccaagtctgagagcagctgcgacgtgaagctggtggaaaagagcttcgagacagacaccaacctga
acttcagaacctgagcgtgatcggttcagaatcctgtctgtgaaggtggccggcttcaacctgtgatgactctgagactgtgtgcc
agctgaattcggatccaagcttaggcctgtctgccttctgtgtccatttctattaaaggttcctttgttc

[0348] E7₁₁₋₁₉ / HLA-A*02:01 Specific TCR AA (SEQ ID NO. 161)

MGPGLLCWALLCLLGAGLVDAQVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQ
QALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDSALYLCAS
SLGWRGGRYNEQFFGPGTRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLAT
GFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNP
RNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSAT
ILYEILLGKATLYAVLVSALVLMAMVKRKDSRGRAKRSGSGATNFSLLKQAGDVEE
NPGPMKSLRVLLVILWLQLSWVWSQGQNIDQPTMTATEGAIVQINCTYQTSGFNG

LFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSKGYSYLLKELQMKDSASYLC
ASVDGNNRLAFGKGNQVVVIPDIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQ
SKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPESS
CDVKLVEKSFETDTNLFQNLVIGFRILLKLVAGFNLLMTLRLWSS

[0349] Axi Cel (KTE-C19) Leader (CSF2RA) DNA (SEQ ID NO. 162)

Atgcttctcctggtgacaagccttctgctctgtgagttaccacaccagcattcctctgatccca

[0350] Axi Cel (KTE-C19) Leader (CSF2RA) AA (SEQ ID NO. 163)

MLLLVTSLLLCELPHPAFLIP

[0351] Axi Cel (KTE-C19) scFv heavy chain DNA (SEQ ID NO. 164)

gacatccagatgacacagactacatcctccctgtctgcctctctgggagacagagtcaccatcagttgcagggcaagtcaggacatta
gtaaatatttaaattggtatcagcagaaaccagatggaactgttaaactcctgatctaccatacatcaagattacactcaggagtcccatc
aaggttcagtggcagtggtctggaacagattattctctcaccattagcaacctggagcaagaagatattgccacttacttttgccaacag
ggtaatacgccttcctacacgttcggaggggggactaagttggaaataaca

[0352] Axi Cel (KTE-C19) scFv heavy chain AA (SEQ ID NO. 165)

DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGV
PSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGGTKLEIT

[0353] Axi Cel (KTE-C19) Linker (Whitlow) DNA (SEQ ID NO. 166)

ggctccacctctggatccggcaagcccggatctggcgagggatccaccaagggc

[0354] Axi Cel (KTE-C19) Linker (Whitlow) AA (SEQ ID NO. 167)

GSTSGSGKPGSGEGSTKG

[0355] Axi Cel (KTE-C19) scFv light chain DNA (SEQ ID NO. 168)

gaggtgaaactgcaggagtcaggacctggcctggtggcgccctcacagagcctgtccgtcacatgcactgtctcaggggtctcattac
ccgactatggtgtaagctggattcgccagcctccacgaaaggtctggagtggctgggagtaatatggggtagtgaaaccacatacta
taattcagctctcaatccagactgaccatcatcaaggacaactccaagagccaagtttcttaaaaatgaacagtctgcaaactgatga
cacagccatttactactgtgccaaacattattactacggtggtagctatgctatggactactgggggtcaaggaacctcagtcaccgtctcc

tca

[0356] Axi Cel (KTE-C19) scFv light chain AA (SEQ ID NO. 169)

EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVWGSETT
YYNSALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQ
GTSVTVSS

[0357] Axi Cel (KTE-C19) Minispace DNA (SEQ ID NO. 170)

gcggccgca

[0358] Axi Cel (KTE-C19) Minispace AA (SEQ ID NO. 171)

AAA

[0359] Axi Cel (KTE-C19) CD28 spacer (extracellular / TM region of CD28) DNA
(SEQ ID NO. 172)

attgaagtattgtatcctcctctacctagacaatgagaagagcaatggaaccattatccatgtgaaagggaacacctttgtccaagtc
ccctatttcccgaccttctaagcccttttgggtgctgggtggttgggggagtcctggcttgctatagcttgctagtaacagtggccttt
attattttctgggtg

[0360] Axi Cel (KTE-C19) CD28 spacer (extracellular / TM region of CD28) AA
(SEQ ID NO. 173)

IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFWVLVVVGGVLACYSLLV
VAFIIFWV

[0361] Axi Cel (KTE-C19) CD28 costimulatory (intracellular region of CD28) DNA
(SEQ ID NO. 174)

aggagtaagaggagcaggctcctgcacagtgactacatgaacatgactccccgccgccccgggccccaccgcaagcattaccagc
cctatgccccaccacgcgacttcgcagcctatcgctcc

[0362] Axi Cel (KTE-C19) CD28 costimulatory (intracellular region of CD28) AA
(SEQ ID NO. 175)

RSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

- [0363]** Axi Cel (KTE-C19) CD3 zeta DNA (SEQ ID NO. 176)
- agagtgaagttcagcaggagcgagacgccccgcgtaccagcagggccagaaccagctctataacgagctcaatctaggacgaa
gagaggagtacgatgttttgacaagagacgtggccgggaccctgagatgggggggaaagccgagaaggaagaaccctcaggaag
gcctgtacaatgaactgcagaaagataagatggcggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaagg
ggcacgatggcctttaccaggggtctcagtacagccaccaaggacacctacgacgcccttcacatgcaggccctgccccctcgc
- [0364]** Axi Cel (KTE-C19) CD3 zeta AA (SEQ ID NO. 177)
- RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR
- [0365]** Axi Cel (KTE-C19) VL CDR1 (Chothia) (SEQ ID NO. 178)
- RASQDISKYLN
- [0366]** Axi Cel (KTE-C19) VL CDR2 (Chothia) (SEQ ID NO. 179)
- HTSRLHS
- [0367]** Axi Cel (KTE-C19) VL CDR3 (Chothia) (SEQ ID NO. 180)
- QQGNTLPYT
- [0368]** Axi Cel (KTE-C19) VH CDR1 (Chothia) (SEQ ID NO. 181)
- GVSLPDY
- [0369]** Axi Cel (KTE-C19) VH CDR2 (Chothia) (SEQ ID NO. 182)
- WGSET
- [0370]** Axi Cel (KTE-C19) VH CDR3 (Chothia) (SEQ ID NO. 183)
- HYYYGGSYAMDY
- [0371]** Axi Cel (KTE-C19) VL CDR1 (Kabat) (SEQ ID NO. 184)
- RASQDISKYLN
- [0372]** Axi Cel (KTE-C19) VL CDR2 (Kabat) (SEQ ID NO. 185)
- HTSRLHS

[0373] Axi Cel (KTE-C19) VL CDR3 (Kabat) (SEQ ID NO. 186)

QQGNTLPYT

[0374] Axi Cel (KTE-C19) VH CDR1 (Kabat) (SEQ ID NO. 187)

DYGVS

[0375] Axi Cel (KTE-C19) VH CDR2 (Kabat) (SEQ ID NO. 188)

VIWGSETTYNSALKS

[0376] Axi Cel (KTE-C19) VH CDR3 (Kabat) (SEQ ID NO. 189)

HYYYGGSYAMDY

[0377] Humanized anti-CD19 CAR CD8 Leader DNA (SEQ ID NO. 190)

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCCG

[0378] Humanized anti-CD19 CAR CD8 Leader AA (SEQ ID NO. 191)

MALPVTALLPLALLHAARP

[0379] Humanized anti-CD19 CAR scFv heavy chain DNA (SEQ ID NO. 192)

GATATTCAAATGACCCAGTCCCCGTCCTCCCTGAGTGCCTCCGTCGGTGACCGTG
TTACGATTACCTGCCGTGCGAGCCAAGACATCTCTAAATACCTGAACTGGTATCA
GCAAAAACCGGATCAGGCACCGAACTGCTGATCAAACATACCTCACGTCTGCA
CTCGGGTGTGCCGAGCCGCTTTAGTGGTTCCGGCTCAGGTACCGATTACACCCTG
ACGATCAGCTCTCTGCAGCCGGAAGACTTTGCCACGTATTACTGCCAGCAAGGTA
ATACCCTGCCGTATACGTTCGGCCAAGGTACCAAACCTGGAAATCAAA

[0380] Humanized anti-CD19 CAR scFv heavy chain AA (SEQ ID NO. 193)

DIQMTQSPSSLSASVGDRVITICRASQDISKYLNWYQQKPDQAPKLLIKHTSRLHSGV
PSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPYTFGQGTKLEIK

[0381] Humanized anti-CD19 CAR Linker (Whitlow) DNA (SEQ ID NO. 194)

GGCTCGACGAGCGGCTCTGGTAAACCGGGCTCTGGTGAAGGCAGTACCAAAGGT

[0382] Humanized anti-CD19 CAR Linker (Whitlow) AA (SEQ ID NO. 195)

GSTSGSGKPGSGEGSTKG

[0383] Humanized anti-CD19 CAR scFv light chain DNA (SEQ ID NO. 196)

GAAGTGCAGCTGGTTGAAAGCGGTGGTGGTCTGGTTCAACCGGGTCGTTCCCTGC
GTCTGTCATGTACGGCGAGTGGTGTCTCCCTGCCGGA CTATGGCGTGTCTGAT
TCGTCAGCCGCCGGGTAAAGGCCTGGAATGGATTGGTGTCTGTTGGGCGAGTGA
AACCACGTATTACAACCTCGGCCCTGAAAAGCCGTTTCACCATCTCTCGCGATAAC
AGTAAAAATACGCTGTACCTGCAGATGAATAGCCTGCGCGCGGAAGACACCGCC
GTTTACTACTGCGCAAAACATTACTACTACGGTGGCAGCTATGCTATGGATTACT
GGGGTCAAGGCACGCTGGTCAACCGTTTCGTCA

[0384] Humanized anti-CD19 CAR scFv light chain AA (SEQ ID NO. 197)

EVQLVESGGGLVQPGRSLRLSCTASGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
YYNSALKSRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHYYYGGSYAMDYWG
QGTLVTVSS

[0385] Humanized anti-CD19 CAR Minispacer DNA (SEQ ID NO. 198)

GCCGCTGCC

[0386] Humanized anti-CD19 CAR Minispacer AA (SEQ ID NO. 199)

AAA

[0387] Humanized anti-CD19 CAR CD28T spacer (extracellular / TM region of
CD28) DNA (SEQ ID NO. 200)

CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC
TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGT
GGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCT
GGGTT

[0388] Humanized anti-CD19 CAR CD28T spacer (extra / TM region of CD28) AA

(SEQ ID NO. 201)

LDNEKSNGTIIHVKGKHLCPSPFLPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWV

[0389] Humanized anti-CD19 CAR CD28 costimulatory (intracellular region of CD28) DNA (SEQ ID NO. 202)

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGC

[0390] Humanized anti-CD19 CAR costimulatory (intracellular region of CD28) AA (SEQ ID NO. 203)

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

[0391] Humanized anti-CD19 CAR CD3 zeta DNA (SEQ ID NO. 204)

AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAAC
CAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGT
ACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAG
CCCTGCCAcctagg

[0392] Humanized anti-CD19 CAR CD3 zeta AA (SEQ ID NO. 205)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR

[0393] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR1 (Chothia) (SEQ ID NO. 206)

RASQSVSSSYLA

[0394] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR2 (Chothia)
(SEQ ID NO. 207)

GASSRAT

[0395] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR3 (Chothia)
(SEQ ID NO. 208)

QQYGSSRFT

[0396] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR1 (Chothia)
(SEQ ID NO. 209)

GGTFSSY

[0397] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR2 (Chothia)
(SEQ ID NO. 210)

IPIFGT

[0398] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR3 (Chothia)
(SEQ ID NO. 211)

EAVAADWLDP

[0399] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR1 (Kabat) (SEQ
ID NO. 212)

RASQSVSSSYLA

[0400] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR2 (Kabat) (SEQ
ID NO. 213)

GASSRAT

[0401] Humanized anti-CD19 CAR VL fully human anti-CD19 CDR3 (Kabat) (SEQ
ID NO. 214)

QQYGSSRFT

[0402] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR1 (Kabat) (SEQ

ID NO. 215)

SYAIS

[0403] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR2 (Kabat) (SEQ

ID NO. 216)

GIPIFGTTNYAQQFQG

[0404] Humanized anti-CD19 CAR VH fully human anti-CD19 CDR3 (Kabat) (SEQ

ID NO. 217)

EAVAADWLDP

[0405] Fully human anti-CD19 CAR Leader (CD8a) DNA (SEQ ID NO. 218)

Atggccctgcctgtgacagctctgctgctgcccctggccctgctgcatgccgccagacct

[0406] Fully human anti-CD19 CAR Leader (CD8a) AA (SEQ ID NO. 219)

MALPVTALLLPLALLHAARP

[0407] Fully human anti-CD19 CAR scFv light chain DNA (SEQ ID NO. 220)

gagatcgtgctgacctgtctcccgccacctgtctctcagcccaggagagagagccacctgagctgcagagccagccagagcgt

gtccagcagctacctggcctggatcagcagaagcccgacaggccccagactgctgatctacggcgccagctctagagccaccg

gcatccccgacagattcagcggcagcggcagtgccaccgacttcacctgacctcagcagactggaacccgaggacttcgccgtg

tactactgccagcagtagcggcagcagccgggtcaccttcggccctggcaccaaggtggacatcaag

[0408] Fully human anti-CD19 CAR scFv light chain AA (SEQ ID NO. 221)

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGI

PDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIK

[0409] Fully human anti-CD19 CAR Linker (Whitlow) DNA (SEQ ID NO. 222)

ggcagcacctccggcagcggcaagcctggctctggcgagggctctaccaagggc

[0410] Fully human anti-CD19 CAR Linker (Whitlow) AA (SEQ ID NO. 223)

GSTSGSGKPGSGEGSTKG

[0411] Fully human anti-CD19 CAR scFv heavy chain DNA (SEQ ID NO. 224)

caggtgcagctggtgcagtctggcgccgaagtgaagaaacccggctctagcgtgaaggtgtcctgcaaggacagcggcgccacctt
cagcagctacgccatcagctgggtgcgccaggccccaggacaggggctggaatggatggcgccatcatccccatcttcggcacc
accactacgcccagcagttccagggcagagtaccatcacccgccgacgagagcaccagcaccgcctacatggaactgagcagcc
tgcggagcagggacacagccgtgtattactgtgcccgcgaggccgtggccgccgactggctggatccttggggacagggcacctt
ggtgacagtgtccagc

[0412] Fully human anti-CD19 CAR scFv heavy chain AA (SEQ ID NO. 225)
QVQLVQSGAEVKKPGSSVKV SCKDSGGTFSSYAISWVRQAPGQGLEWMGGIIPFGT
TNYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQG
TLVTVSS

[0413] Fully human anti-CD19 CAR CD8a spacer and TM region DNA (SEQ ID
NO. 226)
ttcgtgcccgtgttcctgcccgccaaagcctaccaccacccctgcccctagacctcccaccccagccccaacaatgccagccagcct
ctgtccctgcggcccgaagcctgttagacctgctgccggcggagccgtgcacaccagaggcctggacttcgcctgcgatattcatatc
tgggcccctctggccggcacctgtggcgtgctgctgctgagcctggtgatcacctgtactgcaaccaccggaac

[0414] Fully human anti-CD19 CAR CD8a spacer and TM region AA (SEQ ID NO.
227)
FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYW
APLAGTCGVLLLSLVITLYCNHRN

[0415] Fully human anti-CD19 CAR CD28 costim. DNA (SEQ ID NO. 228)
agaagcaagcggagccggctgctgcacagcgactacatgaacatgaccccaagacggcctggccccacccggaagcactaccag
ccttacgcccctcccagagacttcgccgctaccggtcc

[0416] Fully human anti-CD19 CAR CD28 costim. AA (SEQ ID NO. 229)
RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

[0417] Fully human anti-CD19 CAR CD3 zeta DNA (SEQ ID NO. 230)
agagtgaagttcagcagatccgccgacgcccctgcctaccagcaggagacagaaccagctgtacaacgagctgaacctgggcagac

gggaagagtacgacgtgctggacaagcggagaggccgggaccccgagatgggcggaagcccagacggaagaacccccagga
aggcctgtataacgaactgcagaaagacaagatggccgaggcctacagcgagatcggcatgaagggcgagcggaggcgcgga
agggccacgatggcctgtaccagggcctgagcaccgccaccaaggacacctacgacgcctgcacatgcaggccctgccccca
ga

[0418] Fully human anti-CD19 CAR CD3 zeta AA (SEQ ID NO. 231)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR

[0419] MAGE A3 / A6 TCR Construct – Variable alpha chain – AV38-2 DNA (SEQ
ID NO. 232)

atggcatgccctggcttctgtgggcacttgtgatctccacctgtcttgaatttagcatggctcagacagtcactcagtctcaaccagaga
tgtctgtgcaggaggcagagaccgtgaccctgagctgcacatatgacaccagtgaagtgattattatttctgtgtacaagcagcctc
ccagcaggcagatgattctcgttattcgccaagaagcttataagcaacagaatgcaacagagaatcgtttctctgtgaactccagaaag
cagccaaatccttcagtctcaagatctcagactcacagctgggggatgccgcgatgtatttctgtgct

[0420] MAGE A3 / A6 TCR Construct – Variable alpha chain – AV38-2 AA (SEQ
ID NO. 233)

MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL
SCTYDTSESDYYLFWYKQPPSRQMILVIRQEAYKQQNATEN
RFSVNFQKAAKSFSLKISDSQLGDAAMYFCALRSSGTYKYIF
GTGTRLKVLAN

[0421] MAGE A3 / A6 TCR Construct – TRAJ40 DNA (SEQ ID NO. 234)

ctccggagctcaggaacctacaatacatctttggaacaggcaccaggctgaaggtttagcaaat

[0422] MAGE A3 / A6 TCR Construct – Murine constant alpha – Murine CA DNA
(SEQ ID NO. 235)

atccagaaccctgaacctgctgtgtaccagttaaaagatcctcgggtctcaggacagcaccctctgcctgttcaccgactttgactccaa

atcaatgtgccgaaaacatggaatctggaacgttcactgacaaaactgtgctggacatgaaagctatggattccaagagcaatgg
ggccattgcctggagcaaccagacaagcttcacctgccaagatatcttcaaagagaccaacgccacctaccccagttcagacgttccc
tgtgatgccacgttgactgagaaaagctttgaaacagatatgaacctaaactttcaaacctgtcagttatgggactccgaatcctcctgc
tgaaagtagccggatttaacctgctcatgacgctgaggctgtggtccagt

[0423] MAGE A3 / A6 TCR Construct – Murine constant alpha – Murine CA AA
(SEQ ID NO. 236)

I Q N P E P A V Y Q L K D P R S Q D S T L C L F T D F D S Q I N V P K T M E S G T F
I T D K T V L D M K A M D S K S N G A I A W S N Q T S F T C Q D I F K E T N A T Y
P S S D V P C D A T L T E K S F E T D M N L N F Q N L S V M G L R I L L K V A G F
N L L M T L R L W S S

[0424] MAGE A3 / A6 TCR Construct – Furin-SG SG-P2A DNA (SEQ ID NO. 237)
cgggccaaagcgggtccggatccggagccaccaacttcagcctgctgaagcaggccggcgacgtggaggagaacccccggcccc

[0425] MAGE A3 / A6 TCR Construct – Furin-SG SG-P2A AA (SEQ ID NO. 238)
R A K R S G S G A T N F S L L K Q A G D V E E N P G P

[0426] MAGE A3 / A6 TCR Construct – Variable beta chain – BV7-2 DNA (SEQ ID
NO. 239)

atgggcaccaggctcctcttctgggtggccttctgtctcctgggggcagatcacacaggagctggagtctcccagtcccccagtaaca
aggtcacagagaagggaaaggatgtagagctcaggtgtgatccaatttcaggtcatactgccctttactggtagcagagagcctggg
gcagggcctggagtttttaatttactccaaggcaacagtgcaccagacaaatcagggtgcccagtgatcgcttctctgcagagagga
ctgggggatccgtctccactctgacgatccagcgcacacagcaggaggactcggccgtgtatctctgtgccagca

[0427] MAGE A3 / A6 TCR Construct – Variable beta chain – BV7-2 AA (SEQ ID
NO. 240)

M G T R L L F W V A F C L L G A D H T G A G V S Q S P S N K V T E K G K D V E L
R C D P I S G H T A L Y W Y R Q S L G Q G L E F L I Y F Q G N S A P D K S G L P S D
R F S A E R T G G S V S T L T I Q R T Q Q E D S A V Y L C A S I R T G P F F S G N T I

Y F G E G S W L T V V E

[0428] MAGE A3 / A6 TCR Construct – TRBJ1-3 DNA (SEQ ID NO. 241)

tccggacagggcctttttctctggaaacaccatatattttggagaggggaagtggctcactgtttagag

[0429] MAGE A3 / A6 TCR Construct – Murine constant beta – Murine CB1 DNA
(SEQ ID NO. 242)

gacctgagaaacgtgacccacccaaggtctcctgtttgagccatcaaaagcagagattgcaaacaacaaaaggctaccctcgtgt
gcttggccaggggcttctccctgaccacgtggagctgagctggtgggtgaatggcaaggaggtccacagtggggtcagcacggac
cctcaggcctacaaggagagcaattatagctactgcctgagcagccgcctgaggggtctctgctaccttctggcacaatcctcgaacc
acttccgctgccaagtgcagttccatgggctttcagaggaggacaagtggccagagggctcacccaaacctgtcacacagaacatca
gtgcagaggcctggggccgagcagactgtggaatcacttcagcatcctatcatcagggggttctgtctgcaaccatccttatgagatc
ctactggggaaggccaccctatatgtgtgctggtcagtggcctgggtgctgatggctatgggtcaaaagaaagaactcatga

[0430] MAGE A3 / A6 TCR Construct – Murine constant beta – Murine CB1 AA
(SEQ ID NO. 243)

D L R N V T P P K V S L F E P S K A E I A N K Q K A T L V C L A R G F F P D H V E L
S W W V N G K E V H S G V S T D P Q A Y K E S N Y S Y C L S S R L R V S A T F W
H N P R N H F R C Q V Q F H G L S E E D K W P E G S P K P V T Q N I S A E A W G R
A D C G I T S A S Y H Q G V L S A T I L Y E I L L G K A T L Y A V L V S G L V L M A
M V K R K N S Stop

[0431] MAGE A3 / A6 TCR Va CDR1 (SEQ ID NO. 244)

TYDTSESDYYLF

[0432] MAGE A3 / A6 TCR Va CDR2 (SEQ ID NO. 245)

QEAYKQQ

[0433] MAGE A3 / A6 TCR Va CDR3 (SEQ ID NO. 246)

ALRSSGTYKYI

[0434] MAGE A3 / A6 TCR Vb CDR1 (SEQ ID NO. 247)

DPISGHTALY

[0435] MAGE A3 / A6 TCR Vb CDR2 (SEQ ID NO. 248)

FQGNSAPDKSG

[0436] MAGE A3 / A6 TCR Vb CDR3 (SEQ ID NO. 249)

ASIRTGPPFFSGNTIY

[0437] Anti-CLL-1 CAR CD8 Leader DNA (SEQ ID NO. 250)

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCG

[0438] Anti-CLL-1 CAR CD8 Leader AA (SEQ ID NO. 251)

MALPVTALLLPLALLHAARP

[0439] Anti-CLL-1 CAR scFv heavy chain DNA (SEQ ID NO. 252)

CAGGTCCAAGTCAAGAAAGCGGACCCGGACTGGTGAAGCCTTCTGAGACACTT
AGTCTGACGTGCACGGTCAGTGGCGGCTCCATCTCCTCCTATTATTGGTCATGGA
TACGACAACCCCCAGGTAAGGGCCTGGAATGGATTGGCTATATCTACTATTCAGG
AAGCACGAAGTACAATCCCAGCCTGAAGTCCCGAGTGACAATTTTCAGTAGATAC
CAGTAAAAACCAGTTCAGTCTTAACTGTCAAGCGTGACAGCTGCCGACACCGC
TGTGTATTACTGCGTCTCACTGGTGTATTGTGGAGGGGATTGTTATAGCGGGTTC
GATTATTGGGGACAGGGAACCCTGGTGACTGTATCTTCC

[0440] Anti-CLL-1 CAR scFv heavy chain AA (SEQ ID NO. 253)

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTN
YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVSLVYCGGDCYSGFDYWGQ
GTLVTVSS

[0441] Anti-CLL-1 CAR G4S linker DNA (SEQ ID NO. 254)

GGCGGCGGCGGCTCAGGGGGTGGCGGTAGTGGCGGTGGGGGTTCC

[0442] Anti-CLL-1 CAR G4S linker AA (SEQ ID NO. 255)

GGGGSGGGGSGGGGS

[0443] Anti-CLL-1 CAR scFv light chain DNA (SEQ ID NO. 256)

GATATTCAACTGACACAATCCCCCAGCTCACTCAGCGCCAGCGTGGGGGACAGG
GTTAGCTTTACCTGTCAAGCCTCTCAGGATATAAATAACTTTCTGAACTGGTATC
AACAGAAGCCTGGGAAGGCGCCCAAACCTCCTGATCTATGATGCGTCCAACCTGG
AAACTGGCGTGCCTTCACGCTTTAGCGGCTCTGGCAGTGGTACAGACTTCACTTT
TACCATCTCTTCACTTCAGCCGGAGGACATCGCCACATATTACTGTCAACAGTAC
GGAAACTTGCCCTTTACTTTTGGAGGCGGCACCAAAGTTGAAATCAAAAGG

[0444] Anti-CLL-1 CAR scFv light chain AA (SEQ ID NO. 257)

DIQLTQSPSSLSASVGDRVSFTQCASQDINNFLNWYQQKPGKAPKLLIYDASNLETGV
PSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYGNLPFTFGGGTKVEIKR

[0445] Anti-CLL-1 CAR Minispacer DNA (SEQ ID NO. 258)

GCCGCTGCC

[0446] Anti-CLL-1 CAR Minispacer AA (SEQ ID NO. 259)

AAA

[0447] Anti-CLL-1 CAR CD28T (extracellular / TM region of CD28) DNA (SEQ ID NO. 260)

CTGGATAACGAAAAGAGCAATGGGACTATAATACATGTTAAAGGAAAACACCTG
TGTCCATCTCCCCTGTTCCCTGGACCGTCAAAGCCATTTTGGGTGCTCGTGGTTGT
CGGTGGCGTTCTCGCCTGTTATAGCTTGCTGGTGACAGTAGCCTTCATTATCTTTT
GGGTG

[0448] Anti-CLL-1 CAR CD28T (extracellular / TM region of CD28) AA (SEQ ID NO. 261)

LDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWV

[0449] Anti-CLL-1 CAR CD28 (intracellular costimulatory region of CD28) DNA

(SEQ ID NO. 262)

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGC

[0450] Anti-CLL-1 CAR CD28 (intracellular costimulatory region of CD28) AA

(SEQ ID NO. 263)

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

[0451] Anti-CLL-1 CAR CD3 zeta DNA (SEQ ID NO. 264)

CGAGTGAAATTTTCTAGATCAGCTGATGCTCCCGCCTATCAGCAGGGACAGAATC
AACTTTACAATGAGCTGAACCTGGGTCGCAGAGAAGAGTACGACGTTTTGGACA
AACGCCGGGGCCGAGATCCTGAGATGGGGGGGAAGCCGAGAAGGAAGAATCCT
CAAGAAGGCCTGTACAACGAGCTTCAAAAAGACAAAATGGCTGAGGCGTACTCT
GAGATCGGCATGAAGGGCGAGCGGAGACGAGGCAAGGGTCACGATGGCTTGTA
TCAGGGCCTGAGTACAGCCACAAAGGACACCTATGACGCCCTCCACATGCAGGC
ACTGCCCCCACGC

[0452] Anti-CLL-1 CAR CD3 zeta AA (SEQ ID NO. 265)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR

[0453] CLL scFv (24C1) VL CDR1 (SEQ ID NO. 266)

QASQDINNFLN

[0454] CLL scFv (24C1) VL CDR2 (SEQ ID NO. 267)

DASNLET

[0455] CLL scFv (24C1) VL CDR3 (SEQ ID NO. 268)

QQYGNLPFT

[0456] CLL scFv (24C1) VH CDR1 (SEQ ID NO. 269)

GGSISSY

[0457] CLL scFv (24C1) VH CDR2 (SEQ ID NO. 270)

YYSGS

[0458] CLL scFv (24C1) VH CDR3 (SEQ ID NO. 271)

LVYCGGDCYSGFDY

[0459] Anti-BCMA CAR Leader (CD8a) DNA (SEQ ID NO. 272)

ATGGCACTCCCCGTAAGTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCG
CACGCCCCG

[0460] Anti-BCMA CAR Leader (CD8a) AA (SEQ ID NO. 273)

MALPVTALLLPLALLHAARP

[0461] Anti-BCMA CAR scFv heavy chain DNA (SEQ ID NO. 274)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTG
AGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGG
TCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCGTATGATG
GAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAG
ACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACA
CGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCATACGATTATG
GAATGGACGTATGGGGCCAGGGAACAACACTGTCACCGTCTCCTCA

[0462] Anti-BCMA CAR scFv heavy chain AA (SEQ ID NO. 275)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDG
SNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCVKGPLQEPPYDYGM
DVWGQGTTVTVSS

[0463] Anti-BCMA CAR Linker (Whitlow) DNA (SEQ ID NO. 276)

GGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG

[0464] Anti-BCMA CAR Linker (Whitlow) AA (SEQ ID NO. 277)

GSTSGSGKPGSGEGSTKG

[0465] Anti-BCMA CAR scFv light chain DNA (SEQ ID NO. 278)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGA
GCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACC
AGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGG
CCACTGGTATCCCAGCCAGGTTTCACTGGCAGTGGGTCTGGGACAGAGTTCCTCT
CACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCAC
CACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG

[0466] Anti-BCMA CAR scFv light chain AA (SEQ ID NO. 279)

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYSASTRATGI
PARFSGSGSGTEFTLTISSLQSEDFAVYYCQQHHVWPLTFGGGTKVEIKR

[0467] Anti-BCMA CAR Minispace DNA (SEQ ID NO. 280)

GCCGCTGCC

[0468] Anti-BCMA CAR Minispace AA (SEQ ID NO. 281)

AAA

[0469] Anti-BCMA CAR CD28T spacer DNA (SEQ ID NO. 282)

CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC
TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGT
GGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCT
GGGTT

[0470] Anti-BCMA CAR CD28T spacer AA (SEQ ID NO. 283)

LDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWV

[0471] Anti-BCMA CAR CD28 costimulatory region DNA (SEQ ID NO. 284)

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC

CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGC

[0472] Anti-BCMA CAR CD28 costimulatory region AA (SEQ ID NO. 285)

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

[0473] Anti-BCMA CAR CD3 zeta DNA (SEQ ID NO. 286)

AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAAC
CAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGT
ACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAG
CCCTGCCACCTAGG

[0474] Anti-BCMA CAR CD3 zeta AA (SEQ ID NO. 287)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL
PPR

[0475] Anti-BCMA CAR VL CDR1 (SEQ ID NO. 288)

RASQSVSSNLA

[0476] Anti-BCMA CAR VL CDR2 (SEQ ID NO. 289)

SASTRAT

[0477] Anti-BCMA CAR VL CDR3 (SEQ ID NO. 290)

QQHHVWPLTF

[0478] Anti-BCMA CAR VH CDR1 (SEQ ID NO. 291)

GFTFSSY

[0479] Anti-BCMA CAR VH CDR2 (SEQ ID NO. 292)

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VISYDGSNKYYADSVKG

[0480] Anti-BCMA CAR VH CDR3 (SEQ ID NO. 293)

VKGPLQEPPYDYGMDV

[0481] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain variable region
DNA (SEQ ID NO. 294)

atgggcaccagactgttcttttatgtggccctgtgtctgtgtggaccggccacatggatgccggaattacacagagccccagacaaa
agtgaccgagacaggcaccctgtgacactgagatgccaccagaccgagaaccaccgctacatgtactggtacagacaggatccag
gccacggcctgagactgatccactacagctacggcgtgaaggacaccgacaagggcgaagtgtctgacggctacagcgtgtccag
aagcaagaccgaggatttcctgtgacctggaaagcgccacaagcagccagaccagcgtgtacttttgccatcagcggctacaa
gaacaccgaggccttttcggccaaggcaccaggctgacagtggtg

[0482] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain variable region
AA (SEQ ID NO. 295)

MGTRLFFYVALCLLWTGHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMYWYR
QDPGHGLRLIHYSYGKDDTKGEVSDGYSVSRSKTEDFLLTLESATSSQTSVYFCAIS
GYKNTEAFFGQGTRLTVV

[0483] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain constant region
DNA (SEQ ID NO. 296)

gaagatctgaagaacgtgtccacctgaggtggcgtgtttgagccttctgagggccgagatcagccacacagaaagccacactc
gtgtgcctggccaccggctttatcccgatcacgtggaactgtcttggtgggtcaacggcaaagaggtgcacagcggcgtagcacag
accctcagcctctgaaagagcagcccgtctgaacgacagcagatactgtctgagcagcagactgagagtgtccgccaccttctggc
agaaccccagaaaccacttcagatgccaggtgcagttctacggcctgtccgagaatgacgagtgagaccaggatagagccaagcca
gtgacacagattgtgtctgccgaagcctggggcagagccgattgtggctttacaagcgagagctaccagcagggcgctgtgtctgcc
acaatcctgtatgagatcctgctgggcaaagccactctgtacgctgtgctgggtgtctgccctgggtgctgatggccatggtcaagagaaa
ggacagcagagggc

[0484] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain constant region

AA (SEQ ID NO. 297)

EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGV
STDPQPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQD
RAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSALVLM
AMVKRKDSRG

[0485] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – P2A peptide (with Furin cleavage site and linker) DNA (SEQ ID NO. 298)

agagccaagagatctggcagcggcgccacaaacttttagcctgctgaaacaggccggcgacgtggaagagaaccctggacct

[0486] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – P2A peptide (with Furin cleavage site and linker) AA (SEQ ID NO. 299)

RAKRSGSGATNFSLLKQAGDVEENPGP

[0487] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain variable region DNA (SEQ ID NO. 300)

atgaagtcctcgccgtgctgctggtattctgtggctgcagctgagctgggttggagccagggacagcaagtgatgcagatccctca
gtaccagcacgtgcaagaaggcgaggacttcaccacactactgcaacagcagcacaaccctgagcaacatccagtgggtacaagcag
aggcctggcgggcaccctgtgtttctgatccagctggtaagagcggcggaagtgaagaagcagaagcggctgacctttcagttcggc
gaggccaagaagaacagcagcctgcacattaccgccacacagaccaccgacgtgggcacatatTTTTgcgctggcagagaaggcg
gcagcgagaagctggttttggcaagggcaccaaactgacctgaatccc

[0488] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain variable region AA (SEQ ID NO. 301)

MKSLRVLLVILWLQLSWVWSQGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW
YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAG
REGGSEKLVFGKGTKLTVNP

[0489] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain constant region DNA (SEQ ID NO. 302)

gacattcagaaccccgatccagccgtgtaccagctgagagacagcaagagcagcgacaagagcgtgtgtctgttcaccgacttcgac
 tcccagaccaatgtgtcccagagcaaggactccgacgtgtacatcaccgataagaccgtgctggacatgcggagcatggacttcaag
 agcaatagcgccgtggcttggagcaacaagagcgactttgcctgcgccaacgccttcaacaacagcatcatccccgaggacacattc
 ttccaagtctgagagcagctgcgacgtgaagctgggtggaaaagagcttcgagacagacaccaacctgaactccagaacctgagc
 gtgatcggttcagaatcctgctgctgaaggtggccggcttcaacctgctgatgactctgagactgtggtccagctgaattcgatccaa
 gcttaggcctgctcgtttcttctgtgtcccatttctattaaagggttcctttgttc

[0490] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain constant region
 AA (SEQ ID NO. 303)

DIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDF
 KNSNAVAWSNKSDFACANAFNNSIIPEDTFFPSPESSCDVKLVEKSFETDTNLFQNL
 SVIGFRILLKLVAGFNLLMTLRLWSS

[0491] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR1 (SEQ ID NO. 304)
 TTLSN

[0492] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR2 (SEQ ID NO. 305)
 LVKSGEV

[0493] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR3 (SEQ ID NO. 306)
 AGREGGSEKLV

[0494] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR1 (SEQ ID NO. 307)
 ENHRY

[0495] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR2 (SEQ ID NO. 308)
 SYGVKD

[0496] C185 E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR3 (SEQ ID NO. 309)
 AISGYKNTEAF

[0497] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain variable region DNA
 (SEQ ID NO. 310)

atgggacctggattgctttgttgggccctgctgtgtctgcttgagctggacttggatgccggcgtgacacagtctccacacacctg
atcaagaccagaggccagcaagtgacctgagatgtagccctaagagcggccacgacaccgtgtcttggtatcagcaggctcttggc
cagggacctcagttcatcttccagtactacgaggaagaggaacggcagcggggcaacttcctgatagattctctggccatcagttcc
ccaactacagcagcagctgaacgtgaacgctctgctgctgggcgatagcgccctgtatctgtgtgccagttctcttggttgagagggc
ggcagatacaacgagcagttcttggccctggcaccagactgacctgtctg

[0498] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain variable region AA
(SEQ ID NO. 311)

MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQ
QALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDSALYLCAS
SLGWRGGRYNEQFFGPGTRLTVL

[0499] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain constant region DNA
(SEQ ID NO. 312)

gaagatctgaagaacgtgttccacctgaggtggccgtgtttgagccttctgaggccgagatcagccacacagaaagccacactc
gtgtgcctggccaccggcctttatcccgatcacgtggaactgtcttggtgggtcaacggcaaagaggtgcacagcggcgtagcacag
accctcagcctctgaaagagcagcccgctctgaacgacagcagatactgtctgagcagcagactgagagtgtccgccaccttctggc
agaacccagaaaccacttcagatgccaggtgcagttctacggcctgtccgagaatgacgagtggacccaggatagagccaagcca
gtgacacagattgtgtctgccgaagcctggggcagagccgattgtggctttacaagcgagagctaccagcagggcgctgtctgtgcc
acaatcctgtatgagatcctgctgggcaaagccactctgtacgctgtgctgggtgtctgccctgggtgtgatggccatggtcaagagaaa
ggacagcagaggc

[0500] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR beta chain constant region AA
(SEQ ID NO. 313)

EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGV
STDPQPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQD
RAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSALVLM
AMVKRKDSRG

[0501] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – P2A (with Furin cleavage site and linker) DNA (SEQ ID NO. 314)

agagccaagagatctggcagcggcgccacaaactttagcctgctgaaacaggccggcgacgtggaagagaaccctggacct

[0502] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – P2A (with Furin cleavage site and linker) AA (SEQ ID NO. 315)

RAKRSGSGATNFSLLKQAGDVEENPGP

[0503] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain variable region DNA (SEQ ID NO. 316)

atgaagtcctcgccgggtgctgctggtattctgtggctgcagctgagctgggtttggagccagggacagaacatcgaccagcctaccg
agatgacagccaccgaaggcgccatcgatgcagatcaattgcacctaccagaccagcggttcaacggcctgttctggtatcaacagc
atgccggcgaggccccctacctctgagctataatgtgctggacggcctggaagaaaagggcagattcagcagcttctgtccagaa
gcaagggtacagctacctgctgctgaaagaactccagatgaaggacagcgctcctacctgtgtgcctccgtggatggaaacaaca
gactggccttcggcaagggaaccaggtggtggtcatcccc

[0504] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain variable region AA (SEQ ID NO. 317)

MKSLRVLLVILWLQLSWVWSQGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY
QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSKGYSYLLKELQMKDSASYLCASVD
GNNRLAFGKGNQVVVIP

[0505] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain constant region DNA (SEQ ID NO. 318)

gacattcagaaccccgatccagccgtgtaccagctgagagacagcaagagcagcgacaagagcgtgtgtctgttcaccgacttcgac
tccagaccaatgtgtcccagagcaaggactccgacgtgtacatcaccgataagaccgtgctggacatgcggagcatggacttcaag
agcaatagcgccgtggcttgagcaacaagagcgactttgcctgcgccaacgccttcaacaacagcatcatccccgaggacacattc
ttccaagtctgagagcagctgcgacgtgaagctgggtgaaaagagcttcgagacagacaccaacctgaacttcagaacctgagc
gtgatcggttcagaatcctgctgctgaagggtggccggcttcaacctgctgatgactctgagactgtggtccagctgaattcggatccaa

gcttaggcctgctcgtttcttgcgtgtcccatttctattaaaggttcctttgttc

[0506] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – TCR alpha chain constant region AA
(SEQ ID NO. 319)

DIQNPDPVAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDF
KSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPESSCDVKLVEKSFETDTNLFQNL
SVIGFRILLKLVAGFNLLMTLRLWSS

[0507] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR1 (SEQ ID NO. 320)
TSGFNG

[0508] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR2 (SEQ ID NO. 321)
NVLDGL

[0509] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – alpha CDR3 (SEQ ID NO. 322)
ASVDGNNRLA

[0510] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR1 (SEQ ID NO. 323)
SGHDT

[0511] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR2 (SEQ ID NO. 324)
YYEEEE

[0512] E7₁₁₋₁₉/HLA-A*02:01 specific TCR – beta CDR3 (SEQ ID NO. 325)
ASSLGWRGGRYNEQF

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CLAIMS

1. A method for tracking a cell order during an immunotherapy procedure, the method comprising steps of:

initiating a process to create transfected T cells, the initiating comprising:

requesting a timeslot for performing leukapheresis procedure from a remote computing device,

receiving indicia responsive to the requesting, wherein the timeslot is available to perform the leukapheresis procedure, and

confirming acceptance of an available timeslot with the remote computing device;

obtaining T cells by leukapheresis at a material extraction site from a patient's blood collected at the material extraction site;

transferring the T cells collected from the patient's blood by leukapheresis to a container that is labeled with a patient specific identifier;

transmitting the labeled collected T cells to a manufacturing facility;

creating transfected T cells by transfecting the labeled collected T cells with a polynucleotide encoding a chimeric antigen receptor (CAR) to obtain an immune-oncology agent;

receiving the immune-oncology agent from the manufacturing facility for administration,

wherein a tracking event is recorded for each step of the method, each tracking event including the patient specific identifier, and

wherein the tracking events comprise a chain of custody of the patient's T cells during the method.

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2. The method according to claim 1, wherein the CAR comprises an antigen binding molecule that specifically binds to a target molecule.
3. The method of claim 2, wherein the antigen binding molecule is a single chain variable fragment.
4. The method of claim 2 or claim 3, wherein the target molecule is a blood borne cancer-associated antigen.
5. The method of claim 2 or claim 3, wherein the target molecule is a viral infection-associated antigen.
6. The method of any one of claims 2 to 5, wherein the CAR further comprises at least one costimulatory domain.
7. The method of any one of claims 2 to 6, wherein the CAR further comprises at least one activating domain.
8. The method of any one of claims 1 to 7, wherein the polynucleotide encoding a chimeric antigen receptor (CAR) is a component of a vector.
9. The method of any one of claims 1 to 8, further comprising a step of:
receiving a cell order request to create the transfected T cells for the patient.

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10. The method of any one of claims 1 to 9, wherein the patient-specific identifier comprises a patient identity element, a sales order identifier, and a cell order lot number, and wherein the patient identity element comprises a first patient ID associated with the immunotherapy procedure and a second patient ID associated with a facility that administers one or more of: the leukapheresis or administration of the transfected T cells.
11. The method of any one of claims 1 to 10, wherein the tracking event is recorded by a computing device for each step.
12. The method of claim 11, further comprising steps of:
- receiving, by the computing device, indicia that the transfected T cells have been shipped from a first site after being created; and
- receiving indicia that the transfected T cells have been received at a second site before administration.
13. The method of claim 11 or claim 12, wherein the computing device stores the tracking events in an ordered sequence.
14. The method of any one of claims 6 to 13, wherein the at least one costimulatory domain comprises CD28 or CD8.
15. The method of claim 14, wherein the at least one costimulatory domain comprises a sequence of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, or SEQ ID NO. 14.

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16. The method of any one of claims 7 to 15, wherein the at least one activating domain comprises CD3.
17. The method of claim 16, wherein at least one activating domain comprises a sequence of SEQ ID NO. 10.
18. The method according to any one of claims 1 to 17, wherein the CAR comprises: an anti-CD19 scFv, CD8, and 4-1BB; an anti-BCMA scFv and the CD8; the anti-CD19 scFv, CD28, and the 4-1BB; an anti-CD22 scFv and the CD8; the anti-CD19 scFv, the CD28, and EGFRt/19-28z/4-1BB; an anti-MUC16 scFv and the CD28; an anti-CD 171; an anti-CD123 and the CD28; an anti-BCMA, the CD8, and the 4-1BB; an anti-CD 19 and CD28; an anti-CD19 and the CD8; or the CD28.
19. The method according to claim 1, wherein the CAR comprises a CSF2RA leader sequence, an anti-CD 19 scFv, a Whitlow linker, a CD28 spacer, a CD28 costimulatory domain, and CD3 zeta.
20. The method of claim 19, wherein the CAR comprises a sequence of SEQ ID NO. 147.
21. The method according to claim 1, wherein the CAR comprises a CD8 leader sequence, an anti-CD19 scFv, a Whitlow linker, a CD28T spacer, a CD28 costimulatory domain, and CD3 zeta.
22. The method of claim 21, wherein the CAR comprises a sequence of SEQ ID NO. 149.

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23. The method according to claim 1, wherein the CAR comprises a CD8a leader sequence, an anti-CD19 scFv, a Whitlow linker, a CD8a spacer and transmembrane domain, a CD28 costimulatory domain, and CD3 zeta.
24. The method of claim 23, wherein the CAR comprises a sequence of SEQ ID NO. 151.
25. The method according to claim 1, wherein the CAR comprises a CD8 leader sequence, an anti-CLL-1 scFv, a G4S linker, a Minispacer, a CD28T, an intracellular costimulatory region of CD28, and CD3 zeta.
26. The method of claim 25, wherein the CAR comprises a sequence of SEQ ID NO. 155.
27. The method according to claim 1, wherein the CAR comprises a CD8a leader sequence, an anti-BCMA scFv, a Whitlow linker, a CD28T spacer, a CD28 costimulatory domain, and CD3 zeta.
28. The method of claim 27, wherein the CAR comprises a sequence of SEQ ID NO. 157.
29. A method for creating transfected T cells, comprising the steps of:
- obtaining T cells by leukapheresis at a material extraction site from a patient's blood collected at the material extraction site;
 - transferring the T cells collected from the patient's blood by leukapheresis to a container that is labeled with a patient specific identifier;
 - transmitting the labeled collected T cells to a manufacturing facility;

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creating transfected T cells by transfecting the labeled collected T cells with a polynucleotide encoding a chimeric antigen receptor (CAR) to obtain an immune-oncology agent;

receiving the immune-oncology agent from the manufacturing facility for administration,

wherein a tracking event is recorded for each step of the method, each tracking event including the patient specific identifier, and

wherein the tracking events comprise a chain of custody of the patient's T cells during the method.

30. The method according to claim 29 further comprising the step of initiating a process to create transfected T cells prior to obtaining the T cells, the initiating comprising:

requesting a timeslot for performing leukapheresis procedure from a remote computing device,

receiving indicia responsive to the requesting, wherein the timeslot is available to perform the leukapheresis procedure, and

confirming acceptance of an available timeslot with the remote computing device.

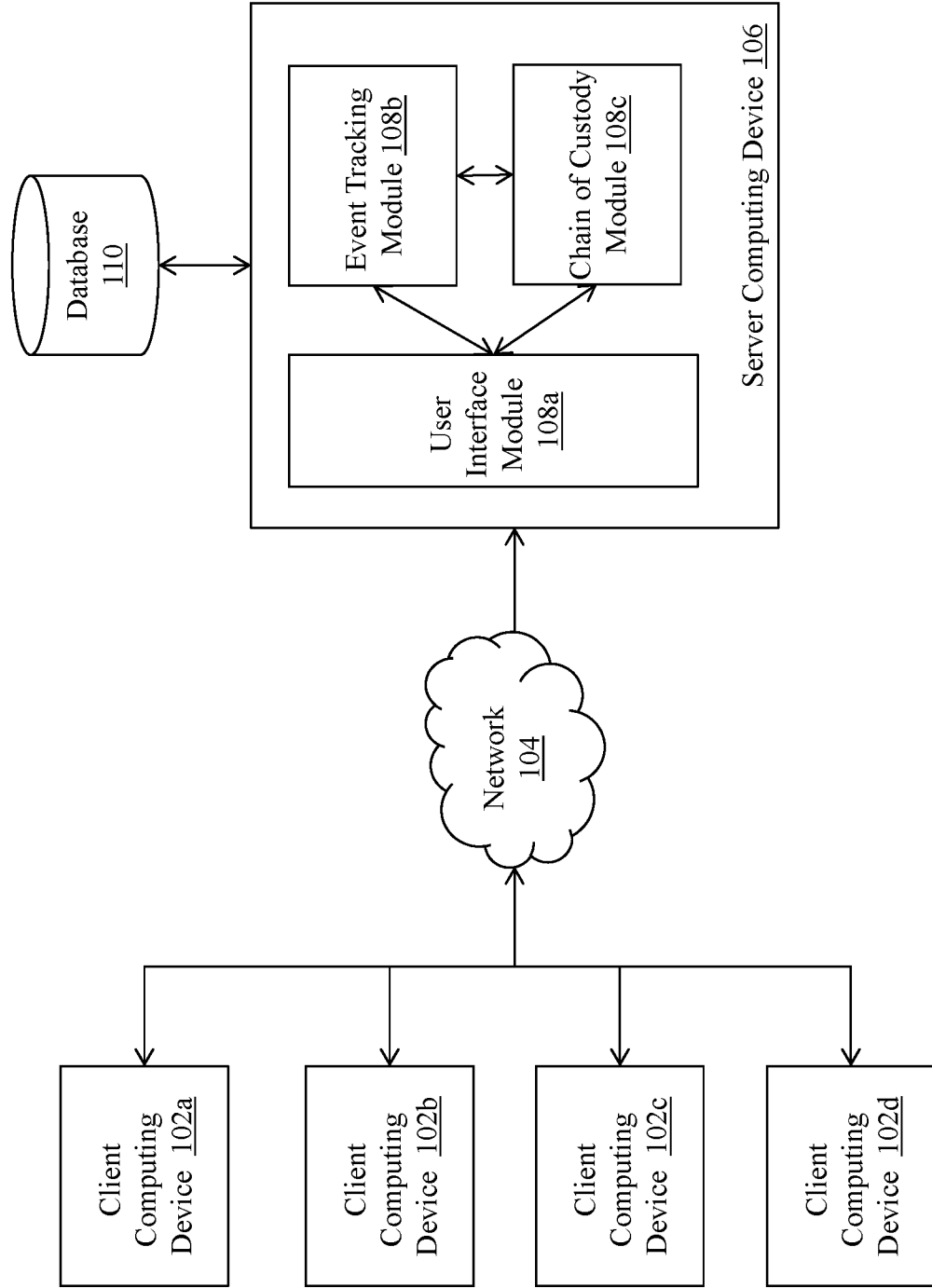


FIG. 1A

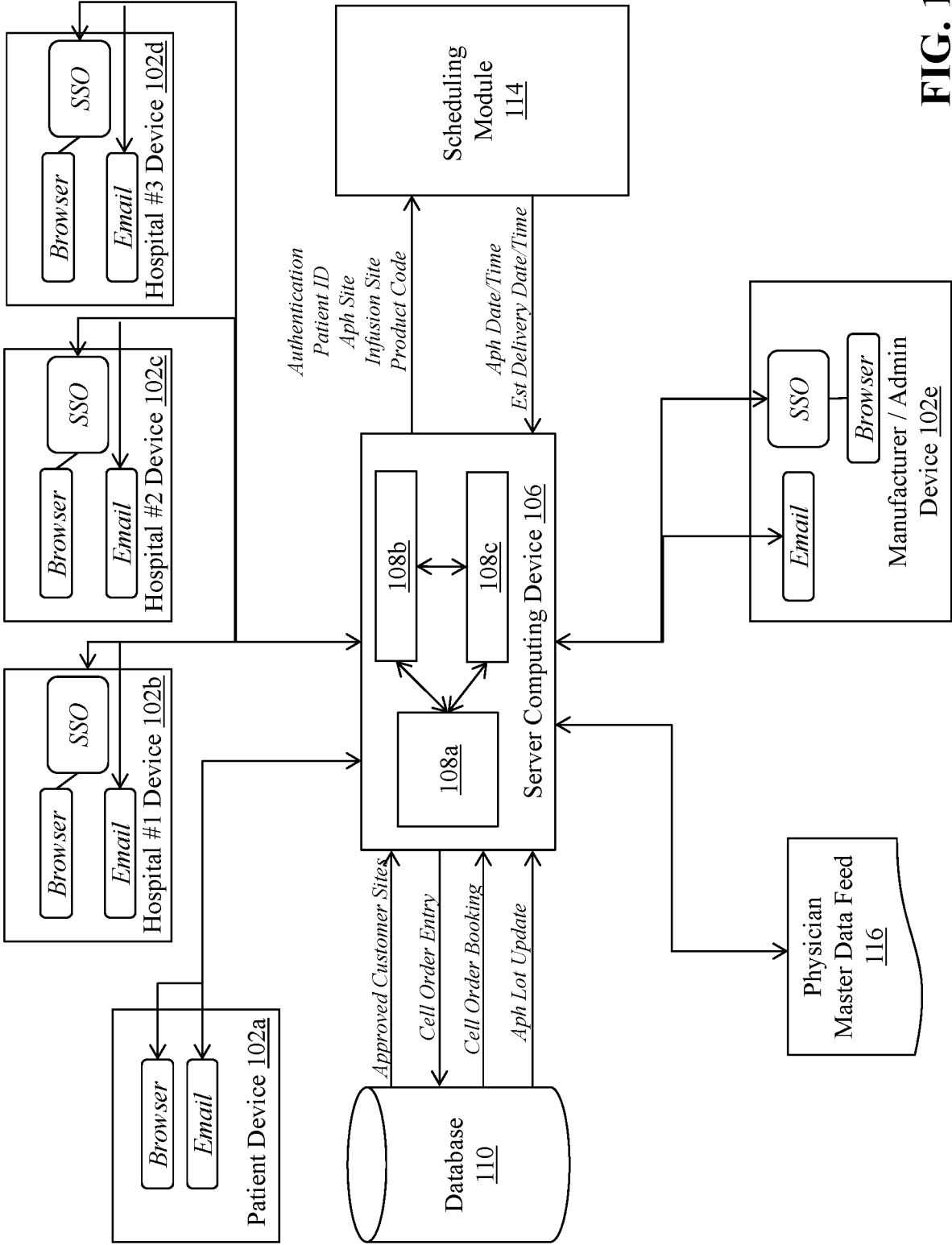


FIG. 1B

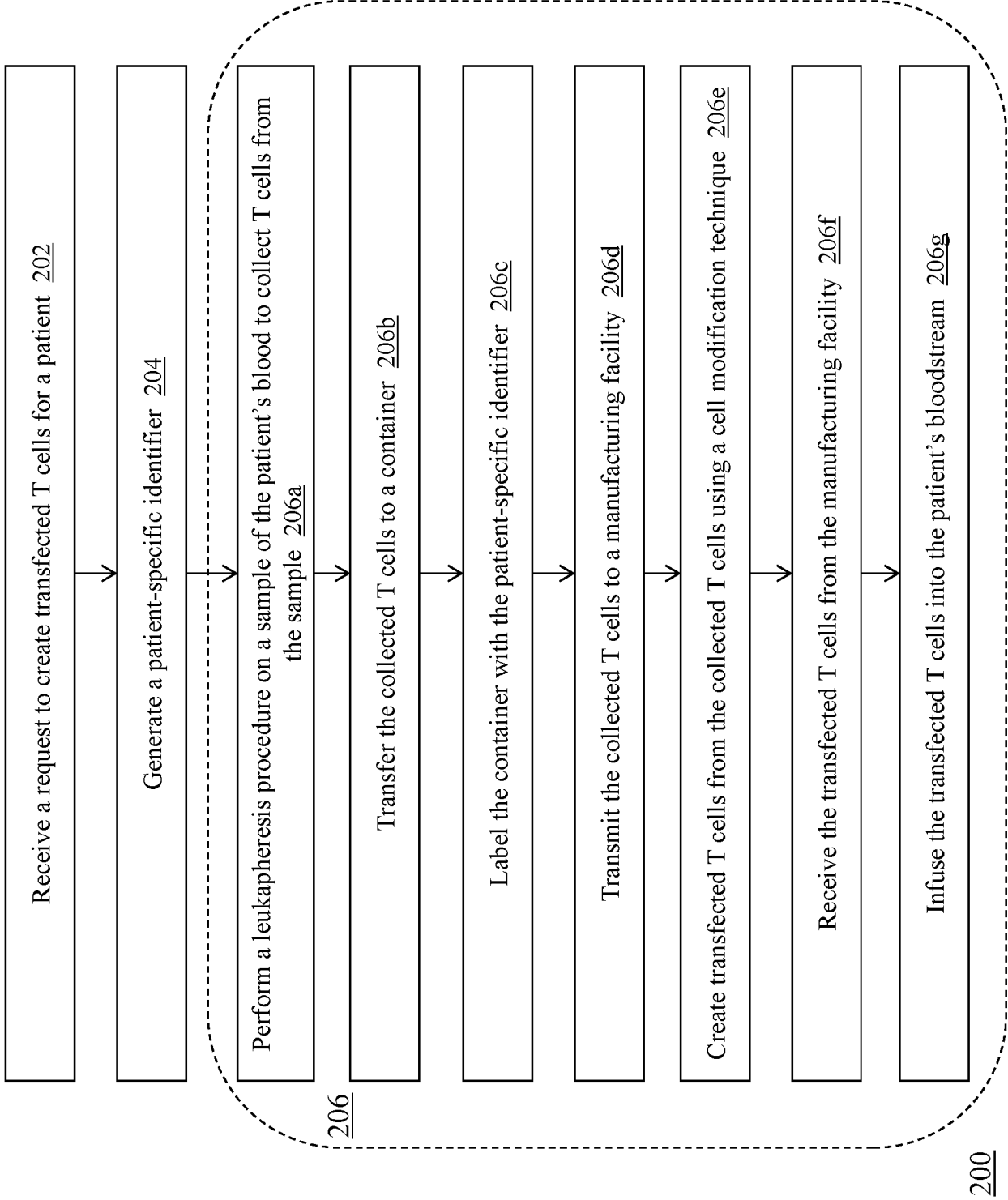


FIG. 2

Please Register Your Patient

First Name*

John

Middle Name

Q.

Last Name*

Public

DOB (Year)*

1985

(Month)*

Sep

(Day)*

24

Gender*

Male

Female

Treating Physician*

Jane Doe

X

Would you like to add your own Hospital Patient ID to the Kite Konnect™ Patient record?*

Yes

No

ID Type

MRN

Patient ID*

12345678

Cancel

Submit

FIG. 3A



Verify Your Patient Information Before Continuing

Patient Name

Public, John Q.

Patient Date of Birth

24-Sep-1985

Physician Name

Doe, Jane

Physician Phone

Hospital Patient ID

MRN: 12345678

Patient Gender

Male

Physician NPI

Physician Email

Back

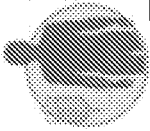
Confirm and Continue to Cell Order

FIG. 3B

Patient Team

Schedule Treatment

Confirm Order



Apheresis Center

Please confirm the address and contact information for the delivery and pickup of your Leukapheresis kit.

Delivery Address

Apheresis Center
7 Elm Street
Anytown, USA 00000

Drop-Off Contact:*

(The Drop-Off Contact is the person who will accept the Leukapheresis Kit.)

Change

Apheresis Contact
(555) 555-5555

Pick-Up Contact:*

(The Pick-Up Contact is the person who will meet the courier with the Leukapheresis material/patient cells.)

Change

Apheresis Contact
(555) 555-5555

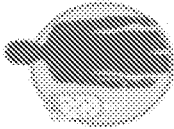
Special Instructions (90 chars max)

Use this area to provide us with any alternate Drop-Off and Pick-Up contacts

Save & Exit

Save & Next

FIG. 4A



Treatment Site

Please confirm the address and contact information for the delivery of your final product.

Delivery Address

Treatment Site
1 Main Street
Anytown, USA 00000

Treatment Site Drop-Off:*

(The Treatment Site Drop-Off Contact is the person who will accept the Final Product from the courier.)

Change

Treatment Pickup
(305) 555-1212

Treatment Site Pick-Up:*

(The Treatment Site Pick-Up Contact is the person who will return the empty LN2 to the courier.)

Change

Treatment Pickup
(305) 555-1212

Special Instructions (90 chars max)

Use this area to provide us with any alternate Drop-Off and Pick-Up contacts

FIG. 4B



Treatment Site

Delivery Address

Treatment Site
1 Main Street
Anytown, USA 00000

Treatment Site Drop-Off:*

(The Treatment Site Drop-Off Contact is the person who will accept the Final Product from the courier.)

Treatment Pickup
(305) 555-1212

Special Instructions

Treatment Site Pick-Up:*

(The Treatment Site Pick-Up Contact is the person who will return the empty LN2 to the courier.)

Treatment Pickup
(305) 555-1212

Click below to schedule your treatment

Open Scheduler

Save & Exit

Confirm and Continue to Customer

FIG. 4C

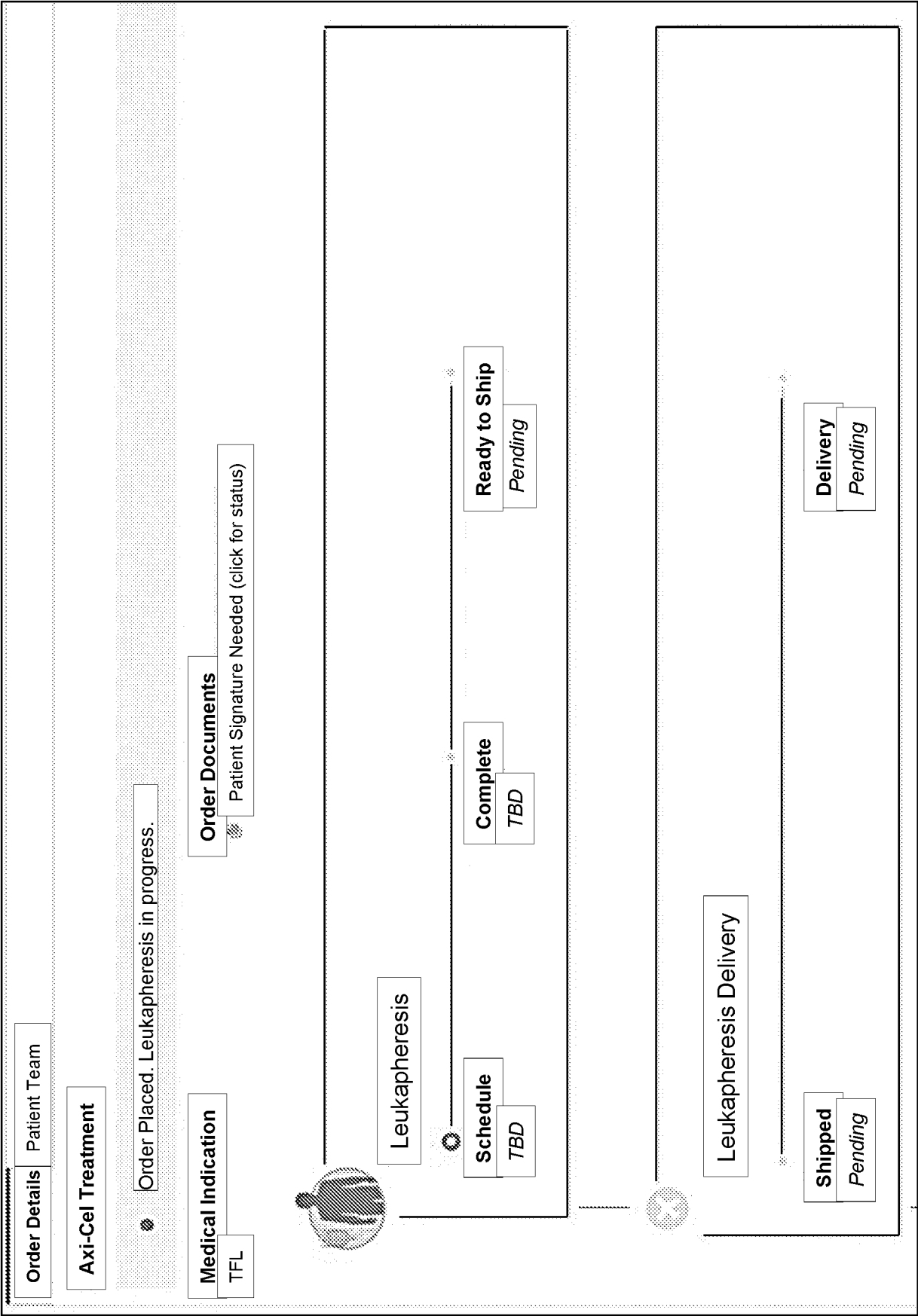


FIG. 5A

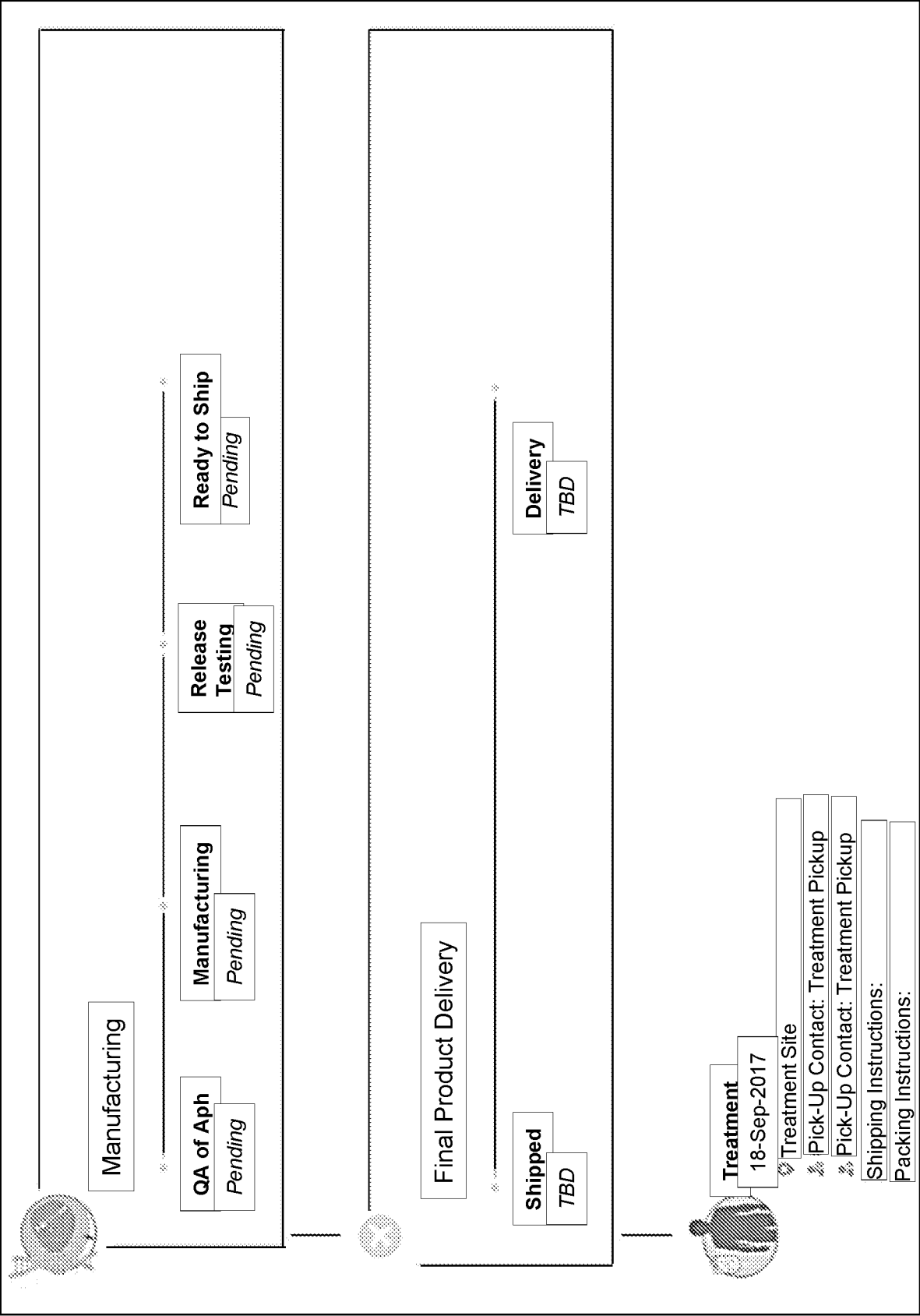


FIG. 5B

Sequence Listing

1	Sequence Listing Information	
1-1	File Name	Sequence listing - M53425856.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.2.0
1-5	Production Date	2023-03-03
1-6	Original free text language code	
1-7	Non English free text language code	
2	General Information	
2-1	Current application: IP Office	AU
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	M53425856
2-5	Earliest priority application: IP Office	US
2-6	Earliest priority application: Application number	62/559330
2-7	Earliest priority application: Filing date	2017-09-15
2-8en	Applicant name	Kite Pharma, Inc.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
2-10en	Invention title	Methods and systems for performing a patient-specific immunotherapy procedure with chain-of-custody and chain-of-identity biological sample tracking
2-11	Sequence Total Quantity	326

3-1 3-1-1 3-1-2 3-1-3 3-1-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	1 DNA 294 misc_feature 1..294 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..294 mol_type=other DNA organism=synthetic construct
3-1-5	NonEnglishQualifier Value Residues	cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60 tcacccttgt tccctgggcc atccaagcca ttctgggtgt tggtcgtagt ggggtggagtc 120 ctcgcttgtt actctctgct cgtcaccgtg gcttttataa tcttctgggt tagatccaaa 180 agaagccgcc tgctccatag cgattacatg aatatgactc cagccgccc tggccccaca 240 aggaaacact accagccta cgcaccacct agagatttcg ctgcctatcg gagc 294
3-2 3-2-1 3-2-2 3-2-3 3-2-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	2 AA 98 REGION 1..98 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..98 mol_type=protein organism=synthetic construct
3-2-5	NonEnglishQualifier Value Residues	LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP FWLVVVGGV LACYSLLVTV AFIIFWVRSK 60 RSRL LHSDYM NMTPRRPGPT RKHYQPYAPP RDFAAYRS 98
3-3 3-3-1 3-3-2 3-3-3 3-3-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	3 DNA 90 misc_feature 1..90 note=source = /note="Description of Artificial Sequence: Synthetic oligonucleotide" source 1..90 mol_type=other DNA organism=synthetic construct
3-3-5	NonEnglishQualifier Value Residues	cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60 tcacccttgt tccctgggcc atccaagcca 90
3-4 3-4-1 3-4-2 3-4-3 3-4-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	4 AA 30 REGION 1..30 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..30 mol_type=protein organism=synthetic construct
3-4-5	NonEnglishQualifier Value Residues	LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP 30
3-5 3-5-1 3-5-2 3-5-3 3-5-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	5 DNA 81 misc_feature 1..81 note=source = /note="Description of Artificial Sequence: Synthetic oligonucleotide" source 1..81 mol_type=other DNA organism=synthetic construct
3-5-5	NonEnglishQualifier Value Residues	ttctgggtgt tggtcgtagt gggtaggagtc ctcgcttgtt actctctgct cgtcaccgtg 60 gcttttataa tcttctgggt t 81
3-6 3-6-1 3-6-2 3-6-3 3-6-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	6 AA 27 REGION 1..27 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..27

3-6-5	NonEnglishQualifier Value Residues	mol_type=protein organism=synthetic construct FWVLVVVGGV LACYSLLVTV AFIIIFWV	27
3-7	Sequences		
3-7-1	Sequence Number [ID]	7	
3-7-2	Molecule Type	DNA	
3-7-3	Length	123	
3-7-4	Features	misc_feature 1..123	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..123 mol_type=other DNA organism=synthetic construct	
3-7-5	NonEnglishQualifier Value Residues	agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgcctt 60 ggccccacaa ggaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120 agc 123	
3-8	Sequences		
3-8-1	Sequence Number [ID]	8	
3-8-2	Molecule Type	AA	
3-8-3	Length	41	
3-8-4	Features	REGION 1..41	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..41 mol_type=protein organism=synthetic construct	
3-8-5	NonEnglishQualifier Value Residues	RSKRSRLLS DYMNTPRRP GPTRKHYQPY APPRDFAAAYR S	41
3-9	Sequences		
3-9-1	Sequence Number [ID]	9	
3-9-2	Molecule Type	DNA	
3-9-3	Length	336	
3-9-4	Features	misc_feature 1..336	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..336 mol_type=other DNA organism=synthetic construct	
3-9-5	NonEnglishQualifier Value Residues	agggtgaagt ttccagatc tgcagatgca ccagcgtatc agcagggccca gaaccaactg 60 tataacgagc tcaacctggg acgcaggga gagtatgacg ttttgacaa gcgcagagga 120 cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180 gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240 agaaggggaa aagggcacga cggtttgtag cagggactca gactgctac gaaggatact 300 tatgacgctc tccacatgca agccctgccca cctagg 336	
3-10	Sequences		
3-10-1	Sequence Number [ID]	10	
3-10-2	Molecule Type	AA	
3-10-3	Length	112	
3-10-4	Features	REGION 1..112	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..112 mol_type=protein organism=synthetic construct	
3-10-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112	
3-11	Sequences		
3-11-1	Sequence Number [ID]	11	
3-11-2	Molecule Type	DNA	
3-11-3	Length	117	
3-11-4	Features	misc_feature 1..117	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..117 mol_type=other DNA organism=synthetic construct	
3-11-5	NonEnglishQualifier Value Residues	attgagggtga tgtatccacc gccttacctg gataacgaaa agagtaacgg taccatcatt 60 cacgtgaaag gtaaacacct gtgtccttct cccctcttcc ccgggccatc aaagccc 117	
3-12	Sequences		

3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	AA
3-12-3	Length	39
3-12-4	Features	REGION 1..39
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"
		source 1..39
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-12-5	Residues	IEVMYPPPYL DNEKSNGTII HVKGKHLCPs PLFPGPSKP 39
3-13	Sequences	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	DNA
3-13-3	Length	288
3-13-4	Features	misc_feature 1..288
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"
		source 1..288
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-13-5	Residues	gctgcagcat tgagcaactc aataatgtat ttagtcact ttgtaccagt gttcttgccg 60 gctaagccta ctaccacacc cgctccacgg ccacctaccc cagctcctac catcgcttca 120 cagcctctgt ccctgcgccc agaggcttgc cgaccggccg cagggggcgc tgttcatacc 180 agaggactgg atttcgcctg cgatatctat atctgggcac ccctggccgg aacctgcggc 240 gtactcctgc tgtccctggt catcacgctc tattgtaatc acaggaac 288
3-14	Sequences	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	AA
3-14-3	Length	96
3-14-4	Features	REGION 1..96
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"
		source 1..96
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-14-5	Residues	AAALSNSIMY FSHFVPVFLP AKPTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT 60 RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCNHRN 96
3-15	Sequences	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	DNA
3-15-3	Length	366
3-15-4	Features	misc_feature 1..366
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"
		source 1..366
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-15-5	Residues	caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60 acgtgtacag ttcttggagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120 cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180 ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240 aaattgtcta gcgtcacagc agctgatata gccgtctatt attgtgtttc tctggtctat 300 tgcggtgggg attgttacag tggcctttgac tattgggggc aggggtactct gggttacagtt 360 tcttcc 366
3-16	Sequences	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	AA
3-16-3	Length	122
3-16-4	Features	REGION 1..122
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-16-5	Residues	QVQLQESGPG LKVPSETLSL TCTVSGGSIS SYYSWIRQP PGKGLEWIGY IYYSGSTNYN 60 PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCVSLVY CGGDCYSGFD YWQGTLVTV 120 SS 122
3-17	Sequences	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	AA

3-17-3	Length	7
3-17-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..7
		mol_type=protein
		organism=synthetic construct
3-17-5	NonEnglishQualifier Value Residues	GGSISSY 7
3-18	Sequences	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	AA
3-18-3	Length	5
3-18-4	Features	REGION 1..5
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..5
		mol_type=protein
		organism=synthetic construct
3-18-5	NonEnglishQualifier Value Residues	YYSGS 5
3-19	Sequences	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	AA
3-19-3	Length	14
3-19-4	Features	REGION 1..14
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..14
		mol_type=protein
		organism=synthetic construct
3-19-5	NonEnglishQualifier Value Residues	LVYCGGDCYS GFDY 14
3-20	Sequences	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	DNA
3-20-3	Length	324
3-20-4	Features	misc_feature 1..324
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..324
		mol_type=other DNA
		organism=synthetic construct
3-20-5	NonEnglishQualifier Value Residues	gacatccagt tgacacagag cccgagttcc ttgtccgcct ccgtcgggga tagagtgtca 60 tttacctgtc aggcctctca ggatattaat aactttctga attggtatca gcaaaagccc 120 ggaaaggcac ccaagctgtt gatttacgac gccagtaacc tggagacagg cgtgccctcc 180 cggtttagtg gtagcggaag cggtagcgat ttaccttta ctatcagctc tctccaaccc 240 gaagacattg caacctacta ttgtcaacaa tatggaaacc tgccttttac atttggcggc 300 ggcaccaagg tggagattaa gcgg 324
3-21	Sequences	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	AA
3-21-3	Length	108
3-21-4	Features	REGION 1..108
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..108
		mol_type=protein
		organism=synthetic construct
3-21-5	NonEnglishQualifier Value Residues	DIQLTQSPSS LSASVGDRVS FTCQASQDIN NFLNWyQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKR 108
3-22	Sequences	
3-22-1	Sequence Number [ID]	22
3-22-2	Molecule Type	AA
3-22-3	Length	11
3-22-4	Features	REGION 1..11
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..11
		mol_type=protein
		organism=synthetic construct
3-22-5	NonEnglishQualifier Value Residues	QASQDINNFL N 11

3-23	Sequences	
3-23-1	Sequence Number [ID]	23
3-23-2	Molecule Type	AA
3-23-3	Length	7
3-23-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-23-5	Residues	DASNLET 7
3-24	Sequences	
3-24-1	Sequence Number [ID]	24
3-24-2	Molecule Type	AA
3-24-3	Length	9
3-24-4	Features	REGION 1..9
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..9 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-24-5	Residues	QQYGNLPFT 9
3-25	Sequences	
3-25-1	Sequence Number [ID]	25
3-25-2	Molecule Type	DNA
3-25-3	Length	1440
3-25-4	Features	misc_feature 1..1440
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1440 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-25-5	Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcaggtcc aactgcaaga aagcggaccc ggactggtga agccttctga gacacttagt 120 ctgacgtgca cggtcagtgg cggctccatc tcctcctatt attggtcatg gatacgacaa 180 ccccaggta agggcctgga atggattggc tatactctact attcaggaag cacgaactac 240 aatcccagcc tgaagtcccg agtgacaatt tcagtagata ccagtaaaaa ccagttcagt 300 cttaaaactgt caagcgtgac agctgccgac accgctgtgt attactgcgt ctacttggtg 360 tattgtggag gggattgtta tagcgggttc gattattggg gacagggaac cctggtgact 420 gtatcttccg gcggcggcgg ctcagggggg ggcggtagtg gcggtggggg ttccgatatt 480 caactgacac aatccccag ctcactcagc gccagcgtgg gggacagggt tagctttacc 540 tgtcaagcct ctcaggatat aaataacttt ctgaactggt atcaacagaa gcctgggaag 600 gcgccccaaac tcctgatcta tgatgctgcc aacctggaaa ctggcgtgcc ttcacgcttt 660 agcggctctg gcagtggtag agacttcact ttaccatct cttcacttca gccggaggac 720 atcgccacat attactgtca acagtacgga aacttgccct ttacttttgg aggcggcacc 780 aaagttgaaa tcaaaagggc cgctgccctg gataacgaaa agagcaatgg gactataata 840 catgttaaa gaaaacact gtgtccatct cccctgttcc ctggaccgtc aaagccattt 900 tgggtgctcg tggttgtcgg tggcgttctc gcctgttata gcttgcgtgt gacagtagcc 960 ttcattatct tttgggtgag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020 atgactccac gccgccctgg cccacaaagg aaacactacc agccttacgc accacctaga 1080 gatttcgctg cctatcggag caggggtgaag ttttccagat ctgcagatgc accagcgtat 1140 cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200 gttttgaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260 cccaggagg gtctctataa tgagctcgag aaggataaga tggctgaagc ctattctgaa 1320 atagggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380 agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440
3-26	Sequences	
3-26-1	Sequence Number [ID]	26
3-26-2	Molecule Type	AA
3-26-3	Length	479
3-26-4	Features	REGION 1..479
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..479 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-26-5	Residues	MALPVTALL PLALLHAAR PQVLQESGP GLVKPSETLS LTCTVSGGSI SSYYWSWIRQ 60 PPGKGLEWIG YIYSGSTNY NPSLKSRTVI SVDTSKNQFS LKLSSVTAAD TAVYYCVSLV 120 YCGGDCYSGF DYWGQGLTVT VSSGGGSGG GSGGGGSDI QLTQSPSSL ASVGDVRSFT 180 CQASQDINN LNYYQKPKG APKLLIYDAS NLETGVPSRF SGSGSGTDF FTISSLQPED 240 IATYYCQYQ NLPFTFGGGT KVEIKRAAL DNEKSNGTII HVKGKHLCP PLFPGPSKPF 300

		WVLVVVGVL ACYSLLVTA FIIFWVRSKR SLLHSDYMN MTPRRPGPTR KHYQPYAPPR 360 DFAAYRSRVK FRSADAPAY QGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGKPRRKN 420 PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHGGLYQGL STATKDTYDA LHMQUALPPR 479
3-27	Sequences	
3-27-1	Sequence Number [ID]	27
3-27-2	Molecule Type	DNA
3-27-3	Length	1374
3-27-4	Features	misc_feature 1..1374
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1374 mol_type=other DNA organism=synthetic construct
3-27-5	NonEnglishQualifier Value Residues	cagggtccaac tgcaagaaag cggacccgga ctggtgaagc cttctgagac acttagtctg 60 acgtgcacgg tcagtggcgg ctccatctcc tcctattatt ggtcatggat acgacaaccc 120 ccaggtaagg gcctggaatg gattggctat atctactatt caggaagcac gaactacaat 180 cccagcctga agtcccagat gacaatttca gtagatacca gtaaaaacca gttcagtctt 240 aaactgtcaa gcgtgacagc tgccgacacc gctgtgtatt actgctctc actggtgtat 300 tgtggagggg attgttatag cgggttcgat tattggggac agggaaacct ggtgactgta 360 tcttccggcg gcggcggctc agggggtggc ggtagtggcg gtgggggttc cgatatctca 420 ctgacacaat ccccagctc actcagcgcc agcgtggggg acagggttag cttacctgt 480 caagcctctc aggatataaa taactttctg aactggtatc aacagaagcc tgggaaggcg 540 cccaaactcc tgatctatga tgcgtccaac ctggaaactg gcgtgccttc acgctttagc 600 ggctctggca gtgtacaga cttcactttt accatctctt cacttcagcc ggaggacatc 660 gccacatatt actgtcaaca gtacggaaac ttgcccttta cttttggagg cggcaccaaa 720 gttgaaatca aaagggccgc tgccctggat aacgaaaaga gcaatgggac tataatacat 780 gttaaaggaa aacacctgtg tccatctccc ctggtccctg gaccgtcaaa gccattttgg 840 gtgctcgtgg ttgtcggtag cgttctcgcc tgttatagct tgtgtgtag agtagccttc 900 attatctttt ggtgagatc caaagaagc cgctgctcc atagcgatta catgaatatg 960 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1020 ttcgtgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1080 cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1140 ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1200 caggaggggtc tctataatga gctgcagaag gataagatgg ctgaagccta tttctgaaata 1260 ggcatgaaaag gagagcggag aaggggaaaa gggcacgacg gttgttacca gggactcagc 1320 actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg 1374
3-28	Sequences	
3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	AA
3-28-3	Length	458
3-28-4	Features	REGION 1..458
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..458 mol_type=protein organism=synthetic construct
3-28-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSSETLSL TCTVSGGSIS SYWWSWIRQP PGKGLEWIGY IYYSGSTNYN 60 PSLKSRTVIS VDTSKNQFSL KLSSVTAADT AVYYCVSLVY CGGDCYSGFD YWQGTLVTV 120 SSGGGSGGGG GSGGGGSDIQ LTQSPSSLSA SVGDRVSFTC QASQDINNFL NWYQQKPGKA 180 PKLLIYDASN LETGVPSRFS GSGSGTDFTF TISSLPEDI ATYYCQYGN LPFTFGGGTK 240 VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFV VLVVVGGVLA CYSLLVTVAF 300 IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK HYQPYAPPR FAAYRSRVKF SRSADAPAYQ 360 QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI 420 GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQUALPPR 458
3-29	Sequences	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	DNA
3-29-3	Length	1467
3-29-4	Features	misc_feature 1..1467
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1467 mol_type=other DNA organism=synthetic construct
3-29-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtgc agctgcagga atccggaccg gggctggtga agcccagcga gactctgagt 120 ctcacgtgta cagtttctgg aggtagcatt agctcctact attggtcatg gataaggcag 180 ccccccggga agggattgga atggatcggc tataatttact acagtgggag caccaattac 240 aaccctcac tgaagtctag agttacaatc agcgttgaca cctcaagaa tcagttcagt 300 ttgaaattgt ctacgctcac agcagctgat acagccgtct attattgtgt ttctctgggtc 360 tattgcgggtg gggattgtta cagtggtctt gactattggg ggcagggtac tctggttaca 420 gtttcttccg gggggggagg ctctgggggc ggaggctcag gtggtggagg cagcgacatc 480

		cagttgacac agagcccagag ttccttgtcc gcctccgctcg gggatagagt gtcatttacc 540 tgtcaggcct ctcaggatat taataacttt ctgaattggt atcagcaaaa gcccggaaaag 600 gcaccaaacg tgttgattta cgacgccagt aacctggaga caggcgtgcc ctcccggttt 660 agtggtagcg gaagcggtag ggattttacc ttactatca gctctctcca acccgaagac 720 attgcaacct actattgtca acaatatgga aacctgcctt ttacatttgg cgggcgacc 780 aaggtggaga ttaagcgggc ggcagctatt gaggtgatgt atccaccgcc ttacctggat 840 aacgaaaaaga gtaacggtag catcattcac gtgaaaggta aacacctgtg tccttctccc 900 ctcttccccg ggccatcaaa gcccttctgg gtctctgtgg tcgtgggagg cgtgcttgct 960 tgttattctc tgctcgttac cgtggcggtt atcatttttt gggttagatc caaaagaagc 1020 cgctgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080 cactaccagc cttacgcacc acctagagat ttcgctgcct atcggagcag ggtgaagttt 1140 tccagatctg cagatgcacc agcgtatcag caggggcaga accaactgta taacgagctc 1200 aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260 atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320 gataagatgg ctgaagccta ttcctgaaata ggcataaaag gagagcggag aaggggaaaa 1380 gggcacgacg gttgtacca gggactcagc actgctacga aggatactta tgacgctctc 1440 cacatgcaag ccctgccacc taggtaa 1467
3-30 3-30-1 3-30-2 3-30-3 3-30-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	30 AA 488 REGION 1..488 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..488 mol_type=protein organism=synthetic construct
3-30-5	NonEnglishQualifier Value Residues	MALPVTALL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SSYYWSWIRQ 60 PPKGLEWIG YIYSGSTNY NPSLKSRTVI SVDTSKNQFS LKLSSVTAAD TAVYVCVSLV 120 YCGGDCYSGF DYWGQGLVT VSSGGGSGG GSGGGGSDI QLTQSPSSLS ASVGRVSFT 180 CQASQDINNF LNWYQKPGK APKLLIYDAS NLETGVPSRF SSGSGSDTFT FTISSLQPED 240 IATYYCQYG NLPFTFGGT KVEIKRAAI EVMYPPPYLD NEKSNGTIIH VKGKHLCPSP 300 LFPGPSKPFV VLVVVGGLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK 360 HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEDV LDKRRGRDPE 420 MGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL 480 HMQALPPR 488
3-31 3-31-1 3-31-2 3-31-3 3-31-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	31 DNA 1401 misc_feature 1..1401 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1401 mol_type=other DNA organism=synthetic construct
3-31-5	NonEnglishQualifier Value Residues	caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60 acgtgtacag tttctggagg tagcattagc tcctactatt ggtcatggaat aaggcagccc 120 cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180 ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240 aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgtttc tctggtctat 300 tgcggtgggg attgttacag tggctttgac tattgggggc aggggtactct ggttacagtt 360 tcttccgggg ggggaggctc tgggggcgga ggctcagggtg gtggaggcag cgacatccag 420 ttgacacaga gcccaggttc cttgtccgcc tccgtcgggg atagagtgtc atttacctgt 480 caggcctctc aggatattaa taactttctg aattggtatc agcaaaagcc cggaaaggca 540 cccaagctgt tgatttacga cgccagtaac ctggagacag cgtgcccctc ccggtttagt 600 ggtagcggaa gcggtacgga ttttaccttt actatcagct ctctccaacc cgaagacatt 660 gcaacctact attgtcaaca atatggaac ctgcctttta catttggcgg cggcaccaag 720 gtggagatta agcgggcggc agctattgag gtgatgtatc caccgcctta cctggataac 780 gaaaagagta acggtaccat cattcacgtg aaaggtaaac acctgtgtcc ttctcccctc 840 ttccccgggc catcaaagcc cttctgggtt cttgtggtcg tgggaggcgt gcttgcctgt 900 tattctctgc tcgttaccgt ggcgtttatc attttttggg ttgatccaa aagaagccgc 960 ctgctccata gcgattacat gaatatgact ccacgcggcc ctagggccac aaggaacac 1020 taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1080 agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1140 ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1200 ggtggcaaac caagacgaaa aaacccccag gagggctctc ataatgagct gcagaaggat 1260 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1320 cacgacggtt tgtaccagg actcagcact gctacgaagg atacttatga cgctctccac 1380 atgcaagccc tgccacctag g 1401
3-32 3-32-1 3-32-2	Sequences Sequence Number [ID] Molecule Type	32 AA

3-32-3	Length	467
3-32-4	Features	REGION 1..467
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..467 mol_type=protein organism=synthetic construct
3-32-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYSWSWIRQP PGKGLEWIGY IYYSGSTNYN 60 PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCVSLVY CGGDCYSGFD YWQGGLVTV 120 SSGGGSGGG GSGGGGSDIQ LTQSPSSLSA SVGDRVSFTC QASQDINNFL NWYQKPKGA 180 PKLLIYDASN LETGVPSRFS GSGSGTDFTF TISSLQPEDI ATYYCQYGN LPFTFGGGTK 240 VEIKRAAAIE VMYPYPYLDN EKSNGTIIHV KGKHLCP SPL FPGSPKPFVW LVVVGGVLAC 300 YSLLVTVAFI IFWVRKRSR LLHSDYMNMT PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS 360 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 420 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 467
3-33	Sequences	
3-33-1	Sequence Number [ID]	33
3-33-2	Molecule Type	DNA
3-33-3	Length	1548
3-33-4	Features	misc_feature 1..1548
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1548 mol_type=other DNA organism=synthetic construct
3-33-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttgccat tgctcctgca cgccgcacgc 60 ccgcagggtgc aattgcaaga gtccggcccc ggactcgtaa aacccagtga gacgcttagc 120 ctgacctgta ccgtctcagg gggcagcatc tcctcttatt actggagctg gatcaggcag 180 cctccaggaa aaggccttga atggattggg tacatctact actctggtc aacaaattat 240 aatccatccc tgaagtcccg cgtgactatc tctgtggaca ccagcaagaa tcagttttca 300 ctgaagttgt ctagtgttac cgcgcccgac accgccgtat actactgtgt gtctcttgtg 360 tactgtggcg gcgactgcta ttccgggttc gactactggg gccaaaggag ctctgtaacc 420 gtgtcctcag gcggcgccgg gtcaggagga ggcggcagtg gaggtggcgg ctccgacatc 480 cagctgacac aatcaccatc ttccctttca gcttcagtcg gggacagagt gtccttcaca 540 tgccaggcca gccaggatat caataacttc ctgaactggt accaacagaa acccggaaag 600 gctccaaagc tcctgatcta tgatgcttcc aacctggaga ccggcgtgcc ctccagggtc 660 agtggttcag gatcaggcac tgactttacg ttcaccatat ccagtcttca gcccgaagac 720 attgcaacct attactgcc acaatacggg aaccttccct ttacattcgg aggcggcacc 780 aaggtggaaa tcaaaaggcg tgcagcattg agcaactcaa taatgtattt tagtcacttt 840 gtaccagtgt tcttgccggc taagcctact accacaccg ctccacggcc acctacccca 900 gctcctacca tcgcttcaca gcctctgtcc ctgcgcccgagg ggtctgccc accggccgca 960 gggggcgctg ttcataccag aggactggat ttgcgctgag atatctatat ctgggacacc 1020 ctggccggaa cctgcggcgt actcctgctg tccctggta tcacgctcta ttgtaatac 1080 aggaacagat ccaaaagaa cgcctgctc catagcgatt acatgaatat gactccacgc 1140 cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgtgccc 1200 tatcgagca gggatgaagt ttccagatct gcagatgcac cagcgtatca gcaggccag 1260 aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag 1320 cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaacc ccaggagggt 1380 ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcataaaa 1440 ggagagcgga gaaggggaaa agggcacgac ggtttgatc agggactcag cactgctacg 1500 aaggatactt atgacgctct ccacatgcaa gccctgccc ctaggtaa 1548
3-34	Sequences	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	AA
3-34-3	Length	515
3-34-4	Features	REGION 1..515
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..515 mol_type=protein organism=synthetic construct
3-34-5	NonEnglishQualifier Value Residues	MALPVTALL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SSYYWSWIRQ 60 PPKGLEWIG IYYSGSTNY NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCVSLV 120 YCGGDCYSGF DYWGQGLVTV VSSGGGSGG GSGGGGSDI QLTQSPSSL ASVGDRVSFT 180 CQASQDINN LNWYQKPKG APKLLIYDAS NLETGVPSRF SGSGSGTDFT FTISSLPED 240 IATYYCQYGN NLPFTFGGGT KVEIKRAAL SNSIMYFSH VPVFLPAKPT TTPAPRPPT 300 APTIASQPLS LRPEACRPAA GGAHVTRGLD FACDIYWAP LAGTCGVLLL SLVITLYCNH 360 RNRSKRSRL HSDYMNMTPR RGPTRKHQY PYAPPRFAA YRSRVKFSRS ADAPAYQQGQ 420 NQLYNELNLG RREEYDVLK RRGDRPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK 480 GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR 515
3-35	Sequences	
3-35-1	Sequence Number [ID]	35

3-35-2	Molecule Type	DNA
3-35-3	Length	1482
3-35-4	Features	misc_feature 1..1482
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1482 mol_type=other DNA organism=synthetic construct
3-35-5	NonEnglishQualifier Value Residues	cagggtgcaat tgcaagagtc cggccccgga ctcgtaaacc ccagtgagac gcttagcctg 60 acctgtaccg tctcaggggg cagcatctcc tcttattact ggagctggat caggcagcct 120 ccaggaaaag gccttgaatg gattgggtac atctactact ctggctcaac aaattataat 180 ccatccctga agtcccgcgt gactatctct gtggacacca gcaagaatca gttttcactg 240 aagttgtcta gtgttaccgc ggccgacacc gccgtatact actgtgtgtc tcttgtgtac 300 tgtggcggcg actgctattc cgggttcgac tactggggcc aagggactct ggtaaccgtg 360 tcctcaggcg gcggcgggtc aggaggaggc ggagtgagg gtggcggctc cgacatccag 420 ctgacacaat caccatcttc cttttcagct tcagtcgggg acagagtgtc cttcacatgc 480 caggccagcc aggatataca taacttcctg aactggtacc aacagaaacc cggaagggt 540 ccaagctcc tgatctatga tgcttccaac ctggagaccg gcgtgccctc caggttcagt 600 ggttcaggat caggcactga ctttacgttc accatatcca gtcttcagcc cgaagacatt 660 gcaacctatt actgccaaca ataccggaac ctcccttcta cattcggagg cggcaccaag 720 gtggaaatca aaagggctgc agcattgagc aactcaataa tgtatttttag tcactttgta 780 ccagtgttct tgccggctaa gcctactacc acaccgctc cacggccacc taccacagct 840 cctaccatcg cttcacagcc tctgtccctg cgccagagg cttgccgacc ggccgcaggg 900 ggcgctgttc ataccagagg actggatttc gcctgcgata tctatatctg ggcacccctg 960 gccggaacct gcggcgtagt cctgctgtcc ctggatcatc cgctctattg taatcacagg 1020 aacagatcca aaagaagcgg cctgctccat agcgattaca tgaatatgac tccacgcccg 1080 cctggcccca caaggaaaaca ctaccagcct tacgcaccac ctatagattt cgctgcctat 1140 cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1200 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1260 agaggacggg accctgagat ggggtggcaa ccaagacgaa aaaaccccca ggagggtctc 1320 tataatgagc tgcaagaagg taagatggct gaagcctatt ctgaaatagg catgaaggga 1380 gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1440 gatacttatg acgctctcca catgcaagcc ctgccaccta gg 1482
3-36	Sequences	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	AA
3-36-3	Length	494
3-36-4	Features	REGION 1..494
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..494 mol_type=protein organism=synthetic construct
3-36-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYVSWIRQP PGKGLEWIGY IYVSGSTNYN 60 PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCVSLVY CGGDCYSGFD YWQGQTLVTV 120 SSGGGSGGG GSGGGGSDIQ LTQSPSSLSA SVGDRVSFTC QASQDINNFL NWYQKPGKA 180 PKLLIYDASN LETGVPSRFS GSGSGDTFTF TISSLPEDI ATYYCQQYGN LPFTFGGGTK 240 VEIKRAAALS NSIMYFSHFV PVFLPAKPTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG 300 GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCNHR NRSKRSRLH SDYMNMTPRR 360 PGPTRKHYQP YAPPRDFAAY RSRVKFSRSA DAPAYQQGN QLYNELNLGR REEYDVLDR 420 RGRDPEMGK PRRKNPQEG LYNELQDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-37	Sequences	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	DNA
3-37-3	Length	1440
3-37-4	Features	misc_feature 1..1440
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1440 mol_type=other DNA organism=synthetic construct
3-37-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccggatatcc agctcacgca atccccctca agcttgagtg cctccgtggg cgaccgggtg 120 tccttcacat gtcaggcaag ccaagacata aataatttcc tgaattggta ccaacaaaaa 180 cccggcaagg ctcccaaact cctgatttat gatgcctcca atctggagac cggggtcctt 240 tctagattca gcggaagtgg cagcggcaca gactttacat ttactatctc ttctctgcaa 300 ccagaggaca tcgccacata ctattgccag caatacggca atctgccctt caccttcgga 360 ggcggaaacca aggtagaat taaaaggggc ggtggaggct ccggaggggg gggctctggc 420 ggagggggct cccaagtaca attgcaggag tcagggcctg gactcgtgaa gccttcagaa 480 actttgtcac tgacatgtac agtgtccggc ggaagcattt ccagttacta ttggtcctgg 540 attagacagc caccgcgcaa aggactggaa tggattggat atatctacta ctctggatct 600

		acaaactata atcccagcct caaatccagg gtcactatta gtgtgggatac atcaaagaat 660 cagttctcct tgaagctgag ctccagtcact gctgccgaca ccgcagtgta ctattgtgtg 720 agcctggtct actgcggcgg agattgctac agcggtttcg attactgggg ccagggcacc 780 ctggttacg ttagttccgc ggctgctctt gataacgaga agtccaacgg tacgattatc 840 cacgttaagg gtaagcact ttgccctagc ccgctgttcc caggccccag taagcccttt 900 tgggtcctcg ttgtggtagg tggggctact gcctgctact ccctgctcgt cactgtcgca 960 ttcatcatct tctgggtcag atccaaaaga agccgcctgc tccatagcga ttcatgaat 1020 atgactccac gccgccctgg cccacaaagg aaacactacc agccttacgc accacctaga 1080 gatttcgctg cctatcggag caggggtgaag ttttccagat ctgcagatgc accagcgtat 1140 cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200 gttttggaac agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260 ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320 ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380 agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440
3-38	Sequences	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	AA
3-38-3	Length	470
3-38-4	Features	REGION 1..470
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..470 mol_type=protein organism=synthetic construct
3-38-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PDIQLTQSPS SLSASVGDRV SFTCQASQDI NNFLNWYQQK 60 PGKAPKLLIY DASNLETGVP SRFSGSGSGT DFTFTISSLQ PEDIATYYCQ QYGNLPFTFG 120 GGTKVEIKRG GGS SGGSGSG GGSQVQLQE SGPGLVKPSE TLSLTCTVSG GSISYYWSW 180 IRQPPGKGLE WIGYIYYS GS TNYNPSLKS RVTISVDTSKN QFSLKLSSVT AADTAVYYCV 240 SLVYCGGDCY SGFDYWGGT LVTVSSAAL DNEKSNGTII HVKGKHLCP S PLFPGPSKPF 300 WVLVVVGVL ACYSLLVTA FIIFWRSKR SLLHSDYMN MTPRRPGPTR KHYQPYAPPR 360 DFAAYRSRVK FRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGKPRRKN 420 PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGH DGLYQGL STATKDTYDA 470
3-39	Sequences	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	DNA
3-39-3	Length	1374
3-39-4	Features	misc_feature 1..1374
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1374 mol_type=other DNA organism=synthetic construct
3-39-5	NonEnglishQualifier Value Residues	gatatccagc tcacgcaatc cccctcaagc ttgagtgcc tccgtgggcga ccgggtgtcc 60 ttcacatgtc aggcgaagcca agacataaat aatttctcta attggtacca acaaaaaccc 120 ggcaaggctc ccaaactcct gatttatgat gcctccaatc tggagaccgg ggtcccttct 180 agattcagcg gaagtggcag cggcacagac ttacattta ctatctcttc tctgcaacca 240 gaggacatcg ccacatacta ttgccagcaa tacggcaatc tgcccttcac cttcggaggc 300 ggaaccaagg tagaaattaa aaggggcggt ggaggctccg gagggggggg ctctggcgga 360 gggggctccc aagtacaatt gcaggagtca gggcctggac tctgtaagcc ttcagaaact 420 ttgtcactga catgtacagt gtccggcgga agcatttcca gttactattg gtccctggatt 480 agacagccac ccggcaaagg actggaatgg attggatata tctactactc tggatctaca 540 aactataatc ccagcctcaa atccagggtc actattagt tggatacatc aaagaatcag 600 ttctccttga agctgagctc agtcaactgt gccgacaccg cagtgtacta ttgtgtgagc 660 ctggtctact gcggcgga ttgctacagc ggtttcgatt actggggcca gggcacccctg 720 gttaccgtta gttccgcggc tgctcttgat aacgagaagt ccaacggtag gattatccac 780 gttaagggtc agcaccttg ccctagcccg ctgttcccag gccccagtaa gcccttttgg 840 gtcctcgttg tggtaggtgg ggtactcgcc tgctactccc tgctcgtcac tgtcgcattc 900 atcatcttct ggtcagatc caaaagaagc cgctgtctcc atagcgatta catgaatatg 960 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1020 ttcgtgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1080 cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1140 ttggacaagc gcagaggac ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1200 caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1260 ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1320 actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg 1374
3-40	Sequences	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	AA
3-40-3	Length	458
3-40-4	Features	REGION 1..458
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..458 mol_type=protein

3-40-5	NonEnglishQualifier Value Residues	organism=synthetic construct DIQLTQSPSS LSASVGDRVS FTCQASQDIN NFLNWXQQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKRGG GSGGGGSGG 120 GGSQVQLQES GPGLVKPSET LSLTCTVSGG SISSYYWSWI RQPPGKGLEW IGYIYYSGST 180 NYNPSLKSRV TISVDTSKNQ FSLKLSSVTA ADTAVYYCVS LVYCGGDCYS GFDYWGGTTL 240 VTVSSAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW VLVVVGGVLA CYSLLVTVAF 300 IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK HYQPYAPRD FAAYRSRVKF SRSADAPAYQ 360 QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI 420 GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR 458
3-41 3-41-1 3-41-2 3-41-3 3-41-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	41 DNA 1467 misc_feature 1..1467 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1467 mol_type=other DNA organism=synthetic construct
3-41-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccggatatcc agctgaccga gtcctcatcc tctttgagtg cctccgtggg tgaccgcgctc 120 tctttcactt gccaaagccag ccaagacatc aacaactttc tgaattggta ccagcagaaa 180 ccaggcaaa caccaaagct cctcatctac gacgcctcca acctggaaac cggggtgccc 240 agcagggtta gcgggagcgg ttctggcacg gattttacgt tcaccatctc ctctctgcag 300 cccaggata tagctactta ttactgtcag cagtacggga atctgccatt tacttttggg 360 ggtggaacta aggtggaat caaaaggggc ggcgggggaa gcgggggcgg gggctcaggt 420 ggcggaggga gccagggtga actccaggaa agtggccag gatggtgaa gccagcgcag 480 accctttccc ttacttgtac tgtagcgga ggcagcataa gcagctacta ttggtcctgg 540 atcagacagc caccaggga agggcttgaa tggattggct acatttacta ttccgggtcc 600 accaactaca acccatccct caagtcccgc gtgacaattt ccgtcgacac aagcaagaac 660 cagtctctcc tgaacttag tagcgctact gctgcagata cagcagtgtg ctatttgtgc 720 agccttgtct actgtggcgg cgactgtac agtggctttg attactgggg acagggcacg 780 ctcgtgacag tgtccagcgc tgcggctatc gaggtaatgt atccgccacc gtatctggac 840 aacgagaagt ctaatgggac aatcattcac gtgaagggga agcacctgtg tccatcccc 900 ctgtttccgg gtcccagtaa acccttctgg gtgcttgttg tcgttggcgg ggtgctggcg 960 tgctattccc tgctggtgac cgtcgctttt attattttct gggttagatc caaaagaagc 1020 cgctgtctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080 cactaccagc cttagcacc acctagagat ttcgctgcct atcggagcag ggtgaagttt 1140 tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200 aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260 atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320 gataagatgg ctgaagccta ttctgaaata ggcataaaag gagagcggag aaggggaaaa 1380 gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc 1440 cacatgcaag ccctgccacc taggtaa 1467
3-42 3-42-1 3-42-2 3-42-3 3-42-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	42 AA 488 REGION 1..488 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..488 mol_type=protein organism=synthetic construct
3-42-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PDIQLTQSPS SLSASVGDRV SFTCQASQDI NNFLNWXQQK 60 PGKAPKLLIY DASNLETGVP SRFSGSGSGT DFTFTISSLQ PEDIATYYCQ QYGNLPFTFG 120 GGTKVEIKRG GSGSGGGSGG GGSQVQLQE SGPGLVKPSE TSLTCTVSG GSIISSYYWSW 180 IRQPPGKGLE WIGYIYYSGS TYNPSLKSR VTISVDTSKN QFSLKLSSVT AADTAVYYCV 240 SLVYCGGDCY SGFDYWQGT LTVSSAAAI EVMYPPPYLD NEKSNGTIIH VKGKHLCPSP 300 LFPGPSKPFW VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK 360 HYQPYAPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE 420 MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL 480 HMQALPPR 488
3-43 3-43-1 3-43-2 3-43-3 3-43-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	43 DNA 1401 misc_feature 1..1401 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1401 mol_type=other DNA

3-43-5	NonEnglishQualifier Value Residues	organism=synthetic construct gatatccagc tgacccagtc tccatcctct ttgagtgcc tccgtgggtga ccgcgtctct 60 ttcacttgcc aagccagcca agacatcaac aactttctga attggtacca gcagaaacca 120 ggcaaagcac caagctcct catctacgac gcctccaacc tggaaaccgg ggtgcccagc 180 agggtttagc ggagcggttc tggcacggat ttacgttca ccatctcctc tctgcagccc 240 gaggatatag ctacttatta ctgtcagcag tacgggaatc tgccatttac ttttgggggt 300 ggaactaagg tggaaatcaa aaggggcggc gggggaagcg ggggcggggg ctcaggtggc 360 ggagggagcc aggtgcaact ccaggaaagt ggcccaggat tggtgaaagg cagcgagacc 420 ctttccctta cttgtactgt tagcggaggc agcataagca gctactattg gtcctggatc 480 agacagccac cagggaaagg gcttgaatgg attggctaca ttactattc cgggtccacc 540 aactacaacc catccctcaa gtcccgcgtg acaatttcg tgcacacaag caagaaccag 600 ttctccctga aacttagtag cgtcactgct gcagatacag cagtgtacta ttgtgtcagc 660 cttgtctact gtggcggcga ctgtacagc ggctttgatt actggggaca gggcacgctc 720 gtgacagtg tccagcgtgc ggctatcgag gtaatgtatc cgccaccgta tctggacaac 780 gagaagtcta atgggacaat cattcacgtg aaggggaagc acctgtgtcc atccccctg 840 tttccgggtc ccagtaaacc cttctgggtg cttgtgtgct ttggcggggg gctggcctgc 900 tattccctgc tggtagccgt cgcgtttatt attttctggg ttagatccaa aagaagccgc 960 ctgctccata gcgattacat gaatatgact ccacgccgcc ctggcccccac aaggaaacac 1020 taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1080 agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1140 ctgggacgca ggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1200 ggtggcaaac caagacgaaa aaaccccag gagggtctct ataatgagct gcagaaggat 1260 aagatggctg aagcctattc tgaatataggc atgaaaggag agcggagaag gggaaaaggg 1320 cacgacggtt tgtaccagg actcagcact gctacgaagg atacttatga cgctctccac 1380 atgcaagccc tgccacctag g 1401
3-44 3-44-1 3-44-2 3-44-3 3-44-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	44 AA 467 REGION 1..467 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..467 mol_type=protein organism=synthetic construct
3-44-5	NonEnglishQualifier Value Residues	DIQLTQSPSS LSASVGDRVS FTCQASQDIN NFLNWFYQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKRGG GSGSGGSGG 120 GGSQVQLQES GPLVKPSET LSLTCTVSGG SISSYYWSWI RQPPGKGLEW IGYIYSGST 180 NYPNPSLKS RV TISVDTSKNQ FSLKLSSVTA ADTAVYVCVS LVYCGGDCYS GFDYWQGT 240 VTVSSAAIE VMYPYLDN EKSNGTIIHV KGKHLCPSP FPGSPKPFV LVVVGGVLAC 300 YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS 360 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GKKPRRKNPQ EGLYNELQKD 420 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDITYDALH MQALPPR 467
3-45 3-45-1 3-45-2 3-45-3 3-45-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	45 DNA 1548 misc_feature 1..1548 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1548 mol_type=other DNA organism=synthetic construct
3-45-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccggacattc aattgaccca gtcccctagc agtctctcag caagtgtggg agataggggtg 120 tcattcacct gtcaggcttc acaggacatc aacaacttcc tcaattggga tcagcagaag 180 ccagggaagg caccaaagct gctcatatat gacgcttcaa accttgaaac cggagtagct 240 agccgcttca gcggaagcgg atcagggact gacttcactt ttaccatctc ttactgtagc 300 cccgaagaca tcgccacata ctactgccag cagtacggaa acttgccctt tacatttggg 360 ggcggcacca aagtggagat taagcgaggg ggaggcggtc caggaggcgg tggctccgga 420 ggcgggggtt ccagggtcca gtcaggagaa tccggccagc gtctgggtta gccagtgtaa 480 actttgtccc tcacgtgtac tgtgagcggg ggttcaatct cctcatacta ttggtcttgg 540 atacggcaac ctcttgaaa ggcctcgag tggatcggtc atatatata tagtggctcc 600 actaattaca acccttcctt caagtccaga gtcaccattt ccgtggacac atctaagaac 660 cagttcagtc tgaagttgtc cagcgttaca gccgcagaca cagccgttta ttactgtgtg 720 tctcttgttt actgcggggg agactgttat agcggcttcg attactgggg ccagggcacc 780 ttggtcacag tctcttcgc ggccgccctc tctaaccagta ttatgtactt ttctattttt 840 gtaccctgtt tccttcccgc taagccaaact actaccccg cccacggcc gcctaccctt 900 gcaccacaaa tagccagtc gcttttgagc ctgagacgtc aggtctgtgc gccggtgctt 960 gggggtgtag tgacacacg aggtcttgat ttgtctgcg acatatacat tagggcccct 1020 ctggccggga cctgtggggg gctgtctctg agcttggta tcacgctcta ttgaaccat 1080 cgcaacagat ccaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1140

		cgccctggcc ccacaaggaa acactaccag ctttacgcac cacctagaga tttcgtgcc 1200 tatcggagca gggtagaagt ttccagatct gcagatgcac cagcgtatca gcagggccag 1260 aaccaactgt ataacgagct caacctggga cgcaggggaag agtatgacgt tttggacaag 1320 cgagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggg 1380 ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcataaaa 1440 ggagagcggg gaaggggaaa agggcacgac ggtttgatc agggactcag cactgctacg 1500 aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa 1548
3-46	Sequences	
3-46-1	Sequence Number [ID]	46
3-46-2	Molecule Type	AA
3-46-3	Length	515
3-46-4	Features	REGION 1..515
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..515 mol_type=protein organism=synthetic construct
3-46-5	NonEnglishQualifier Value Residues	MALPVTALL PLALLLHAAR PDIQLTQSPS SLSASVGD RV SFTCQASQDI NNFLNWYQK 60 PGKAPKLLIY DASNLETGVP SRFSGSGSGT DFTFTISSLQ PEDIATYYCQ QYGNLPFTFG 120 GGTKVEIKRG GGGSGGGGSG GGGSQVLQE SGPGLVKPSE TSLTCTVSG GSISSYYWSW 180 IRQPPGKGLE WIGYIYSGS TNYNPSLKS RTISVDTSKN QFSLKLSSVT AADTAVYYCV 240 SLVYCGGDCY SGFDYWGGT LTVSSAAL SNSIMYFSHF VPVFLPAKPT TTPAPRPPTP 300 APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWP LAGTCGVLL SLVITLYCNH 360 RNRSKRSLR HSDYMNMTPR RGPTRKHYQ PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ 420 NQLYNELNLG RREEYDVL DK RRGDPPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK 480 GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR 515
3-47	Sequences	
3-47-1	Sequence Number [ID]	47
3-47-2	Molecule Type	DNA
3-47-3	Length	1482
3-47-4	Features	misc_feature 1..1482
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1482 mol_type=other DNA organism=synthetic construct
3-47-5	NonEnglishQualifier Value Residues	gacattcaat tgaccagtc ccctagcagt ctctcagcaa gtgtgggaga taggggtgtca 60 ttcacctgtc aggttcaca ggacatcaac aacttcctca attggtatca gcagaagcca 120 gggaaggcac caaagctgct catatatgac gcttcaaacc ttgaaaccgg agtacctagc 180 cgcttcagcg gaagcggatc agggactgac ttcactttta ccatctcttc actgcagccc 240 gaagacatcg ccacatacta ctgccagcag tacggaactc tgccttttac atttgggggc 300 ggcaccaaag tggagattaa gcgaggggga ggcggctcag gagcggtgg ctccggaggc 360 gggggttccc aggtccagct ccaggaatcc ggcccaggtc tggttaagcc cagtgaact 420 ttgtccctca cgtgtactgt gagcgggtgt tcaatctcct catactattg gtcttggata 480 cggcaacctc ctggaagggt cctcgagtgg atcggctata tctactatag tggctccact 540 aattacaacc ctccctcaa gtccagagtc accatttcgg tggacacatc taagaaccag 600 ttcagtcctga agttgtccag cgttacagcc gcagacacag ccgtttatta ctgtgtgtct 660 cttgtttact gcgggggaga ctgttatagc ggcttcgatt actggggcca gggcaccttg 720 gtcacagtct ctcccgggc gccctctct aacagtatta tgtacttttc tcattttgta 780 cccgtgttcc ttcccgctaa gccaactact accccggccc cagggccggc taccctgca 840 cccacaatag ccagtcagcc tttagacctg agacctgagg ctgttcggcc ggctgctggg 900 ggtgcagtgc acacacagg tcttgatttt gcttgcgaca tatacatctg ggccctctg 960 gccgggacct gtgggtgct gcttctgagc ttggtcatca cgctctattg caaccatcgc 1020 aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1080 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1140 cggagcaggg tgaagtttcc cagatctgca gatgcaccag cgtatcagca gggccagaac 1200 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1260 agaggacggg accctgagat gggtgcaaa ccaagacgaa aaaaccccca ggagggtctc 1320 tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1380 gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1440 gatacttatg acgctctcca catgcaagcc ctgccaccta gg 1482
3-48	Sequences	
3-48-1	Sequence Number [ID]	48
3-48-2	Molecule Type	AA
3-48-3	Length	492
3-48-4	Features	REGION 1..492
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..492 mol_type=protein organism=synthetic construct
3-48-5	NonEnglishQualifier Value Residues	DIQLTQSPSS LSASVGD RV FTCQASQDIN NFLNWYQKP GKAPKLLIYD ASNLETGVPS 60

		RFSGSGSGTD FTFTISLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKRGG GSGGGGSGG 120 GGSQVQLQES GPGLVKPSET LSLTCTVSGG SISSYYWSWI RQPPGKGLEW IGYIYSGST 180 NYNPSLKS RV TISVDTSKNQ FSLKLSSVTA DTAVYYCVSL VYCGGDCYSG FDYWGQGT LV 240 TVSSAAALSN SIMYFSHFVP VFLPAKPTTT PAPRPPTPAP TIASQPLSLR PEACRPAAGG 300 AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCNHRN RSKRSRLLSH DYMNMTPRRP 360 GPTRKHYPY APPRDFAAAYR SRVKFSRSAD APAYQQGQNY LYNELNLGRE EYDVLDKRRG 420 RDPEMGGKPR RKNPQEGLYN ELQDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT 480 YDALHMQALP PR 492
3-49 3-49-1 3-49-2 3-49-3 3-49-4 3-49-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	49 DNA 372 misc_feature 1..372 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..372 mol_type=other DNA organism=synthetic construct caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60 acatgtaccg tgagcggcgg aagtataagc agtggaggct tttactggtc ttggatacgg 120 cagcaccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac 180 tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240 agtctcaggc tgcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg 300 gtttactgcg gaggcgactg ttatagcggc ttgattatt gggggcaggg gaccctcgta 360 accgtgagct ct 372
3-50 3-50-1 3-50-2 3-50-3 3-50-4 3-50-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	50 AA 124 REGION 1..124 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..124 mol_type=protein organism=synthetic construct QVQLQESGPG LVKPSQTL SL TCTVSGGSIS SGGFYWSWIR QHPGKGLEWI GYIHHS GSTH 60 YNPSLKS RV TISVDTSKNLF SLRLSSVTAA DTAVYYCASL VYCGGDCYSG FDYWGQGT LV 120 TVSS 124
3-51 3-51-1 3-51-2 3-51-3 3-51-4 3-51-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	51 AA 9 REGION 1..9 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..9 mol_type=protein organism=synthetic construct GGSISSGGF 9
3-52 3-52-1 3-52-2 3-52-3 3-52-4 3-52-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	52 AA 5 REGION 1..5 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..5 mol_type=protein organism=synthetic construct HHS GS 5
3-53 3-53-1 3-53-2 3-53-3 3-53-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value	53 AA 14 REGION 1..14 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..14 mol_type=protein organism=synthetic construct

3-53-5	Residues	LVYCGGDCYS GFDY	14
3-54	Sequences		
3-54-1	Sequence Number [ID]	54	
3-54-2	Molecule Type	DNA	
3-54-3	Length	324	
3-54-4	Features	misc_feature 1..324	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..324	
		mol_type=other DNA	
		organism=synthetic construct	
3-54-5	NonEnglishQualifier Value		
	Residues	gatatccagc tcaactcaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 60 tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 120 ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 180 cgattctctg ggtcagggtc cgggaccgac ttacgttta cgatctcctc tctgcagccc 240 gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 300 gggactaagg ttgaaatcaa gagg 324	
3-55	Sequences		
3-55-1	Sequence Number [ID]	55	
3-55-2	Molecule Type	AA	
3-55-3	Length	108	
3-55-4	Features	REGION 1..108	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..108	
		mol_type=protein	
		organism=synthetic construct	
3-55-5	NonEnglishQualifier Value		
	Residues	DIQLTQSPSS LSASVGDRVS FTCQASQDIN NFLNWYQQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKR 108	
3-56	Sequences		
3-56-1	Sequence Number [ID]	56	
3-56-2	Molecule Type	AA	
3-56-3	Length	11	
3-56-4	Features	REGION 1..11	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
3-56-5	NonEnglishQualifier Value		
	Residues	QASQDINNFL N 11	
3-57	Sequences		
3-57-1	Sequence Number [ID]	57	
3-57-2	Molecule Type	AA	
3-57-3	Length	7	
3-57-4	Features	REGION 1..7	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
3-57-5	NonEnglishQualifier Value		
	Residues	DASNLET 7	
3-58	Sequences		
3-58-1	Sequence Number [ID]	58	
3-58-2	Molecule Type	AA	
3-58-3	Length	9	
3-58-4	Features	REGION 1..9	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
3-58-5	NonEnglishQualifier Value		
	Residues	QQYGNLPFT 9	
3-59	Sequences		
3-59-1	Sequence Number [ID]	59	
3-59-2	Molecule Type	DNA	
3-59-3	Length	1446	
3-59-4	Features	misc_feature 1..1446	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..1446	

3-59-5	NonEnglishQualifier Value Residues	mol_type=other DNA organism=synthetic construct atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcaggtac agctgcagga atctgggccc ggacttgtca agccaagtca gacactttct 120 cttacatgta ccgtgagcgg cggaaagtata agcagtgagg gcttttactg gtctttggata 180 cggcagcacc caggcaaaagg cttggagtggt attggataca ttcattcattc aggatctaca 240 cactataatc catcccttaa gtccccgggtc accattagca ttgatacgtc taagaatctg 300 ttcagttcga ggctgtcctc cgtcactgct gccgacacag ccggtgtacta cttgcgcctcg 360 ttggtttact gcggaggcga ctgttatagc ggcttttgatt attgggggga ggggaccctc 420 gtaaccgtga gctctggagg ggggtgggagc gggggaggag gttcaggggg gggcggtctc 480 gatatccagc tactcaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 540 tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 600 ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 660 cgattctctg ggtcagggtc cgggaccgac ttacgttta cgatctcctc tctgcagccc 720 gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 780 gggactaagg ttgaaatcaa gagggccgct gcactggaca atgagaagtc caacggcacc 840 atcatccacg tgaagggcaa gcacctgtgc cctagtcctc tgttcccagg cccatccaaa 900 cctttttggg ttcttgttgt ggtcgggggg gtgctggcct gctattctct gctggtcacg 960 gtggccttca taattttctg ggtagatcc aaaagaagcc gcctgtcca tagcgattac 1020 atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca 1080 cctagagatt tcgctgccta tcggagcagg gtgaagtttt ccagatctgc agatgcacca 1140 gcgtatcagc agggccagaa ccaactgtat aacgagctca accctggacg cagggaagag 1200 tatgacgttt tggacaagcg cagaggacgg gaccctgaga tgggtggcaa accaagacga 1260 aaaaaccccc aggggggtct ctataatgag ctgcagaagg ataagatggc tgaagcctat 1320 tctgaaatag gcatgaaagg agagcggaga aggggaaaag ggcacgacgg tttgtaccag 1380 ggactcagca ctgctacgaa ggatacttat gacgctctcc acatgcaagc cctgccacct 1440 aggtaa 1446
3-60 3-60-1 3-60-2 3-60-3 3-60-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	60 AA 481 REGION 1..481 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..481 mol_type=protein organism=synthetic construct
3-60-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI SSGGFYWSWI 60 RQHPGKGLEW IGYIHHSST HYNPSLKSRLV TISIDTSKNL FSLRLSSVTA ADTAVYYCAS 120 LVYCGGDCYS GFDYWQQTLL VTVSSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVS 180 FTCQASQDIN NFLNWWYQKPK GKAPKLLIYD ASNLETGVPS RFSGSGSGSTD FTFTISSLP 240 EDIATYYCQY YGNLPFTFGG GTKVEIKRAA ALDNEKSNST IIHVKGKHLK PSPLFPGPSK 300 PFVWLVVVGG VLACYSLLVV VAFIIFWVRS KRSRLHSDY MNMTPRRPGP TRKHYPYAP 360 PRDFAAYRSR VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR 420 KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY DALHMQALPP 480 R 481
3-61 3-61-1 3-61-2 3-61-3 3-61-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	61 DNA 1380 misc_feature 1..1380 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1380 mol_type=other DNA organism=synthetic construct
3-61-5	NonEnglishQualifier Value Residues	caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60 acatgtaccg tgaaggcgcg aagtataagc agtggaggct tttactggtc ttggatacgg 120 cagcaccagc gcaaaggctt ggagtgattt ggatacattc atcattcagg atctacacac 180 tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240 agtctcaggc tgcctccgtt cactgctgcc gacacagccg tgtactactg cgcctccttg 300 gtttactgcg gaggcgactg ttatagcggc ttgtattatt gggggcaggg gacctcctga 360 accgtgagct ctggaggggg tgggagcggg ggaggaggtt cagggggggg cggctccgat 420 atccagctca ctcaaagccc ctctagtctc tctgcctcag tgggggatcg ggtcagtttt 480 acttgtcaag cttcacagga tatcaacaac ttccttaatt ggtatcagca gaagccagga 540 aaagcaccga agctgctcat ctatgatgcc tcaaatttgg agacgggtgt tcccagtcga 600 ttctctgggt cagggtccgg gaccgacttt acgtttacga tctcctctct gcagcccgaa 660 gacatcgcca catactattg tcaacagtac ggcaacttgc ctttcacatt tggggggcgg 720 actaaggttg aatcaagag ggccgctgca ctggacaatg agaagtccaa cggcaccatc 780 atccacgtga agggcaagca cctgtgccct agtcctctgt tcccaggccc atccaaacct 840 ttttgggttc ttgttgtggt cgggggggtg ctggcctgct attctctgct ggtcagcgtg 900 gccttcataa ttttctgggt tagatccaaa agaagccgcc tgctccatag cgattacatg 960

		aatatgactc cacgccgccc tggccccaca aggaaacact accagcctta cgcaccacct 1020 agagatttcg ctgcctatcg gagcagggtg aagttttcca gatctgcaga tgcaccagcg 1080 tattcagcagg gccagaacca actgtataac gagctcaacc tgggacgcag ggaagagtat 1140 gacgtttttg acaagcgtag aggacgggac cctgagatgg gtggcaaacc aagacgaaaa 1200 aacccccagg aggggtctcta taatgagctg cagaaggata agatggctga agcctattct 1260 gaaataggca tgaaggaga gcggagaagg ggaaaagggc acgacggttt gtaccaggga 1320 ctcagcactg ctacgaagga tacttatgac gctctccaca tgcaagccct gccacctagg 1380
3-62	Sequences	
3-62-1	Sequence Number [ID]	62
3-62-2	Molecule Type	AA
3-62-3	Length	460
3-62-4	Features	REGION 1..460
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..460 mol_type=protein organism=synthetic construct
3-62-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGFYWSWIR QHPGKGLEWI GYIHHSGSTH 60 YNPSLKSRTV ISIDTSKNLF SLRLSSVTAA DTAVYYCASL VYCGGDCYSG FDYWGQGTLV 120 TVSSGGGGSG GGGSGGGGSD IQLTQSPSSL SASVGDVRSF TCQASQDINN FLNWFYQKPG 180 KAPKLLIYDA SNLETGVPSR FSGSGSGTDF TFTISSLQPE DIATYYCQQY GNLPFTFGGG 240 TKVEIKRAAA LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP FWLVVVGGV LACYSLLVTV 300 AFIIFWVRSK RSRLHSDYM NMTPRRPGPT RKHYQPYAPP RDFAAYRSRV KFSRSADAPA 360 YQQGQNQLYN ELNLGRREEY DVLDKRRGRD PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS 420 EIGMKGERRR GKGDGLYQG LSTATKDTYD ALHMQALPPR 460
3-63	Sequences	
3-63-1	Sequence Number [ID]	63
3-63-2	Molecule Type	DNA
3-63-3	Length	1473
3-63-4	Features	misc_feature 1..1473
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1473 mol_type=other DNA organism=synthetic construct
3-63-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtg agctgcagga aagcgggtccg ggacttgta agccgtccca aacgtgagtg 120 ctgacgtgta ctgtctctgg tggtctctatt tcttccgggg gcttttattg gtcttggatc 180 agacaacacc ctggcaaagg gctggagtgg atagggtata ttcaccactc tgggtccact 240 cactacaacc catcattgaa atccagagtg actatctcaa tcgacacatc caagaacctt 300 ttcagcctga ggttgtcatc agttaccgcc gctgacaccg cgggtgatta ttgcgcctct 360 ctcgtgtact gcggtggcga ttgttatagt ggctttgact actgggggca ggggacattg 420 gttaccgttt caagtggagg cgggtgggtct ggcgggggcg gtagcggagg tggggggagc 480 gacatacagc ttacgcagag cccctccagc ctttcagcct ccgtggggga taggggtgtc 540 tttacctgcc aggccttcca ggacataaac aacttcctca attggtatca gcaaaagccc 600 gggaaagcac caaagctgct catctacgat gccagcaacc tggaaaaccg agtgccgtct 660 cgcttctctg gaagtggcag tgggaccgat ttcactttta caatctcaag ttgcagcca 720 gaagacattg caacatacta ctgtcaacag tacggcaatc tcccctttac atttgggggg 780 ggaaactaaag tggagattaa gcgcgctgca gccattgaag ttatgtatcc gcccccgtat 840 ctggataacg agaaatctaa tggtagcata atacatgtga aggggaagca cctctgtcca 900 tcaccgctgt tccccggccc ttcaaaacct ttctgggtac tcgttgtcgt ggggtggagtt 960 ctggcctgct atagtctgct ggtgaccgtg gcgtttatca tcttctgggt aagatccaaa 1020 agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 1080 aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1140 aagttttcca gatctgcaga tgcaccagcg tattcagcagg gccagaacca actgtataac 1200 gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgtag aggcaggac 1260 cctgagatgg gtggcaaacc aagacgaaaa aacccccagg aggggtctcta taatgagctg 1320 cagaaggata agatggctga agcctattct gaaataggca tgaaggaga gcggagaagg 1380 ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac 1440 gctctccaca tgcaagccct gccacctagg taa 1473
3-64	Sequences	
3-64-1	Sequence Number [ID]	64
3-64-2	Molecule Type	AA
3-64-3	Length	490
3-64-4	Features	REGION 1..490
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..490 mol_type=protein organism=synthetic construct
3-64-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI SSGGFYWSWI 60 RQHPGKGLEW IGYIHHSGST HYNPSLKSRTV TISIDTSKNL FSLRLSSVTA ADTAVYYCAS 120

		LVYCGGDCYS GFDYWQGQTL VTVSSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVS 180 FTCQASQDIN NFLNWWYQKP GKAPKLLIYD ASNLETGVPS RFSGSGSGTD FTFTISSLQP 240 EDIATYYCQQ YGNLPFTFGG GTKVEIKRAA AIEVMYPPPY LDNEKSNGTI IHVKGKHLCP 300 SPLFPGPSKP FWLVVVVGGV LACYSLLVTV AFIIFWVRSK RSRLHSDYM NMTPRRPGPT 360 RKHYQPYAPP RFAAYRSRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY DVLDKRRGRD 420 PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGDHGLYQG LSTATKDTYD 480 ALHMQUALPPR 490
3-65	Sequences	
3-65-1	Sequence Number [ID]	65
3-65-2	Molecule Type	DNA
3-65-3	Length	1407
3-65-4	Features	misc_feature 1..1407
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1407 mol_type=other DNA organism=synthetic construct
3-65-5	NonEnglishQualifier Value Residues	cagggtgcagc tgcaggaagc cgggtccggga cttgtcaagc cgtcccaaac gctgagtctg 60 acgtgtactg tctctgggtg cctctatttct tccgggggct tttatttggc ttggatcaga 120 caacaccctg gcaaagggct ggagtggata gggatatatt accactctgg gtccactcac 180 tacaacccat cattgaaatc cagagtgact atctcaatcg acacatccaa gaaccttttc 240 agcctgaggt tgtcatcagt taccgccgct gacaccgagg tgtattattg cgctctcttc 300 gtgtactgag gtggcgattg ttatagtggc ttgtactact gggggcaggg gacattgggt 360 accgtttcaa gtggaggcgg tgggtctggc gggggcggta gcggagggtg ggggagcgac 420 atacagctta cgcagagccc ctccagcctt tcagcctccg tgggggatag ggtgtccttt 480 acctgccagg ctcccagga cataaacaac ttctctcaatt ggtatcagca aaagcccggg 540 aaagcaccaa agctgctcat ctacgatgcc agcaacctgg aaaccggagt gccgtctcgc 600 ttctctggaa gtggcagtg gaccgatttc acttttaca tctcaagttt gcagccagaa 660 gacattgcaa cactactctg tcaacagtac ggcaatctcc cctttacatt tgggggggga 720 actaaagtgg agattaagcg cgctgcagcc attgaagtta tgtatccgcc cccgtatctg 780 gataacgaga aatctaattg taccataata catgtgaagg ggaagcacct ctgtccatca 840 ccgctgttcc ccggcccttc aaaacctttc tgggtactcg ttgtcgtggg tggagtctctg 900 gcctgctata gtctgctggt gaccgtggcg tttatcatct tctgggtaag atccaaaaga 960 agccgcctgc tccatagcga ttacatgaat atgactccac gccgccttgg ccccaacaag 1020 aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag cagggtgaag 1080 ttttccagat ctgcagatgc accagcgat cagcagggcc agaaccaact gtataacgag 1140 ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1200 gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag 1260 aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1320 aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1380 ctccacatgc aagccctgcc acctagg 1407
3-66	Sequences	
3-66-1	Sequence Number [ID]	66
3-66-2	Molecule Type	AA
3-66-3	Length	469
3-66-4	Features	REGION 1..469
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..469 mol_type=protein organism=synthetic construct
3-66-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGFYWSWIR QHPGKGLEWI GYIHHSGSTH 60 YNPSLKSRVT ISIDTSKNLF SLRLSSVTAA DAVYYCASL VYCGGDCYSY GFDYWQGQTLV 120 TVSSGGGGSG GGGSGGGGSD IQLTQSPSSL SASVGDRVSF TCQASQDINN FLNWWYQKPG 180 KAPKLLIYDA SNLETGVPSR FSGSGSGTDF TFTISSLQPE DIATYYCQY GNLPTFTGGG 240 TKVEIKRAAA IEVYPPPYL DNEKSNGTII HVKGKHLCP PLFPGPSKPF WLVVVVGGVL 300 ACYSLLVTVA FIIFWVRSKR SRLHSDYMN MTPRRPGPTR KHYQPYAPPR DFAAYRSRVK 360 FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ 420 KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQUALPPR 469
3-67	Sequences	
3-67-1	Sequence Number [ID]	67
3-67-2	Molecule Type	DNA
3-67-3	Length	1554
3-67-4	Features	misc_feature 1..1554
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1554 mol_type=other DNA organism=synthetic construct
3-67-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtg agttgcagga aagcgggcct ggccttgta aaccaagcca gacactgagc 120 ctgacatgca ctgtgtccgg cgggtccata tcttccgggg gtttttattg gtcctggata 180

		cgccagcatc ccgggaaaagg acttgaatgg attggtatata tccaccattc cggaagcacc 240 cactacaatc caagccttaa atcccgggtg acaatctcca tcgacacctc aaagaatctt 300 ttttccctgc ggttgtcttc agtaactgcc gccgataccg ctgtgtacta ctgtgccagc 360 ctcgtctatt gcggcggaga ttgttatctt gggttcgatt attgggggtca aggcacactg 420 gtaactgtca gcagcggagg cggcgggttc gggggcgggg gcagtggagg gggcggatct 480 gacattcagc ttacgcagtc cccatcttca cttagcgcca gcgttggcga tcgggtcagc 540 ttcacgtgtc aagcaagtca ggatatcaac aactttctta actggtacca gcagaagcca 600 ggcaaggcac ccaagttgct gatttacgat gcttctaacc tcgagacggg agtgcctagc 660 cgcttctccg ggagcggcag cggcacagac ttaccttta cgatttccag tctgcagcca 720 gaggatatag caacttatta ctgtcagcag tatggcaacc tcccttttac cttcgggtgt 780 ggcacaaaagg tcgagattaa aagagccgca gcgttgtcca actccataat gtatttttct 840 cattttgtgc ccgtctttct gcctgccaaa cctaccacca cccccgcccc acgaccacct 900 actccagccc ccaccatcgc ctcccagccc ctccagcctga ggccagaggc ttgtcgccct 960 gctgcggggg gcgctgtcca taccagagga ctcgacttcg cctgcgatat ttatatatgg 1020 gccccctcg ccggcacctg cggagtcttg ctccctgagcc ttgtgatcac gctttattgt 1080 aaccatcgga atagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact 1140 ccacgccgcc ctggcccccac aaggaaacac taccagcctt acgcaccacc tagagatttc 1200 gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag 1260 ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg 1320 gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag 1380 gagggctctc ataagagct gcagaaggat aagatggtg aagcctattc tgaaataggc 1440 atgaaaggag agcggagaag gggaaaaggg cagcaggtt tgtaccaggg actcagcact 1500 gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag gtaa 1554
3-68	Sequences	
3-68-1	Sequence Number [ID]	68
3-68-2	Molecule Type	AA
3-68-3	Length	515
3-68-4	Features	REGION 1..515
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..515 mol_type=protein organism=synthetic construct
3-68-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI SSGGFYWSWI 60 RQHPGKGLEW IGYIHHSGST HYNPSLKS RV TISIDTSKNL FSLRLSSVTA ADTAVYYCAS 120 LVYCGGDCYS GFDYWQGT L VTVSSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGRVS 180 FTCQASQDIN NFLNWYQKP GKAPKLLIYD ASNLETGVP R FSGSGSGTDF TFTISSLQPE 240 DIATYYCQYG NLPFTFGG GT KVEIKRAAL SNSIMYFSHF VPVFLPAKPT TTPAPRPPTP 300 APTIASQPLS LRPEACRPAA GGAHVTRGLD FACDIYIWAP LAGTCGVLLL SLVITLYCNH 360 RNRSKRSRL HSDYMNMP R RPGPTRKHYQ PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ 420 NQLYNELNLG RREEYDVL DK RRGDRPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK 480 GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR 515
3-69	Sequences	
3-69-1	Sequence Number [ID]	69
3-69-2	Molecule Type	DNA
3-69-3	Length	1488
3-69-4	Features	misc_feature 1..1488
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1488 mol_type=other DNA organism=synthetic construct
3-69-5	NonEnglishQualifier Value Residues	caggtgcagt tgcaggaagg cgggcctggc cttgtgaaac caagccagac actgagcctg 60 acatgcactg tgtccggcgg gtccatatct tccgggggtt tttattgggtc ctggatagcg 120 cagcatcccg ggaaaggact tgaatggatt ggatatatcc accattccgg aagcaccac 180 tacaatccaa gccttaaatc ccgggtgaca atctccatcg acacctcaaa gaatctttt 240 tccctgcggt tgtcttcagt aactgccgcc gataccgctg tgtactactg tgccagcctc 300 gtctattgcg gcggagattg ttattctggg ttcgattatt ggggtcaagg cacactggta 360 actgtcagca gcggaggcgg cggttccggg ggcgggggca gtggaggggg cggtatctgac 420 attcagctta cgagtcccc atcttactt agcgccagcg ttggcgatcg ggtagcttc 480 acgtgtcaag caagtcagga tatcaacaac ttctttaact ggtaccagca gaagccaggc 540 aaggcaccga agttgctgat ttacgatgct tctaacctcg agacgggagt gcctagccg 600 ttctccggga gcggcagcg cagagacttt accctttacga ttcccatgct tcgagccagag 660 gatatagcaa ctattactg tcagcagtat ggcaacctcc cttttacctt cgggtgtggc 720 acaaaggtcg agattaaaag agccgcagcg ttgtccaact ccataatgta tttttctcat 780 tttgtgccg tctttctgcc tgccaaacct accaccacc ccgccccacg accactact 840 ccagccccca ccatgcctc ccagcccctc agcctgaggc cagaggcttg tcgcctgct 900 gcggggggcg ctgtccatac cagaggactc gacttcgct gcgatattta tatatgggc 960 ccctcgccg gcacctcgg agtcttgct ctgagcctg tgatcacgt ttattgtaa 1020 catcggaata gatccaaaag aagccgcctg ctccatagcg attacatgaa tatgactcca 1080 cgccgccctg gcccacaa gaaacactac cagccttacg caccacctag agatttcgct 1140 gcctatcgga gcagggtgaa gttttccaga tctgcagatg caccagcgta tcagcagggc 1200 cagaaccaac tgtatacga gctcaacctg ggacgcaggg aagagtatga cgttttggac 1260

		aagcgagag gacgggaccc tgagatgggt ggcaaaccaa gacgaaaaaa ccccccaggag 1320 ggtctctata atgagctgca gaaggataag atggctgaag cctattctga aataggcatg 1380 aaaggagagc ggagaagggg aaaagggcac gacggtttgt accagggact cagcactgct 1440 acgaaggata cttatgacgc tctccacatg caagccctgc cacctagg 1488
3-70 3-70-1 3-70-2 3-70-3 3-70-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	70 AA 496 REGION 1..496 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..496 mol_type=protein organism=synthetic construct
3-70-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGFYWSWIR QHPGKGLEWI GYIHHSGSTH 60 YNPSLKSRVT ISIDTSKNLF SLRLSSVTAA DTAVYYCASL VYCGGDCYSG FDYWGQGTLV 120 TVSSGGGGSG GGGSGGGGSD IQLTQSPSSL SASVGDVRSF TCQASQDINN FLNWFYQKPG 180 KAPKLLIYDA SNLETGVPSR FSGSGSGTDF TFTISSLQPE DIATYYCQQY GNLPFTFGGG 240 TKVEIKRAAA LSNSIMYFSH FVPVFLPAKP TTTPAPRPPT PAPTIASQPL SLRPEACRPA 300 AGGAVHTRGL DFACDIYIWA PLAGTCGVLL LSLVITLYCN HRNRSKRSRL LHSDYMNMTPT 360 RRPGPTRKHY QPYAPPRDFA AYRSRVKFSR SADAPAYQQG QNQLYNELNL GRREYDVLD 420 KRRGRDPEMG GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA 480 TKDTYDALHM QALPPR 496
3-71 3-71-1 3-71-2 3-71-3 3-71-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	71 DNA 363 misc_feature 1..363 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..363 mol_type=other DNA organism=synthetic construct
3-71-5	NonEnglishQualifier Value Residues	caggtccaac tgggtgcagtc cggagccgaa gtcaagaaac caggtgcctc cgtaaagtgt 60 agttgcaaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120 cccggaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180 gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240 atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300 aggggcattg gatggcccta cttcgattac tggggtcagg gaactctggt gactgtctcc 360 agc 363
3-72 3-72-1 3-72-2 3-72-3 3-72-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	72 AA 121 REGION 1..121 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..121 mol_type=protein organism=synthetic construct
3-72-5	NonEnglishQualifier Value Residues	QVQLVQSGAE VKKPGASVKV SCKVSGYTLT ELSMHWVRQA PGKGLEWMGG FDPEDGETIY 60 AQKFQGRVTV TEDTSTDYAY MELSSLRSED TAVYYCATES RGIGWPYFDY WGQGTLVTVS 120 S 121
3-73 3-73-1 3-73-2 3-73-3 3-73-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	73 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..7 mol_type=protein organism=synthetic construct
3-73-5	NonEnglishQualifier Value Residues	GYTLTEL 7
3-74 3-74-1 3-74-2 3-74-3 3-74-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	74 AA 6 REGION 1..6 note=source = /note="Description of Artificial Sequence: Synthetic peptide"

3-74-5	NonEnglishQualifier Value Residues	source 1..6 mol_type=protein organism=synthetic construct DPEDGE	6
3-75 3-75-1 3-75-2 3-75-3 3-75-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	75 AA 12 REGION 1..12 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..12 mol_type=protein organism=synthetic construct	
3-75-5	NonEnglishQualifier Value Residues	ESRGIGWPYF DY	12
3-76 3-76-1 3-76-2 3-76-3 3-76-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	76 DNA 324 misc_feature 1..324 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..324 mol_type=other DNA organism=synthetic construct	
3-76-5	NonEnglishQualifier Value Residues	gatattcaga tgactcaatc tccttcttct ctgtccgctt ccgtgggcca tagagtgacc 60 attacttgta gggcgtcca gtcaatctcc agttattga attggtatca gcagaagccc 120 gggaaagcac ctaagctgtt gatcagcggg gcttctagcc tgaagagtgg ggtaccttca 180 cggttcagcg gaagcggag cggaaccgat ttcaccctga ctatcagcag cctgcccact 240 gaggactttg caacttacta ctgccaacag tcatacagca ctccgatcac tttcggccag 300 ggcaccggcg tcgaaatcaa gcgc 324	
3-77 3-77-1 3-77-2 3-77-3 3-77-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	77 AA 108 REGION 1..108 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..108 mol_type=protein organism=synthetic construct	
3-77-5	NonEnglishQualifier Value Residues	DIQMTQSPSS LSASVGDRVT ITCRASQSI SYLNWYQQKP GKAPKLLISG ASSLKSGVPS 60 RFGSGSGSTD FTLTISSLPP EDFATYYCQQ SYSTPITFGQ GTRLEIKR 108	
3-78 3-78-1 3-78-2 3-78-3 3-78-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	78 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-78-5	NonEnglishQualifier Value Residues	RASQSISSYL N	11
3-79 3-79-1 3-79-2 3-79-3 3-79-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	79 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct	
3-79-5	NonEnglishQualifier Value Residues	GASSLKS	7
3-80 3-80-1 3-80-2	Sequences Sequence Number [ID] Molecule Type	80 AA	

3-80-3	Length	9
3-80-4	Features	REGION 1..9
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide"
		source 1..9
		mol_type=protein
		organism=synthetic construct
3-80-5	NonEnglishQualifier Value Residues	QSYSTPIT 9
3-81	Sequences	
3-81-1	Sequence Number [ID]	81
3-81-2	Molecule Type	DNA
3-81-3	Length	1437
3-81-4	Features	misc_feature 1..1437
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"
		source 1..1437
		mol_type=other DNA
		organism=synthetic construct
3-81-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcaggtcc aactgggtgca gtccggagcc gaagtcaaga aaccaggtgc ctccgttaaa 120 gtgagttgca aagtctctgg atacactctg accgagctct ctatgcactg ggtccggcag 180 gcccccgga agggattgga atggatggc gggttcgatc ctgaggacgg agagactatc 240 tacgctcaaa aattccaggg acgagtgact gtgaccgaag acactagtac cgacactgcc 300 tacatggaac ttctctctct gcgatcagaa gataccgcag tgtactactg tgctactgaa 360 tctaggggca ttgatggccc ctacttcgat tactggggtc agggaaactct ggtgactgtc 420 tccagcggtg gaggtggcag cggtggtggc ggaagcgggg ggggcggctc tgatattcag 480 atgactcaat ctcttcttc tctgtccgct tccgtgggcg atagagtgc cattacttgt 540 agggcgtccc agtcaatctc cagttatttg aattggtatc agcagaagcc cgggaaagca 600 cctaagctgt tgatcagcgg ggcttctagc ctgaagagtg gggtagcttc acggttcagc 660 ggaagcggaa gcggaaccga ttccaccctg actatcagca gcctgccacc tgaggacttt 720 gcaacttact actgccaaac gtcatacagc actccgatca ctttcggcca gggcaccgg 780 ctcgaatca agcgcgctgc tgctttggac aatgagaagt caaacggcac catcatacat 840 gttaaaggta aacatctgtg tccttcccgc ctgttcccgc gcccttccaa accgttctgg 900 gttctgggtg tggtcggagg cgtactcgct tgctatagtc tgctggtaac tgtcgcttc 960 atcatctttt gggtagatc caaaagaagc cgctgctcc atagcgatta catgaatatg 1020 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080 ttcgtgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140 cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1200 ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260 caggaggggc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320 ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1380 actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggttaa 1437
3-82	Sequences	
3-82-1	Sequence Number [ID]	82
3-82-2	Molecule Type	AA
3-82-3	Length	478
3-82-4	Features	REGION 1..478
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"
		source 1..478
		mol_type=protein
		organism=synthetic construct
3-82-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSKVSGYTL TELSMHWVRQ 60 APGKGLEWMG GFDPEDGETI YAKFQGRVT VTEDTSTDTA YMELSSLRSE DTAVYYCATE 120 SRGIGWPYFD YWQGTLVTV SSGGGGSGGG GSGGGGSDIQ MTQSPSSLSA SVGDRVITIC 180 RASQSISSYL NWYQKPGKA PKLLISGASS LKSGVPSRFS GSGSGDFTL TISSLPEDF 240 ATYYCQSYS TPITFGQGTR LEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW 300 VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMMN TPRRPGPTRK HYQPYAPPRD 360 FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP 420 QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR 478
3-83	Sequences	
3-83-1	Sequence Number [ID]	83
3-83-2	Molecule Type	DNA
3-83-3	Length	1371
3-83-4	Features	misc_feature 1..1371
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"
		source 1..1371
		mol_type=other DNA
		organism=synthetic construct
3-83-5	NonEnglishQualifier Value Residues	cagggtccaac tgggtgcagtc cggagccgaa gtcaagaaac cagggtcctc cgtaaagtg 60

		agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120 cccggcaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180 gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240 atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300 aggggcattg gatggcccta ctctgattac tggggtcagg gaactctggt gactgtctcc 360 agcgggtggag gtggcagcgg tgggtggcga agcggggggg gcggctctga tattcagatg 420 actcaatctc cttcttctct gtccgcctcc gtgggcgata gagtgacct tacttgtagg 480 gcgtcccagt caatctccag ttatttgaat tggtatcagc agaagcccg gaaagcacct 540 aagctgttga tcagcggggc ttctagcctg aagagtgggg taccttcacg gttcagcggg 600 agcgggaagcg gaaccgattt caccctgact atcagcagcc tgccacctga ggactttgca 660 acttactact gccaacagtc atacagcact ccgatcactt tcggccaggg caccgggctc 720 gaaatcaagc gcgtgctgc tttggacaat gagaagtcaa acggcaccat catacatggt 780 aaaggtaaac atctgtgtcc ctccccgctg tcccccgcc ctccaacc gttctgggtt 840 ctgggtggtg tcggaggcgt actgcctgc tatagtctgc tggtaactgt cgccttcac 900 atcttttggg tgagatccaa aagaagccgc ctgctccata gctattacat gaatatgact 960 ccacgccgcc ctggcccccac aaggaaacac taccagcctt acgcaccacc tagagatttc 1020 gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag 1080 ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg 1140 gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag 1200 gaggggtctc ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc 1260 atgaaaggag agcggagaag gggaaaaggg cagcaggtt tgtaccaggg actcagcact 1320 gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag g 1371
3-84	Sequences	
3-84-1	Sequence Number [ID]	84
3-84-2	Molecule Type	AA
3-84-3	Length	457
3-84-4	Features	REGION 1..457
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..457 mol_type=protein organism=synthetic construct
3-84-5	NonEnglishQualifier Value Residues	QVQLVQSGAE VKKPGASVKV SCKVSGYTLT ELSMHWVRQA PGKGLEWMGG FDPEDGETIY 60 AQKFQGRVTV TEDTSTDYAT MELSSLRSED TAVYYCATES RGIGWPYFDY WQGGLTVTVS 120 SGGGGSGGGG SGGGGSIDIQ TQSPSSLSAS VGDRVITICR ASQSISSYLN WYQKPKGKAP 180 KLLISGASSL KSGVPSRFSG SGSGTDFLT ISSLPPEFDA TYQCQSYST PITFGQGTRL 240 EIKRAALDN EKSNGTIIHV KGKHLCP SPL FPGPSKPFV LVVVGGVLAC YSLLVTVAFI 300 IFWVRSKRSR LLHSDYMMNT PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ 360 GQNQLYNELN LGRREEYDVL DKRRGRDPEM GKGPRRKNPQ EGLYNELQKD KMAEAYSEIG 420 MKGERRRGKG HDGLYQLGST ATKDITYDALH MQALPPR 457
3-85	Sequences	
3-85-1	Sequence Number [ID]	85
3-85-2	Molecule Type	DNA
3-85-3	Length	1464
3-85-4	Features	misc_feature 1..1464
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1464 mol_type=other DNA organism=synthetic construct
3-85-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcaggtgc agcttgtgca gagcggggcc gaggtgaaga agccccgggc cagcgtcaaa 120 gtgtcctgta aggtcagcgg ttacaccctc accgagctga gcatgactg ggtacggcag 180 gtccccggca aaggtcttga gtggatgggt ggatttgatc cagaagatgg agagactatc 240 tacgcccaga agttccaggg ccgggtcacc gtaacagaag acacctcaac tgaccgcgt 300 tacatggagc tgagttcact gcggtccgag gacacggccg tgtattattg tgccaccgag 360 agccgcggaa tcggatggcc ttacttcgac tactggggac aggggtacact tgttacagta 420 tcatccgggg gtggcggctc tgggtggggc ggctccggag ggggtggatc agatatccaa 480 atgactcaaa gtccaagtcc cctgtctgcc tcagtcggag atagagtcac cataacctgc 540 agggcaagtc agtccatctc ctccatctc aactggtacc aacagaaacc tggaaaggcg 600 cctaagctcc tgatctccgg agcctcatct ttgaaatccg gtgtcccatc tcgcttcagt 660 ggctctggaa gcggtacaga ttttacttga accattagca gcctccacc ggaagacttt 720 gctacatatt actgccagca gtcttactca accccaatca ccttcgggca aggcaccaga 780 ctcgaaataa aaagagcagc tgctatcgag gttatgtacc caccgcgta cttggataac 840 gaaaaaagca atgggaccat cattcatgtg aagggtgaag acctttgccc tagccactg 900 tttctggcc cgagtaaac cttttgggta ctgtgtgctg tcggcggcgt gctggcctgc 960 tactcactcc tggttaccgt gcattcatc atcttttggg tgagatccaa aagaagccgc 1020 ctgctccata gcgattacat gaatatgact ccacgccgc ctggcccccac aaggaaacac 1080 taccagcctt acgcaccacc tagagatttc gctgcctat ggagcagggt gaagttttcc 1140 agatctgcag atgcaccagc gtatcagcag gccagaaacc aactgtataa cgagctcaac 1200 ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1260 ggtggcaaac caagacgaaa aaacccccag gagggctctc ataatgagct gcagaaggat 1320 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

		cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440 atgcaagccc tgccacctag gtaa 1464
3-86	Sequences	
3-86-1	Sequence Number [ID]	86
3-86-2	Molecule Type	AA
3-86-3	Length	487
3-86-4	Features	REGION 1..487
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..487 mol_type=protein organism=synthetic construct
3-86-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSKVSGYTL TELSMHWVRQ 60 APGKGLEWMG GFDPEDGETI YAKKFQGRVT VTEDTSTDTA YMELSSLRSE DTAVYYCATE 120 SRGIGWPYFD YWQGTLVTV SSGGGGSGGG GSGGGGSDIQ MTQSPSSLSA SVGDRVITITC 180 RASQSISSYL NWYQKPGKA PKLLISGASS LKSGVPSRFS GSGSGTDFTL TISSLPPEDF 240 ATYYCQSYS TPITFGQGR LEIKRAAAIE VMYPYPYLDN EKSNGTIIHV KGKHLCP SPL 300 FPGPSKPFVW LVVVGGLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT PRRPGPTRKH 360 YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM 420 GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDITYDALH 480 MQALPPR 487
3-87	Sequences	
3-87-1	Sequence Number [ID]	87
3-87-2	Molecule Type	DNA
3-87-3	Length	1398
3-87-4	Features	misc_feature 1..1398
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1398 mol_type=other DNA organism=synthetic construct
3-87-5	NonEnglishQualifier Value Residues	cagggtgcagc ttgtgcagag cggggccgag gtgaagaagc ccggggccag cgtcaaagtg 60 tcctgtaagg tcagcgggta caccctcacc gagctgagca tgcactgggt acggcagggt 120 cccggaag gtcttgagtg gatgggtgga ttgatccag aagatggaga gactatctac 180 gccagaagt tccagggccg ggtcaccgta acagaagaca cctcaactga caccgcttac 240 atggagctga gttcactcgc gtcgaggac acggccgtgt attattgtgc caccgagagc 300 cgcggaatcg gatggcctta cttcgactac tggggacagg gtacacttgt tacagtatca 360 tccgggggtg gcggctctgg tggggcggc tccggagggg gtggatcaga tatccaaatg 420 actcaaagtc caagttccct gtctgcctca gtcggagata gagtcaccat aacctgcagg 480 gcaagtcagt ccatctcctc ctatctgaac tggtagaac agaaacctgg aaaggcgccct 540 aagctcctga tctccggagc ctcatctttg aaatccgggtg tcccatctcg cttcagtggc 600 tctggaagcg gtacagattt tactttgacc attagcagc tccaccgga agactttgct 660 acataattact gccagcagtc ttactcaacc ccaatcacct tcgggcaagg caccagactc 720 gaaataaaaa gacgagctgc tatcgaggtt atgtaccac cgccgtactt ggataacgaa 780 aaaagcaatg ggaccatcat tcatgtgaag ggtaagcacc ttgcccctag cccactgttt 840 cctggcccga gtaaaccctt ttgggtactt gtggtcgtcg gcggcgtgct ggcctgctac 900 tactcctggt ttaccgtcgc attcatcatc ttttgggtga gatccaaaag aagccgcctg 960 ctccatagcg attacatgaa tatgactcca cgccgcctg gccccacaag gaaacactac 1020 cagccttacg caccacctag agatttcgct gcctatcgga gcagggtgaa gttttccaga 1080 tctgcagatg caccagcgtg tcagcagggc cagaaccaac tgtataacga gctcaacctg 1140 ggacgcaggg aagagtatga cgttttggac aagcgcagag gacgggaccc tgagatgggt 1200 ggcaaaccaa gacgaaaaaa cccccaggag ggtctctata atgagctgca gaaggataag 1260 atggctgaag cctattctga aataggcatg aaaggagagc ggagaagggg aaaagggcac 1320 gacggtttgt accagggact cagcactgct acgaaggata cttatgacgc tctccacatg 1380 caagccctgc cacctagg 1398
3-88	Sequences	
3-88-1	Sequence Number [ID]	88
3-88-2	Molecule Type	AA
3-88-3	Length	466
3-88-4	Features	REGION 1..466
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..466 mol_type=protein organism=synthetic construct
3-88-5	NonEnglishQualifier Value Residues	QVQLVQSGAE VKKPGASVKV SCKVSGYTLT ELSMHWVRQA PGKGLEWMGG FDPEDGETIY 60 AQKFQGRVTV TEDTSTDYAY MELSSLRSED TAVYYCATES RGIGWPYFDY WGQGLTVTVS 120 SGGGGSGGGG SGGGGSDIQM TQSPSSLSAS VGDRVITICR ASQSISSYLN WYQKPGKAP 180 KLLISGASSL KSGVPSRFSG SSGTDFTLT ISSLPPEFDA TYCQSYS PITFGQTRL 240 EIKRAAAIEV MYPPPYLDNE KSNGTIIHV KGHLCPSPLF PGPSKPFVWL VVVGGLV LACY 300 SLLVTVAFI FWVRSKRSRL LHSDYMNMT PRRPGPTRKH QPYAPPRDFA AYRSRVKFSR 360 SADAPAYQQG QNQLYNELNL GRREEYDVL D KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 420

		MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDLYDALHM QALPPR	466
3-89	Sequences		
3-89-1	Sequence Number [ID]	89	
3-89-2	Molecule Type	DNA	
3-89-3	Length	1545	
3-89-4	Features	misc_feature 1..1545	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..1545	
		mol_type=other DNA	
		organism=synthetic construct	
3-89-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccggttggcat tgctcctgca cgccgcacgc 60 ccgcaggtgc agttggtgca aagcggcgca gaagttaaga aacctggggc gtcagttaag 120 gtgtcttgca aagtatctgg ctataccctc actgagctgt ccatgcattg ggtaaggcag 180 gctcctggaa aggggctcga atggatggga ggatttgacc ctgaagacgg agagaccatc 240 tacgcccaga aattccaggg tagagtaaca gtgactgagg acactagcac tgacacagcg 300 tacatggagc tgagttctct gagaagttag gacacagccg ttactactct cgctaccgag 360 tccagaggta ttggctggcc atacttcgac tattggggtc agggcaccct ggttacagtg 420 agttcaggag gcgggggctc tggggggggc gggtccggag ggggggggctc agatatacac 480 atgacgcaga gtccatcaag tctctcagcc agcgtgggag atcgcgtgac tattacttgc 540 cgcgccagcc agagtattag ctctatctg aattggtagc agcaaaagcc cgggaaggcc 600 cctaagcttc tgatttctgg cgctctctt ttgaagttag gtgtgccaag cagatttagc 660 gggtctggaa gtggcactga ctttacactt actatctcca gcctgcccc agaggatttt 720 gccacatatt actgtcagca aagctactct actccaatca ctttcggcca gggcacaaga 780 ttggagatta agagggtgc cgcacttcca aattccatca tgtatttcag ccattttgtg 840 cctgtttttc ttccggccaa acctacaacc actcccggcc cagcggccacc tactcccgcc 900 cctaccattg cctcccagcc tctgtctctt agacctgagg cttgtagacc tgctgccggc 960 ggagccgtgc acactcgcg tctggacttc gcctgcgaca tctatatctg ggcccctctg 1020 gccggcacct gcggcgctct cttctctcca ctcgtaatca cactctattg caatcacagg 1080 aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1140 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1200 cggagcaggg tgaggttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1260 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1320 agaggacggg accctgagat ggggtggcaa ccaagacgaa aaaaccccca ggagggtctc 1380 tataatgagc tgcaagaaga taagatggct gaagcctatt ctgaaatagg catgaaagga 1440 gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1500 gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1545	
3-90	Sequences		
3-90-1	Sequence Number [ID]	90	
3-90-2	Molecule Type	AA	
3-90-3	Length	514	
3-90-4	Features	REGION 1..514	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..514	
		mol_type=protein	
		organism=synthetic construct	
3-90-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSKVSGYTL TELSMHWVRQ 60 APGKGLEWMG GFDPEDGETI YAKKFQGRVT VTEDTSTDTA YMELSSLRSE DTAVYYCATE 120 SRGIGWPYFD YWGQGLVTV SSGGGGSGGG GSGGGGSDIQ MTQSPSSLSA SVGDRVITITC 180 RASQSISSYL NWYQKPKGA PKLLISGASS LKSGVPSRFS GSGSGDFTL TISSLPEDF 240 ATYYCQSYS TPITFGQTR LEIKRAAALS NSIMYFSHFV PVFLPAKPTT TPAPRPPTPA 300 PTIASQPLSL RPEACRPAAG GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCNHR 360 NRSKRSRLH SDYMNMPRR PGPTRKHYQP YAPPRDFAAY RSRVKFSRSA DAPAYQQQN 420 QLYNELNLGR REEYDVLDR RGRDPEMGGK PRRKNPQEGE YNELQKDKMA EAYSEIGMKG 480 ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 514	
3-91	Sequences		
3-91-1	Sequence Number [ID]	91	
3-91-2	Molecule Type	DNA	
3-91-3	Length	1479	
3-91-4	Features	misc_feature 1..1479	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..1479	
		mol_type=other DNA	
		organism=synthetic construct	
3-91-5	NonEnglishQualifier Value Residues	caggtgcagt tggtgcaag cggcgcgaaa gttaagaaac ctggggcgctc agttaagggtg 60 tcttgcaag tatctggcta taccctcact gagctgtcca tgcatgggtt aaggcaggct 120 cctggaaagg ggctcgaat gatgggagga ttgacctg aagacggaga gaccatctac 180 gccagaaaat tccagggtag agtaacagt actgaggaca ctgactga cacagcgta 240 atggagctga gttctctgag aagtgaggac acagccgttt actactgcgc taccgagtcc 300 agaggatttg gctggccata cttcgactat tggggtcagg gcaccctggt tacagtgagt 360	

		tcaggaggcg ggggctctgg ggggggcggt tccggagggg ggggctcaga tatacagatg 420 acgcagagtc catcaagtct ctccagccagc gtgggagatc gcgtgactat tacttgccgc 480 gccagccaga gtattagctc ctatctgaat tggtagcagc aaaagcccgg gaaggccctt 540 aagcttctga tttctggcgc ctctctcttg aagtcagggtg tgccaagcag atttagcggg 600 tctggaagtg gactgactt tacacttact atctccagcc tgccccaga ggattttgcc 660 acatattact gtcagcaaa gctacttact ccaatcactt tcggccaggg cacaagattg 720 gagattaaga gggctgccgc actttcaaat tccatcatgt atttcagcca ttttgtgcct 780 gtttttcttc cggccaaacc tacaaccact cccgcccac gccacctac tcccgccctt 840 accattgcct cccagcctct gtctcttaga cctgaggctt gtagacctgc tgccggcgga 900 gccgtgcaca ctgcgggtct ggacttcgcc tgcgacatct atatctgggc ccctctggcc 960 ggcacctgcg gcgttctcct tctctcactc gtaatcacac tctattgcaa tcacaggaac 1020 agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 1080 ggccccacaa ggaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1140 agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1200 ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgccaga 1260 ggacgggacc ctgagatggg tggcaaacca agacgaaaa acccccagga gggctcttat 1320 aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1380 cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat 1440 acttatgacg ctctccacat gcaagccctg ccacctagg 1479
3-92 3-92-1 3-92-2 3-92-3 3-92-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	92 AA 493 REGION 1..493 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..493 mol_type=protein organism=synthetic construct
3-92-5	NonEnglishQualifier Value Residues	QVQLVQSGAE VKKPGASVKV SCKVSGYTLT ELSMHWVRQA PGKGLEWMGG FDPEDGETIY 60 AQKFQGRVTV TEDTSTDYAY MELSSLRSED TAVYYCATES RGIGWPYFDY WGQGLVTVTS 120 SGGGSGGGG SGGGSDIQM TQSPSSLSAS VGDRVITICR ASQSISSYLN WYQKPGKAP 180 KLLISGASSL KSGVPSRFSG SSGGTDFTLT ISSLPPEDEFA TYQCQSYST PITFGQGTRL 240 EIKRAAALSN SIMYFSHFVP VFLPAKPTTT PAPRPPTPAP TIASQPLSLR PEACRPAAGG 300 AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCNHRN RSKRSRLHS DYMNMTPRRP 360 GPTRKHYQPY APPRDFAAAY SRVKFSRSAD APAYQQGQNY LYNELNLGRR EEDVLDKRR 420 GRDPEMGGKP RRKNPQEGLY NELQDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD 480 TYDALHMQAL PPR 493
3-93 3-93-1 3-93-2 3-93-3 3-93-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	93 DNA 351 misc_feature 1..351 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..351 mol_type=other DNA organism=synthetic construct
3-93-5	NonEnglishQualifier Value Residues	caggtccagt tggtcgaaag tggcggtggt gtagtcagc cgggccgcag tttgaggctt 60 tcctgtgcgg cttcaggctt tactttttcc agctatggaa tgcactgggt gcggcaggcc 120 cccggaag gacttgagt ggtggccgtc atttcttatg acggatcaga taagtactac 180 gtggacagcg tcaagggcag atccaccatc tctagggaca acagtaaaaa tagactctac 240 ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300 tatagtggca gagactactg ggggcagggc acactcgta cagtgaagtag c 351
3-94 3-94-1 3-94-2 3-94-3 3-94-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	94 AA 117 REGION 1..117 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..117 mol_type=protein organism=synthetic construct
3-94-5	NonEnglishQualifier Value Residues	QVQLVESGGG VVQGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV ISYDGS DKYY 60 VDSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCARER YSGRDYWGQG TLVTVSS 117
3-95 3-95-1 3-95-2 3-95-3 3-95-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	95 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"

3-95-5	NonEnglishQualifier Value Residues	source 1..7 mol_type=protein organism=synthetic construct GFTFSSY	7
3-96 3-96-1 3-96-2 3-96-3 3-96-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	96 AA 6 REGION 1..6 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..6 mol_type=protein organism=synthetic construct	
3-96-5	NonEnglishQualifier Value Residues	SYDGSD	6
3-97 3-97-1 3-97-2 3-97-3 3-97-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	97 AA 8 REGION 1..8 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..8 mol_type=protein organism=synthetic construct	
3-97-5	NonEnglishQualifier Value Residues	ERYSGRDY	8
3-98 3-98-1 3-98-2 3-98-3 3-98-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	98 DNA 324 misc_feature 1..324 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..324 mol_type=other DNA organism=synthetic construct	
3-98-5	NonEnglishQualifier Value Residues	gagattgtta tgaccagag tcttgcgacc ctctcagtca gccccgggga ggcgcgaact 60 ttgtcttgca gagctagtca gtcggtgtcc tctcttctga catggtacca gcaaaagccc 120 gggcaggctc cgcgcctttt gatctttggg gcttcaacaa gagccactgg gattcccgca 180 cgattctctg gctccggggag cggtagctgg ttcaccctga cgattagcag tctccagagc 240 gaggacttcg ccgtatacta ctgccagcag tacgatacgt ggccattcac ttttggacca 300 gggactaaag tggattttaa gcgc 324	
3-99 3-99-1 3-99-2 3-99-3 3-99-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	99 AA 108 REGION 1..108 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..108 mol_type=protein organism=synthetic construct	
3-99-5	NonEnglishQualifier Value Residues	EIVMTQSPAT LSVSPGERAT LSCRASQSVS SLLTWYQQKP GQAPRLLIFG ASTRATGIPA 60 RFSGSGSGTG FTLTISSLQS EDFAVYQCQ YDTWPFTFGP GTKVDFKR 108	
3-100 3-100-1 3-100-2 3-100-3 3-100-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	100 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-100-5	NonEnglishQualifier Value Residues	RASQSVSSLL T	11
3-101 3-101-1 3-101-2	Sequences Sequence Number [ID] Molecule Type	101 AA	

3-101-3	Length	7
3-101-4	Features Location/Qualifiers	REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct
3-101-5	NonEnglishQualifier Value Residues	GASTRAT 7
3-102	Sequences	
3-102-1	Sequence Number [ID]	102
3-102-2	Molecule Type	AA
3-102-3	Length	9
3-102-4	Features Location/Qualifiers	REGION 1..9 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..9 mol_type=protein organism=synthetic construct
3-102-5	NonEnglishQualifier Value Residues	QQYDTWPFT 9
3-103	Sequences	
3-103-1	Sequence Number [ID]	103
3-103-2	Molecule Type	DNA
3-103-3	Length	1425
3-103-4	Features Location/Qualifiers	misc_feature 1..1425 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1425 mol_type=other DNA organism=synthetic construct
3-103-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtcc agttggtcga aagtggcggg ggtgtagtgc agccggggccg cagtttgagg 120 ctttcctgtg cggttcagg ctttactttt tccagctatg gaatgcactg ggtgcggcag 180 gcccccgga aaggacttga gtgggtggcc gtcatttctt atgacggatc agataagtac 240 tacgtggaca gcgtcaaggg cagattcacc atctctaggg acaacagtaa aaatagactc 300 tacctccaga tgaatagcct cagagctgaa gacacggccg tctactattg tgctcgggag 360 cggtatagtg gcagagacta ctggggggcag ggcacactcg ttacagttag tagcggcgga 420 ggagggagtg ggggcggtggt ctccggtgga ggaggttctg agattgttat gaccagagt 480 cctgcgaccc tctcagtcag ccccggggag cgcgcaactt tgtcttgtag agctagttag 540 tccgtgtcct ctcttctgac atgggtaccag caaaagcccg ggcaggctcc ggccttttg 600 atctttgggg ctcaacaag agccactggg attcccgcac gattctctgg ctccgggagc 660 ggtagctggt tcaccctgac gattagcagt ctccagagcg aggcattcgc cgtatactac 720 tgccagcagt acgatactg gccattcact tttggaccag ggactaaagt ggattttaag 780 cgcgccgccc ctctcgataa cgaaaagtca aatggcacca taatccacgt caaaggcaag 840 cacctgtgcc cttccccgct ctccccgga cccagtaaac cattttgggt gctggttgtt 900 gtggggggcg tgctggcctg ctatagcctt ttggtcactg tagccttcat tattttttgg 960 gtcagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1020 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080 cggagcaggg tgaagtttcc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1200 agaggacggg accctgagat ggttggaaca ccaagacgaa aaaaccccca ggagggtctc 1260 tataatgagc tgcaagaaga taagatggct gaagcctatt ctgaaatagg catgaaagga 1320 gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1380 gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1425
3-104	Sequences	
3-104-1	Sequence Number [ID]	104
3-104-2	Molecule Type	AA
3-104-3	Length	474
3-104-4	Features Location/Qualifiers	REGION 1..474 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..474 mol_type=protein organism=synthetic construct
3-104-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ 60 APKGKLEWVA VISYDGS DKY YVDSVKGRFT ISRDNSKNRL YLQMNSLRAE DTAVYYCARE 120 RYSGRDYWGQ GTLTVVSSGG GSGSGGSGSG GGSEIVMTQS PATLSVSPGE RATLSCRASQ 180 SVSSLLTWYQ QKPGQAPRLI IFGASTRATG IPARFSGSGS GTGFTLTISS LQSEDAFVYY 240 CQQYDTWPFT FPGTKVDFK RAAALDNEKS NGTIIHVKGK HLCPSPLFPG PSKPFWVLV 300 VGGVLACYSL LVTVAFIIFW VRSKRSLRH SDYMNMTPRR PGPTRKHYQP YAPPRDFAAY 360 RSRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDR RGRDPEMGGK PRRKNPQEG 420 YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 474

3-105	Sequences	
3-105-1	Sequence Number [ID]	105
3-105-2	Molecule Type	DNA
3-105-3	Length	1359
3-105-4	Features	misc_feature 1..1359
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1359 mol_type=other DNA organism=synthetic construct
3-105-5	NonEnglishQualifier Value Residues	cagggtccagt tggtcgaaa tggcgggtggt gtagtgacgc cgggccgcag tttgaggctt 60 tcctgtgcgg cttcaggctt tactttttcc agctatggaa tgcactgggt gcggcaggcc 120 cccggcaaa gacttgagt ggtggccgtc atttcttatg acggatcaga taagtactac 180 gtggacacgc tcaagggcag attcaccatc tctagggaca acagtaaaaa tagactctac 240 ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300 tatagtggca gagactactg ggggcagggc acactcgtta cagttagtag cggcggagga 360 gggagtggg gcggtggctc cggtggagga ggttctgaga ttgttatgac ccagagtcct 420 gcgaccctct cagtcagccc cggggagcgc gcaactttgt cttgcagagc tagtcagtc 480 gtgtcctctc ttctgacatg gtaccagcaa aagcccgggc aggtcccgcg ccttttgatc 540 tttggggctt caacaagagc cactgggatt ccgcacgat tctctggctc cgggagcgg 600 actgggttca cctgacgat tagcagtctc cagagcgag acctcgccgt actactatgc 660 cagcagtagc atacgtggcc attcactttt ggaccaggga ctaaagtgg ttttaagcgc 720 gccgccgtc tcgataacga aaagtcaaat ggcaccataa tccacgtcaa aggcaagcac 780 ctgtgccctt cccgctctt ccccgagccc agtaaaccat ttgggtgct ggttgttgtg 840 gggggcgtgc tggcctgcta tagccttttg gtcactgtag ccttcattat tttttgggtc 900 agatccaaaa gaagccgctt gtcctatagc gattacatga atatgactcc acgccgccct 960 ggccccacaa ggaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020 agcagggtag agttttccag atctgcagat gcaccagcgt atcagcagg ccagaaccaa 1080 ctgtataacg agtcaacct gggacgcagg gaagagtatg acgttttgg caagcgacga 1140 ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggctctat 1200 aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260 cggagaagg gaaaagggca cgacggttg taccagggac tcagcactgc tacgaaggat 1320 acttatgacg ctctccacat gcaagccctg ccacctagg 1359
3-106	Sequences	
3-106-1	Sequence Number [ID]	106
3-106-2	Molecule Type	AA
3-106-3	Length	453
3-106-4	Features	REGION 1..453
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..453 mol_type=protein organism=synthetic construct
3-106-5	NonEnglishQualifier Value Residues	QVQLVESGGG VVQPGSRSLR SCAASGFTFS SYGMHWVRQA PGKGLEWVAV ISYDGS DKYY 60 VDSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCARER YSGRDYWGQG TLVTYSSGGG 120 GSGGGGSGGG GSEIVMTQSP ATLSVSPGER ATLSCRASQS VSSLLTWYQQ KPGQAPRLLI 180 FGASTRATGI PARFSGSGSG TGFTLTISL QSEDAVYYV QYDTWPFTF GPGTKVDFKR 240 AAALDNEKSN GTIIHVKGKH LCPSPFPGP SKPFWLVVV GGVLCYSLV VTVAFIIFWV 300 RSKRSLRLHS DYMNMTPRRP GPTRKHYQPY APPRDFAYR SRVKFSRSAD APAYQQGQNQ 360 LYNELNLGRR EEDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQDKMAE AYSEIGMKGE 420 RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR 453
3-107	Sequences	
3-107-1	Sequence Number [ID]	107
3-107-2	Molecule Type	DNA
3-107-3	Length	1452
3-107-4	Features	misc_feature 1..1452
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1452 mol_type=other DNA organism=synthetic construct
3-107-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtc agctcgtgga gtctggcggc gccgtggtcc agccccggcg gtccctgcgc 120 ctgtcctgcg ccgccagcgg gtttactttt tcctcctacg gcatgcactg ggtgcgccag 180 gtccccggca agggcctcga gtgggtcgcc gtgatctcat acgatgggtc agacaatac 240 tatgtcgatt ctgttaaaag gcggtttacc atttcaagag ataactctaa gaataggctg 300 tatttgcaga tgaacagcct gagggctgaa gataccgcag tgtactattg cgctaggagg 360 cggtatagtg gccgcgatta ctggggacag ggtacactgg tgaccgtgag ctctgggggt 420 ggcggaagcg ggggtggcgg aagcggcgga gggggtagtg aaattgtgat gaccagtc 480 ccggctacac tttcagtcct ccctggggag agagctacac tgtcatgcag agcgtccag 540 tccgtctctt ctctccttac ctggtatcag cagaagccc gccaggctcc tcgactgctg 600 atcttcggtg cctccacaag ggcgaccggg attccagccc gcttctcagg ttctgggagc 660

		ggaactggtt tcactttgac aatcagttca ctgcagtcag aggatttcgc cgtgtactac 720 tgccagcaat acgacacatg gccattcact ttcggaccgc gtaccaaaagt cgattttcaag 780 agagccgcgc ccacgcaggt tatgtaccca ccaccatact tggacaatga aaaaagcaat 840 ggaaccatta tccatgtgaa gggtaaacac ctctgcccta gccacttttt ccctggccca 900 tcaaagccct tctgggtcct ggtgggtcgt ggggggtgtgc tggcctgtta cagccttctg 960 gtgacggttg ctttcattat cttctgggtt agatccaaaa gaagccgcct gctccatagc 1020 gattacatga atatgactcc acgccgccct ggccccacaa ggaacacta ccagccttac 1080 gcaccaccta gagatttcgc tgccatcgcg agcagggtga agttttccag atctgcagat 1140 gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200 gaagagtatg acgttttga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260 agacgaaaaa acccccagga ggtctctat aatgagctgc agaaggataa gatggctgaa 1320 gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380 taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440 ccacctaggt aa 1452
3-108 3-108-1 3-108-2 3-108-3 3-108-4 3-108-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	108 AA 483 REGION 1..483 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..483 mol_type=protein organism=synthetic construct MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ 60 APGKGLEWVA VISYDGS DKY YVDSVKGRFT ISRDNSKNRL YLQMNSLRAE DTAVYYCARE 120 RYSGRDYWGQ GTLVTVSSGG GSGSGGSGSGG GGSEIVMTQS PATLSVSPGE RATLSCRASQ 180 SVSLLTWTYQ QKPGQAPRLL IFGASTRATG IPARFSGSGS GTGFTLTISS LQSEDFAVYY 240 CQQYDTPFT FPGTKVDFK RAAAEVMP PPYLDNEKSN GTIIHVKGKH LCPSPLFPGP 300 SKPFWLVVV GGLVACYLL VTAFIIFWV RSKRSRLHS DYMNMTPRRP GPTRKHYQPY 360 APPRDFAAYR SRVKFSRSAD APAYQQGQNG LYNELNLGRR EEYDVLDRR GRDPEMGGKP 420 RRKNPQEGLY NELQDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL 480 PPR 483
3-109 3-109-1 3-109-2 3-109-3 3-109-4 3-109-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	109 DNA 1386 misc_feature 1..1386 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1386 mol_type=other DNA organism=synthetic construct caggtgcagc tcgtggagtc tggcggcggc gtggtccagc ccggccggtc cctgcgcctg 60 tcctgcgcgc ccagcgggtt tactttttcc tcctacggca tgcactgggt gcgccaggct 120 cccggcaagg gcctcagtg ggtcgccgtg atctcatacg atgggtcaga caaatactat 180 gtcgattctg ttaaaggcg gttaccatt tcaagagata actctaagaa taggctgtat 240 ttgcagatga acagcctgag ggctgaagat accgcagtgt actattgcgc tagggagcgg 300 tatagtggcc gcgattactg gggacagggt acactggtga ccgtgagctc tgggggtggc 360 ggaagcgggg gtggcggaag cggcggaggg ggtagtgaat ttgtgatgac ccagtcctcg 420 gctacacttt cagtctcccc tggggagaga gctacactgt catgcagagc gtcccagtc 480 gtctcttctc tccttacctg gtatcagcag aagcccggcc aggctcctcg actgtgatc 540 ttcggtgccct ccacaaggcg gaccgggatt ccagcccgtc tctcagggtt tgggagcgga 600 actggtttca ctttgacaat cagttcactg cagtcagagg atttcgccgt gtactactgc 660 cagcaatacg acacatggcc attcactttc ggaccgggta ccaaagtga tttcaagaga 720 gccgcggcca tcgaggttat gtaccacca ccatatctg acaatgaaaa aagcaatgga 780 accattatcc atgtgaaggg taaacacctc tgccctagcc cacttttccc tggcccatca 840 aagcccttct ggtcttgggt ggtcgtgggg ggtgtgctgg cctgttacag ccttctggtg 900 acggttgctt tcattatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 960 tacatgaata tgactccacg ccgccctggc ccacaagga aacactacca gccttacgca 1020 ccacctagag atttcgtgc ctatcggagc aggggtgaagt tttccagatc tgcagatgca 1080 ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140 gagtatgacg ttttgacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1200 cgaaaaaacc ccaggagggt tctctataat gagctgcaga aggataagat ggctgaagcc 1260 tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1320 cagggactca gcactgtctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380 cctagg 1386
3-110 3-110-1 3-110-2 3-110-3 3-110-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	110 AA 462 REGION 1..462 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"

3-110-5	NonEnglishQualifier Value Residues	source 1..462 mol_type=protein organism=synthetic construct QVQLVESGGG VVQPGRSRLR SCAASGFTFS SYGMHWVRQA PGKGLEWVAV ISYDGS DKYY 60 VDSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCARER YSGRDYWGQG TLVTVSSGGG 120 GSGGGSGSGG GSEIVMTQSP ATLSVSPGER ATLSCRASQS VSSLLTWYQQ KPGQAPRLLI 180 FGASTRATGI PARFSGSGSG TGFTLTISL QSEDFAVYYC QQYDTPWFTF GPGTKVDFKR 240 AAAEVMPYP PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWLVVVG GVLACYSLLV 300 TVAFIIFWVR SKRSRLHSD YNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA 360 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGKPR RKNPQEGLYN ELQKDKMAEA 420 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 462
3-111 3-111-1 3-111-2 3-111-3 3-111-4 3-111-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	111 DNA 1533 misc_feature 1..1533 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1533 mol_type=other DNA organism=synthetic construct atggcactcc ccgtaactgc tctgctgctg ccgttggtcat tgctcctgca cgccgcacgc 60 ccgcaggtgc agttggttga atcaggaggg ggtgtggtgc aaccggctcg gtcactgcgc 120 ctcagttgtg ctgcttcggt gtttactttc agctcatatg ggatgcactg ggtacggcag 180 gctccaggta aaggcttga atgggtggcg gtgatcagct atgacggctc tgacaaatat 240 tatgtggact ccgtgaaagg cagattcacc atcagtcgag acaactcaaa gaatagactc 300 tacttgacaga tgaatagcct ccggggccgaa gatactgcag tctattattg cgcccgggag 360 cgctacagtg gaagagacta ttggggggcaa ggaactcttg tcacagtctc atctggcggc 420 ggcggcagcg gtggggcggt atctggcggg ggcggcagcg aaatcgttat gactcagagt 480 cctgccacac tgagcgtag ccctggtgag agagcaacac tttagctgcag agctagtcag 540 agtgtttcca gtcttttgac atgggtaccaa cagaagcccg gtcaagctcc acgactgctc 600 atcttcggtg catccaccgg cgcaaccggg ataccggccc ggttttcggt tttctggaagt 660 ggcacaggat tcacgctcac catttcttct ctgcagtctg aagactttgc cgtgtattac 720 tgccagcagt acgatactg gccctttacc tttggccag gtactaaagt ggattttaaa 780 cgagctgctg cactttccaa tagtattatg tacttttcac attttgtgcc cgtgttcctg 840 cctgcgaagc ctacgacaac ccagcccctc aggcgcgcca caccggcccc aactattgcc 900 tcccagccat tgtctctgag acccgaaagt tgcagacctg ctgctggagg cgccgttcac 960 acccgaggat tggatttcgc atgtgacatt tacatctggg cccctttggc cggaacctgc 1020 ggtgtgctgc tgctgtcact cgtgattaca ctttactgca accaccgaaa cagatccaaa 1080 agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 1140 aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200 aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260 gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgagc aggacgggag 1320 cctgagatgg gtggcaaac aagacgaaaa aacccccagg agggctctcta taatgagctg 1380 cagaaggata agatggctga agcctattct gaaataggca tgaaggaga gcgggagaagg 1440 ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac 1500 gctctccaca tgcaagccct gccacctagg taa 1533
3-112 3-112-1 3-112-2 3-112-3 3-112-4 3-112-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	112 AA 509 REGION 1..509 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..509 mol_type=protein organism=synthetic construct MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSRLR LSCAASGFTF SSYGMHWVRQ 60 APGKGLEWVA VISYDGS DKY YVDSVKGRFT ISRDNSKNRL YLQMNSLRAE DTA VYYCARE 120 RYSGRDYWG TLVTVSSGG GSGGGSGSGG GSEIVMTQSP ATLSVSPGER ATLSCRASQS 180 VSSLLTWYQQ KPGQAPRLLI FGASTRATGI PARFSGSGSG TGFTLTISL QSEDFAVYYC 240 QQYDTPWFTF GPGTKVDFKR AAALSNSIMY FSHFVPVFLP AKPTTTPAPR PPTPAPTIAS 300 QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCNHRNRSKR 360 SRLHSDYMN MTPRRPGPTR KHYQPYAPPR DFAAYRSRVK FSRADAPAY QQGQNQLYNE 420 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 480 KGHDGLYQGL STATKDTYDA LHMQUALPPR 509
3-113 3-113-1 3-113-2 3-113-3 3-113-4	Sequences Sequence Number [ID] Molecule Type Length Features	113 DNA 1467 misc_feature 1..1467

	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1467 mol_type=other DNA organism=synthetic construct
3-113-5	NonEnglishQualifier Value Residues	cagggtgcagt tggttgaatc aggagggggt gtggtgcaac ccggtcggtc actgcgcctc 60 agttgtgctg cttccggggt tactttcagc tcatatggga tgcactgggt acggcagggt 120 ccaggtaaag gcttggaatg ggtggcggtg atcagctatg acggctctga caaatattat 180 gtggactccg tgaaggcag attcaccatc agtcgagaca actcaaagaa tagactctac 240 ttgcagatga atagcctccg ggccgaagat actgcagtct attattgcgc ccgggagcgc 300 tacagtggaa gagactattg ggggcaagga actcttgtca cagtctcatc tggcggcggc 360 ggcagcgggt ggggcggatc tggcgggggc ggcagcga aa tcgttatgac tcagagtcc 420 gccacactga gcgttagccc tggtagagaga gcaacactta gctgcagagc tagtcagagt 480 gtttccagtc ttttgacatg gtaccaacag aagcccggtc aagctccacg actgctcatc 540 ttcgggtgcat ccaccgcgc aaccgggata cccggccggt tttccgggtc tgggaagtggc 600 acaggattca cgctcaccat tcttctctg cagtctgaag actttgccgt gtattactgc 660 cagcagtacg atacctggcc ctttacctt ggcccaggta ctaaagtgga ttttaaacga 720 gctgtgcac tttccaatag tattatgtac tttcacatt ttgtgcccg gttcctgcct 780 gcgaagccta cgacaacccc agcccctagg ccgccacac cggcccaac tattgcctcc 840 cagccattgt ctctgagacc cgaagcttgc agacctgtg ctggaggcgc cgttcacacc 900 cgaggattgg atttcgcatg tgacatttac atctgggccc ctttggccgg aacctgcggt 960 gtgctgctgc tgtcactcgt gattacactt tactgcaacc accgaaacag atccaaaaga 1020 agccgcctgc tccatagcga ttacatgaat atgactccac gccgccttgg cccacaagg 1080 aaacactacc agccttacgc accacctaga gatttcgctg cttatcgga cagggtgaag 1140 ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1200 ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggacct 1260 gagatgggtg gcaaaccaag acgaaaaaac cccaggagag gtctctataa tgagctcgag 1320 aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1380 aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1440 ctccacatgc aagccctgcc acctagg 1467
3-114	Sequences	
3-114-1	Sequence Number [ID]	114
3-114-2	Molecule Type	AA
3-114-3	Length	489
3-114-4	Features	REGION 1..489
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..489 mol_type=protein organism=synthetic construct
3-114-5	NonEnglishQualifier Value Residues	QVQLVESGGG VVQGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV ISYDGS DKYY 60 VDSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCARER YSGRDYWGQG TLVTVSSGGG 120 GSGGGSGGGG GSEIVMTQSP ATLSVSPGER ATLSCRASQS VSSLLTWYQQ KPGQAPRLLI 180 FGASTRATGI PARFSGSGSG TGFTLTISL QSEDFAVYYC QQYDTWPFTE GPGTKVDFKR 240 AAALNSIMY FSHFVPVFLP AKPTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT 300 RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCNHRNRSKR SRLHSDYMN MTPRRPGPTR 360 KHYQPYAPPR DFAAYRSRVK FSRADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQUALPPR 489
3-115	Sequences	
3-115-1	Sequence Number [ID]	115
3-115-2	Molecule Type	DNA
3-115-3	Length	1425
3-115-4	Features	misc_feature 1..1425
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1425 mol_type=other DNA organism=synthetic construct
3-115-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgtgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccggagattg tgatgacca gtcccctgct accctgtccg tcagtccggg cgagagagcc 120 accttgtcat gccgggccag ccagtccgtc agcagtctcc tgacttggtg tcagcaaaaa 180 ccagggcagg caccgcggct tttgattttt ggtgcaagca cacgcgccac tggcattcca 240 gctaggtttt ctggaagtgg atctgggaca ggcttcactc tgacaatcag tagcctcgag 300 agtgaggact ttgctgttta ctactgtcaa cagtacgaca cactggcatt caccattcggg 360 cccgccacca aggtcgactt caagaggggc ggtggagggt cagggtggtg cgggtcaggc 420 ggcgggtgggt ctcaggttca actggtggaa tcagggtggc gcgttgtcca accggggcga 480 tcacttcgac tttcctgtgc tgcctcaggc tttactttt catcctatgg gatgcactgg 540 gttcggcagg ctcccggaaa aggactcgag tgggttgag tgatctctta cgatggctca 600 gacaagtatt atgtggactc agtcaagggg agattcacaa taagccgaga caactccaaa 660 aaccgcgttt atctccagat gaacagcctt agagcggaag ataccgcggt atactactgt 720 cccgccgaga ggtattccgg cagagactac tggggacagg gcacactggt caccgtgagt 780 tctgccgcag cgctcgataa cgaaaagagc aacggaacca ttatccacgt taagggcaag 840

		cacctgtgcc ccagtccctt cttcccagga ccatctaaac ccttctgggt tctggtagta 900 gttggagggg tccttgcatt ttactccctt ttggtcaccg tcgccttcat tattttctgg 960 gtgagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1020 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080 cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1200 agaggacggg accctgagat ggggtggcaa ccaagacgaa aaaaccccca ggagggtctc 1260 tataatgagc tgacagaaga taagatggct gaagcctatt ctgaaatagg catgaaagga 1320 gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1380 gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1425
3-116	Sequences	
3-116-1	Sequence Number [ID]	116
3-116-2	Molecule Type	AA
3-116-3	Length	474
3-116-4	Features	REGION 1..474
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..474 mol_type=protein organism=synthetic construct
3-116-5	NonEnglishQualifier Value Residues	MALPVTALL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV SLLTWYQQK 60 PGQAPRLLIF GASTRATGIP ARFSGSGSGT GFTLTISLQ SEDFAVYQC QYDTWPFTFG 120 PGTKVDFKRG GGGSGGGSGG GGGSQVQLVE SGGGVQVQGR SLRLSCAASG FTFSSYGMHW 180 VRQAPGKGLE WVAVISYDGS DKYYVDSVKG RFTISRDNK NLRLYLQMSL RAEDTAVYIC 240 ARERYSGRDY WQGTLVTVS SAAALDNEKS NGTIIHVKGK HLCPSPLFPG PSKPFWLVV 300 VGGVLACYSL LVTVAFIIFW VRSKRSRLH SDYMMNTPRR PGPTRKHYQP YAPPRDFAAY 360 RSRVKFERSA DAPAYQQQN QLYNELNLGR REEYDVLDR RGRDPEMGK PRRKNPQEG 420 YNELQDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 474
3-117	Sequences	
3-117-1	Sequence Number [ID]	117
3-117-2	Molecule Type	DNA
3-117-3	Length	1359
3-117-4	Features	misc_feature 1..1359
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1359 mol_type=other DNA organism=synthetic construct
3-117-5	NonEnglishQualifier Value Residues	gagattgtga tgacccagtc cctgtctacc ctgtccgtca gtccgggcga gagagccacc 60 ttgtcatgcc gggccagcca gtccgtcagc agtctcctga ctgggtatca gcaaaaacca 120 gggcaggcac cgcggctttt gatttttggt gcaagcacac gcgccactgg cattccagct 180 aggttttctg gaagtggatc tgggacaggc ttcactctga caatcagtag cctgcagagt 240 gaggactttg ctgtttacta ctgtcaacag tacgacacct ggccattcac attcggggccc 300 ggcaccaagg tcgacttcaa gaggggcggt ggaggttcag gtggtggcgg gtcaggcggc 360 ggtgggtctc aggttcaact ggtggaatca ggtggcgcg ttgtccaacc ggggcgatca 420 cttcgacttt cctgtgctgc ctcaggcttt actttttcat cctatgggat gcactgggtt 480 cggcaggctc ccgaaaagg actcgagtgg gtgacagtga tctcttacga tggctcagac 540 aagtattatg tggactcagt caaggggaga ttcacaataa gccgagacaa ctccaaaaac 600 cgcctttatc tcagatgaa cagccttaga gcggaagata ccgcggtata ctactgtgcc 660 cgcgagaggt attccggcag agactactgg ggacaggcca cactggtcac cgtgagttct 720 gccgcagcgc tcgataacga aaagagcaac ggaaccatta tccacgttaa gggcaagcac 780 ctgtgcccc gtccctctt ccaggacca tctaaacct tctgggttct ggtagtagtt 840 ggaggggtcc ttgatgtta ctcccttttg gtcaccgtcg ccttcattat tttctgggtg 900 agatccaaaa gaagccgctt gctccatagc gattacatga atatgactcc acgccgccct 960 ggccccacaa ggaacacta ccagccttac gcaccacga gagatttcgc tgcctatcgg 1020 agcagggtga agttttccag atctgcagat gcaccagcgt atcagcagg ccagaaccaa 1080 ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttga caagcgaga 1140 ggacgggacc ctgagatggg tggcaacca agacgaaaa acccccagga gggctcttat 1200 aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260 cggagaagg gaaaaggcca cgacggtttg taccagggac tcagcactgc tacgaaggat 1320 acttatgacg ctctccacat gcaagccctg ccacctagg 1359
3-118	Sequences	
3-118-1	Sequence Number [ID]	118
3-118-2	Molecule Type	AA
3-118-3	Length	453
3-118-4	Features	REGION 1..453
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..453 mol_type=protein organism=synthetic construct
3-118-5	NonEnglishQualifier Value Residues	EIVMTQSPAT LSVSPGERAT LSCRASQSVS SLLTWYQQK GPAPRLLIFG ASTRATGIPA 60

		RFSGSGSGTG FTLTISSLQS EDFAVYYCQQ YDTWPFTEFG GTKVDFKRGG GSGGGGSGG 120 GGSQVQLVES GGGVVQPGRS LRLSCAASGF TFSSYGMHWV RQAPGKGLEW VAVISYDGS 180 KYYVDSVKGR FTISRDN SKN RLYLQMNSLR AEDTAVYYCA RERYSGRDYWG QGGLTVTVSS 240 AAALDNEKSN GTIIHVKGKH LCPSPLFPGP SKPFWLVVV GGV LACYSLL VTVAFIIFWV 300 RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY APPRDFAAAYR SRVKFSRSAD APAYQQGQNQ 360 LYNELNLGRR EEDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE 420 RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR 453
3-119	Sequences	
3-119-1	Sequence Number [ID]	119
3-119-2	Molecule Type	DNA
3-119-3	Length	1452
3-119-4	Features	misc_feature 1..1452
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1452 mol_type=other DNA organism=synthetic construct
3-119-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttgccat tgctcctgca cgccgcacgc 60 ccggagatcg tcatgacaca gaggccagct accctgagcg tgctccctgg agagagagcc 120 accctgtcct gtagggctag tcagagtgtg tccagcctcc tcacctggta tcaacagaag 180 cctggtcaag ctccccggtc gcttatcttc ggggccagca cgcgagccac aggcattccc 240 gccagattct ctggctctgg cagtggcacc gggttcactc tcacgatctc atccctgcag 300 tcagaggatt tcgctgtgta ttactgtcag cagtacgata catggccctt caccttcggc 360 ccgggcacaa aagtagattt caagcgcggc ggccggggta gtggggggcg gggatcagga 420 ggagggggct cccaagtaca gctggttag agcggcggcg ggggtggtca gcccgggcgc 480 agcctcaggc tgagttgcgc agcatcagga ttcacattca gttcttatgg aatgcattgg 540 gtcagacagg ctcccgggaa gggccttgaa tgggtggcag tcattagcta cgacggaagc 600 gataagtact atgtggactc agttaaagg agatttacta tcagccgcga caattccaaa 660 aacagattgt atttgcagat gaactccctc agggcgagg acactgctgt atattactgc 720 gcacgagaga gatactccgg ccgagactat tggggccaag gaacattggt aactgtgagc 780 tccgccgcag ctattgaggt catgtacccc ccaccttacc tcgataatga gaagagtaat 840 gggactataa ttcacgtaaa gggcaaacac ctgtgccctt ccccgctgtt tccaggtcca 900 agtaagccgt tctgggtcct ggttgtggtg ggaggggtgc tggcctgcta ttctctgttg 960 gttaccgtgg cctttatcat tttctgggtg agatccaaaa gaagccgcct gctccatagc 1020 gattacatga atatgactcc acgcccgcct ggccccacaa ggaacacta ccagccttac 1080 gcaccaccta gagatttcgc tgccctatcg agcaggtgta agttttccag atctgcagat 1140 gcaccagcgt atcagcagg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200 gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260 agacgaaaaa acccccagga ggtctctat aatgagctgc agaaggataa gatggtctga 1320 gcctattctg aaataggcat gaaaggagag cggaaggagg gaaaagggca cgacggtttg 1380 taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440 ccacctaggt aa 1452
3-120	Sequences	
3-120-1	Sequence Number [ID]	120
3-120-2	Molecule Type	AA
3-120-3	Length	483
3-120-4	Features	REGION 1..483
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..483 mol_type=protein organism=synthetic construct
3-120-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PEIVMTQSPA TSVSPGERA TLSCRASQSV SLLTWYQQK 60 PGQAPRL LIF GASTRATGIP ARFSGSGSGT GFTLTISSLQ SEDFAVYYCQ QYDTWPFTEFG 120 PGTKVDFKRG GSGSGGGSG GGSQVQLVE SGGVVQPGR SLRLSCAASG FTFSSYGMHW 180 VRQAPGKGLE WAVISYDGS DKYYVDSVKG RFTISRDN SK NRLYLQMNSL RAEDTAVYYC 240 ARERYSGRDY WQGLTVTVS SAAAEVMYP PPYLDNEKSN GTIIHVKGKH LCPSPLFPGP 300 SKPFWLVVV GVLACYSLL VTVAFIIFWV RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY 360 APPRDFAAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR EEDVLDKRR GRDPEMGGKP 420 RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRGKGHDGL YQGLSTATKD TYDALHMQAL 480 PPR 483
3-121	Sequences	
3-121-1	Sequence Number [ID]	121
3-121-2	Molecule Type	DNA
3-121-3	Length	1386
3-121-4	Features	misc_feature 1..1386
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1386 mol_type=other DNA organism=synthetic construct
3-121-5	NonEnglishQualifier Value Residues	gagatcgta tgacacagag tccagctacc ctgagcgtgt cccctggaga gagagccacc 60

		ctgtcctgta gggctagtca gagtgtgtcc agcctcctca cctggtatca acagaagcct 120 ggtaagctc cccggctgct tatcttcggg gccagcacgc gagccacagg catcccggcc 180 agattctctg gctctggcag tggcaccggg ttcactctca cgatctcatc cctgcagtca 240 gaggatttcg ctgtgtatta ctgtcagcag tacgatacat ggcccttcac cttcggcccc 300 ggcacaaaag tagatttcaa gcgcggcggc gggggtagtg gggggcgggg atcaggagga 360 gggggctccc aagtacagct ggttgagagc ggcggcgggg tggttcagcc cgggcgcagc 420 ctcaggctga gttgcgcagc atcaggattc acattcagtt cttatggaat gcattgggtc 480 agacaggctc ccgggaaggg ccttgaatgg gtggcagtca ttagctacga cggaagcgat 540 aagtactatg tggactcagt taaagggaga ttactatca gccgcgacaa ttccaaaaac 600 agattgtatt tgcagatgaa ctccctcagg gcggaggaca ctgctgtata ttactgcgca 660 cgagagagat actccggccg agactattgg ggccaaggaa cattggtaac tgtgagctcc 720 gccgcagcta ttgaggtcat gtacccccca cttatctcgc ataatgagaa gagtaatggg 780 actataattc acgtaaaagg caaacacctg tgcccttccc cgctgtttcc aggtccaagt 840 aagccgttct gggctctggt tgtggtggga ggggtgctgg cctgctattc tctgttggtt 900 accgtggcct ttatcatttt ctgggtgaga tccaaaagaa gccgcctgct ccatagcgat 960 tacatgaata tgactccacg ccgccctggc ccacaaagga aacactacca gccttacgca 1020 ccacctagag atttcgctgc ctatcgagc aggggtgaagt tttccagatc tgcagatgca 1080 ccagcgtatc agcagggccca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140 gagtatgacg ttttggaaca gcgcagagga cgggacctg agatgggtgg caaaccaaga 1200 cgaaaaaacc ccaggagggt tctctataat gagctgcaga aggataagat ggctgaagcc 1260 tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgatc 1320 cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380 cctagg 1386
3-122 3-122-1 3-122-2 3-122-3 3-122-4 3-122-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	122 AA 462 REGION 1..462 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..462 mol_type=protein organism=synthetic construct EIVMTQSPAT LSVSPGERAT LSCRASQSVS SLLTWYQQKP GQAPRLLIFG ASTRATGIPA 60 RFSGSGSGTG FTLTISSLQS EDFAVYYCQQ YDTWPFTHGP GTKVDFKRGG GSGGGGSGG 120 GGSQVQLVES GGGVVPGRS LRLSCAASGF TFSSYGMHWV RQAPGKGLEW VAVISYDGSD 180 KYYVDSVKGR FTISRDNKSN RLYLQMNSLR AEDTAVYYCA RERYSGRDYW GQGLTIVTSS 240 AAAEIVMYPY PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWLVVVG GVLACYSLLV 300 TVAFIIFWVR SKRSRLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA 360 PAYQQGQNL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQDKMAEA 420 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 462
3-123 3-123-1 3-123-2 3-123-3 3-123-4 3-123-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	123 DNA 1533 misc_feature 1..1533 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1533 mol_type=other DNA organism=synthetic construct atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccggaaatag tgatgactca gtccccggcc accctcagcg tgtcccccg ggagcgagcg 120 accctgtcat gcagggttc ccagagtgtc agctccctgc tcaattggta tcagcaaaag 180 ccggggcagg ctccccgct cctcatcttc ggggcatcaa ctagggccac cggcattcct 240 gcaagatttt ccgggtctgg cagcggcacc ggcttcacc ttaccattag ctctctgcag 300 tctgaggact tcgccgttta ctattgtcag cagtatgata cttggccctt taccttcggt 360 cccgaacta aggtggactt caagcgcggg ggggtggat ctggaggtgg tggctccggg 420 ggcgggtgaa gccaggtcca gttggttag agcggcggcg gagtggtgca gcccgggagg 480 tccttgccgc tgagctgtgc agcctccggt ttacttttt ctagctatgg aatgcattgg 540 gtaagacagg ctcccgaaa aggcctcgag tgggtggcgg tcattagcta tgatggatct 600 gataaatact atgtgactc agttaagggt cgcttcacaa tctcaagaga caatagcaaa 660 aatagactgt acctgcagat gaatagtctg cgcgccgagg acactgccgt ctactactgc 720 gcccgcgaga gatacagcgg acgggattac tggggccagg gtacctcgt aacggtgtcc 780 tccgctgccg cccttagcaa cagcattatg tacttttctc atttcgtgcc agtctttctc 840 ccagcaaaag ccaccactac ccgggccccc aggcgccta ctctgcccc cactatcgcg 900 tctcagcctc tctccttcg gcccgaggcc tgccggccag ccgcaggggg cgccgtacat 960 actcggggtt tggatttcgc ttgcgacata tatatttggg cccctctgc cggcacatgt 1020 ggagtgtgct tcctgagctc cgttataacc ctctattgca accatagaaa catagccaaa 1080 agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgcc tggccccaca 1140 aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200 aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260 gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgag aggacgggac 1320

		cctgagatgg gtggcaaaccc aagacgaaaa aacccccagg aggggtctcta taatgagctg 1380 cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1440 ggaaaagggc acgacggttt gtaccagga ctcagcactg ctacgaagga tacttatgac 1500 gctctccaca tgcaagccct gccacctagg taa 1533
3-124 3-124-1 3-124-2 3-124-3 3-124-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	124 AA 510 REGION 1..510 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..510 mol_type=protein organism=synthetic construct
3-124-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV SLLTWYQK 60 PGQAPRLLIF GASTRATGIP ARFSGSGSGT GFTLTISLQ SEDFAVYYCQ QYDTPFTFG 120 PGTKVDFKRG GGGSGGGSGG GGSQVQLVE SGGGVVQGR SLRLSCAASG FTFSSYGMHW 180 VRQAPGKGL E WVAVISYDGS DKYYVDSVKG RFTISRDN SK NRLYLQMN SL RAEDTAVYYC 240 ARERYSGRDY WGQGLTVTS SAAALSNSIM YFSHFVPVFL PAKPTTTPAP RPPTPAPTIA 300 SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC GVLLLSLVIT LYCNHRNRSK 360 RSRLHSDY NMTPRRPGPT RKHYQPYAPP RDFSRSADAPA YQQGQQLYN 420 ELNLGRREEY DVLDKRRGRD PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMGERRR 480 GKGHDGLYQG LSTATKDTYD ALHMQALPPR 510
3-125 3-125-1 3-125-2 3-125-3 3-125-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	125 DNA 1467 misc_feature 1..1467 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1467 mol_type=other DNA organism=synthetic construct
3-125-5	NonEnglishQualifier Value Residues	gaaatagtga tgactcagtc cccggccacc ctcagcgtgt cccccgggga gcgagcgacc 60 ctgtcatgca gggcttccca gagtgtcagc tccctgctca cttggtatca gcaaaagccg 120 gggcaggctc cccgcctcct catcttcggg gcatcaacta gggccaccgg cattcctgca 180 agattttccg ggtctggcag cggcaccggc ttcaccctta ccattagctc tctgcagtct 240 gaggacttcg ccgtttacta ttgtcagcag tatgatactt ggccctttac cttcggctcc 300 ggaactaagg ttgacttcaa gcgcgggggg ggtggatctg gaggtggtgg ctccgggggc 360 ggtggaagcc aggtccagtt ggttgagagc ggcggcggag tgggtgcagcc cgggagggtc 420 ttgcggctga gctgtgcagc ctccggtttt actttttcta gctatggaat gcattgggta 480 agacaggctc ccggaagg cctcgagtgg gtggcggtca ttagctatga tggatctgat 540 aaatactatg ttgactcagt taaggggcgc ttcacaaatc caagagacaa tagcaaaaat 600 agactgtacc tgcagatgaa tagtctgcgc gccgaggaca ctgccgtgta ctactcgcgc 660 cgcgagagat acagcggacg ggattactgg ggccagggta ccctcgtaac ggtgtcctcc 720 gctgccgccc ttagcaacag cattatgtac ttttctcatt tcgtgccagt ctttctccca 780 gcaaagccca ccactacccc ggccccagg ccgcctactc ctgcccccac tatcgcgtct 840 cagcctctct ctttgcggcc cgaggcctgc cggccagcgc cagggggcgc cgtacatact 900 cggggtttgg atttcgcttg cgacatatat atttgggccc ccctcgccgg cacatgtgga 960 gtgctgtccc tgagtctcgt tataaccctc tattgaacc atagaacag atccaaaaga 1020 agccgcctgc tccatagcga ttacatgaat atgactccac gccgccttgg cccacaagg 1080 aaacactacc agccttacgc accacctaga gatttcgctg cctatcgag caggtggaag 1140 ttttccagat ctgcagatgc accagcgat cagcagggcc agaaccaact gtataacgag 1200 ctcaacctgg gacgcagga agagtatgac gttttggaca agcgcagagg acgggaccct 1260 gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag 1320 aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1380 aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1440 ctccacatgc aagccctgcc acctagg 1467
3-126 3-126-1 3-126-2 3-126-3 3-126-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	126 AA 489 REGION 1..489 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..489 mol_type=protein organism=synthetic construct
3-126-5	NonEnglishQualifier Value Residues	EIVMTQSPAT LSVSPGERAT LSCRASQSVS SLLTWYQKQP QAPRLLIFG ASTRATGIPA 60 RFSGSGSGTG FTLTISLQS EDFAVYYCQ YDTPFTFGP GTKVDFKRG GSGGGSGG 120 GGSQVQLVES GGGVVQGRS LRLSCAASGF FTFSSYGMHW RQAPGKGLEW VAVISYDGS 180 KYYVDSVKG RFTISRDN SK RLYLQMN SLR AEDTAVYYCA RERYSGRDYWG QGGLTVTVSS 240

		AAALSNSIMY FSHFVPVFLP AKPTTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT 300 RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCNHRNRSKR SRLHSDYMN MTPRRPGPTR 360 KHYQPYAPPR DFAAYRSRVK FRSADAPAY QGQGNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRR KGHGGLYQGL STATKDTYDA 480 LHMQUALPPR 489
3-127	Sequences	
3-127-1	Sequence Number [ID]	127
3-127-2	Molecule Type	DNA
3-127-3	Length	63
3-127-4	Features	misc_feature 1..63
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"
		source 1..63
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-127-5	Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccg 63
3-128	Sequences	
3-128-1	Sequence Number [ID]	128
3-128-2	Molecule Type	AA
3-128-3	Length	21
3-128-4	Features	REGION 1..21
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..21
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-128-5	Residues	MALPVTALLL PLALLHAAR P 21
3-129	Sequences	
3-129-1	Sequence Number [ID]	129
3-129-2	Molecule Type	DNA
3-129-3	Length	45
3-129-4	Features	misc_feature 1..45
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"
		source 1..45
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-129-5	Residues	ggcgggtggag gctccggagg ggggggctct ggcggagggg gctcc 45
3-130	Sequences	
3-130-1	Sequence Number [ID]	130
3-130-2	Molecule Type	AA
3-130-3	Length	15
3-130-4	Features	REGION 1..15
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..15
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-130-5	Residues	GGGGSGGGGS GGGGS 15
3-131	Sequences	
3-131-1	Sequence Number [ID]	131
3-131-2	Molecule Type	DNA
3-131-3	Length	54
3-131-4	Features	misc_feature 1..54
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"
		source 1..54
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-131-5	Residues	gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggg 54
3-132	Sequences	
3-132-1	Sequence Number [ID]	132
3-132-2	Molecule Type	AA
3-132-3	Length	18
3-132-4	Features	REGION 1..18
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..18
		mol_type=protein

3-132-5	NonEnglishQualifier Value Residues	organism=synthetic construct GSTSGSGKPG SGEGSTKG	18
3-133 3-133-1 3-133-2 3-133-3 3-133-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	133 AA 152 REGION 1..152 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..152 mol_type=protein organism=synthetic construct	
3-133-5	NonEnglishQualifier Value Residues	MLRLLLALNL FPSIQVTGNK ILVKQSPMLV AYDNAVNLSK KYSYNLFSRE FRASLHKGLD 60 SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP 120 PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KP 152	
3-134 3-134-1 3-134-2 3-134-3 3-134-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	134	
3-134-5	NonEnglishQualifier Value Residues	000	3
3-135 3-135-1 3-135-2 3-135-3 3-135-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	135	
3-135-5	NonEnglishQualifier Value Residues	000	3
3-136 3-136-1 3-136-2 3-136-3 3-136-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	136	
3-136-5	NonEnglishQualifier Value Residues	000	3
3-137 3-137-1 3-137-2 3-137-3 3-137-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	137 AA 11 MOD_RES 1 note=Any amino acid MOD_RES 5..9 note=Any amino acid MOD_RES 11 note=Any amino acid REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic peptide"	
3-137-5	NonEnglishQualifier Value Residues	organism=synthetic construct XASQXXXXXL X	11
3-138 3-138-1 3-138-2 3-138-3 3-138-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	138	
3-138-5	NonEnglishQualifier Value Residues	000	3
3-139 3-139-1 3-139-2	Sequences Sequence Number [ID] Molecule Type	139 AA	

3-139-3	Length	9	
3-139-4	Features	MOD_RES 3..6 note=Any amino acid	
	Location/Qualifiers	MOD_RES 8 note=Any amino acid	
		REGION 1..9 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..9 mol_type=protein organism=synthetic construct	
3-139-5	NonEnglishQualifier Value Residues	QXXXXPXT	9
3-140	Sequences		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	DNA	
3-140-3	Length	126	
3-140-4	Features	misc_feature 1..126	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..126 mol_type=other DNA organism=synthetic construct	
3-140-5	NonEnglishQualifier Value Residues	aagcgcggca ggaagaagct cctctacatt tttaagcagc cttttatgag gcccgtagag 60 acaacacagg aggaagatgg ctgtagctgc agatttcccg aggaggagga aggtgggtgc 120 gagctg 126	
3-141	Sequences		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	AA	
3-141-3	Length	42	
3-141-4	Features	REGION 1..42	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..42 mol_type=protein organism=synthetic construct	
3-141-5	NonEnglishQualifier Value Residues	KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC EL	42
3-142	Sequences		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	AA	
3-142-3	Length	37	
3-142-4	Features	REGION 1..37	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..37 mol_type=protein organism=synthetic construct	
3-142-5	NonEnglishQualifier Value Residues	RRDQRLPPDA HKPPGGGSFR TPIQEEQADA HSTLAKI	37
3-143	Sequences		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	AA	
3-143-3	Length	21	
3-143-4	Features	REGION 1..21	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..21 mol_type=protein organism=synthetic construct	
3-143-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR P	21
3-144	Sequences		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	AA	
3-144-3	Length	20	
3-144-4	Features	REGION 1..20	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..20 mol_type=protein organism=synthetic construct	
	NonEnglishQualifier Value		

3-144-5	Residues	GGGGS GGGGS GGGGS GGGGS	20
3-145	Sequences		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	AA	
3-145-3	Length	112	
3-145-4	Features	REGION 1..112	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..112	
		mol_type=protein	
		organism=synthetic construct	
3-145-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYKQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGDGLY QGLSTATKDT YDALHMQALP PR 112	
3-146	Sequences		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	DNA	
3-146-3	Length	1467	
3-146-4	Features	misc_feature 1..1467	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"	
		source 1..1467	
		mol_type=other DNA	
		organism=synthetic construct	
3-146-5	NonEnglishQualifier Value Residues	atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60 atcccagaca tccagatgac acagactaca tcctccctgt ctgcctctct gggagacaga 120 gtcaccatca gttgcagggc aagtcaggac attagtaaat atttaaatg gtatcagcag 180 aaaccagatg gaactgttaa actcctgata taccatacat caagattaca ctcaggagtc 240 ccatcaaggt tcagtggcag tgggtctgga acagattatt ctctcaccat tagcaacctg 300 gagcaagaag atattgccac ttacttttgc caacagggtg atacgcttcc gtacacgttc 360 ggagggggga ctaagtgtga aataacaggc tccacctctg gatccggcaa gcccggatct 420 ggcgagggat ccaccaaggc cgaggtgaaa ctgcaggagt caggacctgg cctggtggcg 480 ccctcacaga gcctgtccgt cacatgcact gtctcagggg tctcattacc cgactatggt 540 gtaagctgga ttcgccagcc tccacgaag ggtctggagt ggctgggagt aatatggggt 600 agtgaacca catactataa ttcagctctc aaatccagac tgaccatcat caaggacaac 660 tccaagagcc aagttttctt aaaaatgaac agtctgcaaa ctgatgacac agccatttac 720 tactgtgcca aacattatta ctacggtggt agctatgcta tggactactg gggtcaagga 780 acctcagtca ccgtctctc agcgccgcca attgaagtta tgtatcctcc tccttaccta 840 gacaatgaga agagcaatgg aaccattatc catgtgaaag ggaaacacct ttgtccaagt 900 cccctatttc ccggaccttc taagcccttt tgggtgctgg tgggtggttg gggagtcctg 960 gcttgctata gcttgctagt aacagtgccc tttattattt tctgggtgag gagtaagagg 1020 agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gccaccgccg 1080 aagcattacc agccctatgc cccaccagc gacttcgcag cctatcgctc cagagtgaag 1140 ttcagcagga gcgcagacgc cccgcgtac cagcagggcc agaaccagct ctataacgag 1200 ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccggggacct 1260 gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 1320 aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc 1380 aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1440 cttcacatgc aggccctgcc ccctcgc 1467	
3-147	Sequences		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	AA	
3-147-3	Length	489	
3-147-4	Features	REGION 1..489	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..489	
		mol_type=protein	
		organism=synthetic construct	
3-147-5	NonEnglishQualifier Value Residues	MLLLVTSLLL CELPHPAFL IPDIQMTQTT SLSASLGDR VTISCRASQD ISKYLNWYQQ 60 KPDGTVKLLI YHTSRLHSGV PSRFSGSGSG TDYSLTISNL EQEDIATYFC QQGNLPTYTF 120 GGGKLEITG STSGSGKPGS GEGSTKGEVK LQESGPLVA PSQSLSVTCT VSGVSLPDYG 180 VSWIRQPPRK GLEWLGVIWG SETTYNSAL KSRLTIKDN SKSQVFLKMN SLQTDDTAIY 240 YCAKHYYYGG SYAMDYWGQG TSVTVSSAAA IEVMYPPPYL DNEKSNGTII HVKGKHLCP 300 PLFPGPSKPF WLVVVGVLV ACYSLLVTVA FIIFWVRSKR SLLHSDYMN MTPRRPGPTR 360 KHYQPYAPPR DFAAYRSRVK FRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRR KGDGLYQGL STATKDTYDA 480 LHMQALPPR	
3-148	Sequences		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	DNA	
3-148-3	Length	1437	
3-148-4	Features	misc_feature 1..1437	

	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1437 mol_type=other DNA organism=synthetic construct
3-148-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgatatatc aaatgaccga gtccccgtcc tccctgagtg cctccgtcgg tgaccgtgtt 120 acgattacct gccgtgcgag ccaagacatc tctaaatacc tgaactggta tcagcaaaaa 180 ccggatcagg caccgaaact gctgatcaaa catacctcac gtctgcactc ggggtgtgccg 240 agccgccttta gtggttccgg ctcaggtacc gattacaccc tgacgatacag ctctctgcag 300 ccggaagact ttgccacgta ttactgccag caaggtaata ccctgccgta tacgttcggc 360 caaggtacca aactggaaat caaaggctcg acgagcggct ctggtaaacc gggctctggt 420 gaaggcagta ccaaaggatga agtgcagctg gttgaaagcg gtgggtgtct ggttcaaccg 480 ggtcgttccc tgcgtctgtc atgtacggcg agtgggtgtct ccctgccgga ctatggcgtg 540 tcctggattc gtcagccgcc gggtaaaagg ctggaatgga ttggtgtcat ctggggcagt 600 gaaaccacgt attacaactc ggccctgaaa agccgtttca ccatctctcg cgataacagt 660 aaaaatacgc tgtacctgca gatgaatagc ctgcgcgcgg aagacacccg cgtttactac 720 tgcgcaaaac attactacta cgggtggcagc tatgctatgg attactgggg tcaaggcacg 780 ctggtcaccg tttcgtcagc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt 840 cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctgggtccatc caagccattc 900 tgggtgttgg tcgtagtggg tggagtcctc gcttgttact ctctgtctgt caccgtggct 960 tttataatct tctgggttag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020 atgactccac gccgccttg cccacaaggg aaacactacc agccttacgc accacctaga 1080 gatttcgctg cctatcggag cagggtgaag tttccagat ctgcacatgc accagcgtat 1140 cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200 gttttgaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260 cccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320 ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380 agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctagg 1437
3-149	Sequences	
3-149-1	Sequence Number [ID]	149
3-149-2	Molecule Type	AA
3-149-3	Length	479
3-149-4	Features	REGION 1..479
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..479 mol_type=protein organism=synthetic construct
3-149-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PDIQMTQSPS SLSASVGDV TITCRASQDI SKYLNWYQQK 60 PDQAPKLLIK HTSRLHSGVP SRFSGSGSGT DYTTLTISLQ PEDFATYYCQ QGNTLPYTFG 120 QGTKLEIKGS TSGSGKPGSG EGSTKGEVQL VESGGGLVQP GRSLRLSCTA SGVSLPDYGV 180 SWIRQPPGKG LEWIGVIWGS ETTYNSALK SRFTISRDNS KNTLYLQMNS LRAEDTAVYY 240 CAKHYYYGGS YAMDYWGQGT LVTVSSAAAL DNEKSNGTII HVKGKHLCPs PLFPGPSKPF 300 WVLVVVGVL ACYSLLVTV FIIFWRSKR SLLHSDYMN MTPRRPGPTR KHYQPYAPPR 360 DFAAYRSRVK FSRADAPAY QGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRN 420 PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDYDA LHMQUALPPR 479
3-150	Sequences	
3-150-1	Sequence Number [ID]	150
3-150-2	Molecule Type	DNA
3-150-3	Length	1506
3-150-4	Features	misc_feature 1..1506
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1506 mol_type=other DNA organism=synthetic construct
3-150-5	NonEnglishQualifier Value Residues	atggccctgc ctgtgacagc tctgctgctg cccctggccc tgctgtgtgca tgccgccaga 60 cctgagatcg tgctgaccga gtctcccggc accctgtctc tcagcccagg agagagagcc 120 accctgagct gcagagccag ccagagcgtg tccagcagct acctggcctg gtatcagcag 180 aagcccgagc agggcccccag actgctgac tacggcgcca gctctagagc caccggcatc 240 cccgacagat tcagcgcgag cggcagtggc accgacttca ccctgaccat cagcagactg 300 gaacccgagg acttcgccgt gtactactgc cagcagtagc gcagcagccg gttcaccttc 360 ggccctggca ccaaggtgga catcaagggc agcacctccg gcagcggcaa gcctggctct 420 ggcgagggct ctaccaaggg ccaggtgcag ctgggtgcagt ctggcgccga agtgaagaaa 480 cccggctcta gcgtgaagggt gtcctgcaag gacagcggcg gcaccttcag cagctacgcc 540 atcagctggg tgcgccaggc cccaggacag gggctggaat ggatgggcgg catcatcccc 600 atcttcggca ccaccaacta cgcccagcag ttccagggca gagtgaccat caccgccgac 660 gagagcacca gcaccgccta catggaactg agcagcctgc ggagcgagga cacagccgtg 720 tattactgtg cccgcgaggc cgtggccgcc gactggctgg atccttgggg acagggcacc 780 ctgggtgacag tgtccagctt cgtgcccggt ttcttgcccc ccaagcctac caccacccct 840 gcccctagac ctcccacccc agccccaaca atcgccagcc agcctctgtc ctgcggcccc 900 gaagcctgta gacctgtgtc cggcggagcc gtgcacacca gaggcctgga cttcgccctg 960

		gatatctaca tctgggcccc tctggccggc acctgtggcg tgctgtgtgt gagcctgggtg 1020 atcacccctgt actgcaacca ccggaacaga agcaagcgga gccggctgtgt gcacagcgac 1080 tacatgaaca tgacccaag acggcctggc cccaccggga agcactacca gccttacgcc 1140 cctcccagag acttcgccgc ctaccggtcc agagtgaagt tcagcagatc cgccgacgcc 1200 cctgcctacc agcagggaca gaaccagctg tacaacgagc tgaacctggg cagacgggaa 1260 gagtacgagc tgctggacaa gcggagaggg cgggaccccg agatggggcg aaagcccaga 1320 cggaagaacc ccaggaagg cctgtataac gaactgcaga aagacaagat ggccgaggcc 1380 tacagcgaga tcggcatgaa gggcgagcgg aggcgcggca agggccacga tggcctgtac 1440 cagggcctga gcaccgccac caaggacacc tacgacgccc tgcacatgca ggccctgccc 1500 cccaga 1506
3-151 3-151-1 3-151-2 3-151-3 3-151-4 3-151-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	151 AA 502 REGION 1..502 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..502 mol_type=protein organism=synthetic construct MALPVTALL PLALLLHAAR PEIVLTQSPG TSLSPGERA TLSCRASQSV SSSYLAWYQQ 60 KPGQAPRLLI YGASSRATGI PDRFSGSGSG TDFTLTISR EPEDFAVYYC QYGGSSRFTF 120 GPGTKVDIKG STSGSGKPGS GEGSTKGQVQ LVQSGAEVKK PGSSVKVSK DSGGTFSSYA 180 ISWVRQAPGQ GLEWMGGIIP IFGTTNYAQQ FQGRVTITAD ESTSTAYMEL SSLRSEDVAV 240 YYCAREAVAA DWLDPWGGGT LVTVSSFVPV FLPAKPTTTP APRPPTPAPT IASQPLSLRP 300 EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCNHRNR SKRSRLHSD 360 YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNL YNELNLGRRE 420 EYDVLDKRRG RDPENGGKPR RKNPQEGLYN ELQKDKMAEA YEIGMKGER RRGKGHDGLY 480 QGLSTATKDT YDALHMQALP PR 502
3-152 3-152-1 3-152-2 3-152-3 3-152-4 3-152-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	152 DNA 1824 misc_feature 1..1824 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1824 mol_type=other DNA organism=synthetic construct atggcatgcc ctggcttcct gtgggcactt gtgactctca cctgtcttga atttagcatg 60 gctcagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gaccgtgacc 120 ctgagctgca catatgacac cagtgcagag gattattatt tattctggta caagcagcct 180 cccagcaggc agatgattct cgttattcgc caagaagcct ataagcaaca gaatgcaaca 240 gagaatcgtt tctctgtgaa cttccagaaa gcagccaaat ccttcagtc caagatctca 300 gactcacagc tgggggatgc cgcgatgat ttctgtgtct tccggagctc aggaacctac 360 aaatacatct ttggaacagg caccaggctg aagggttttag caaatatcca gaacctgaa 420 cctgctgtgt accagttaaa agatcctcgg tctcaggaca gcacctctg cctgttcacc 480 gactttgact cccaaatcaa tgtgccgaaa accatggaat ctggaacgtt catcactgac 540 aaaactgtgc tggacatgaa agctatggat tccaagagca atggggccat tgcctggagc 600 aaccagacaa gcttcacctg ccaagatatt ttcaaagaga ccaacgccac ctacccagc 660 tcagacgttc cctgtgatgc cacgttgact gagaaaagct ttgaaacaga tatgaacct 720 aactttcaaa acctgtcagt tatgggactc cgaatcctcc tgctgaaagt agccggattt 780 aacctgctca tgacgctgag gctgtgtgcc agtcgggcca agcggtcagg atccggagcc 840 accaacttca gcctgtgtaa gcaggccggc gacgtggagg agaaccctcg cccatgggc 900 accaggctcc tcttctgggt ggccttctgt ctccctgggg cagatcacac aggagctgga 960 gtctcccagt ccccgagtaa caaggtcaca gagaagggaa aggatgtaga gctcagggtg 1020 gatccaattt caggtcatac tgccctttac tggtagcgac agagcctggg gcagggcctg 1080 gagtttttaa ttactttcca aggcaacagt gcaccagaca aatcagggtt gccagtgat 1140 cgcttctctg cagagaggac tgggggatcc gtctccactc tgacgatcca gcgcacacag 1200 caggaggact cggccgtgta tctctgtgcc agcatccgga cagggccttt tttctctgga 1260 aacaccatat attttgaga gggaagtgg ctactgttg tagaggacct gagaacgtg 1320 acccacccta aggtctcctt gtttgagcca tcaaaagcag agattgcaaa caaacaaga 1380 gctaccctcg tgtgcttggc caggggcttc ttccctgacc acgtggagct gactgggtg 1440 gtgaatggca aggaggtcca cagtgggttc agcacggacc ctacggccta caaggagagc 1500 aattatagct actgcctgag cagccgcctg aggttctct ctacctctg gcacaatcct 1560 cgaaaccact tccgctgcca agtgagctc catgggcttt cagaggagga caagtggcca 1620 gagggctcac ccaaacctgt cacacagaac atcagtcgag aggcctgggg ccgagcagac 1680 tgtggaatca cttcagcatc ctatcatcag ggggttctgt ctgcaaccat cctctatgag 1740 atcctactgg ggaaggccac cctatatgct gtgctggcca gtggcctggg gctgatggct 1800 atggtcaaaa gaaagaactc atga 1824
3-153 3-153-1 3-153-2	Sequences Sequence Number [ID] Molecule Type	153 AA

3-153-3	Length	607
3-153-4	Features	REGION 1..607
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..607 mol_type=protein organism=synthetic construct
3-153-5	NonEnglishQualifier Value Residues	MACPGFLWAL VISTCLEFSM AQTVTQSQPE MSVQEAETVT LSCTYDTSES DYFLFWYKQP 60 PSRQMILVIR QEAYKQQNAT ENRFSVNFQK AAKSFSLKIS DSQLGDAAMY FCALRSSGTY 120 KYIFGTGTRL KVLANIQNPE PAVYQLKDPR SQDSTLCLFT DFDSQINVPK TMESGTFITD 180 KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL 240 NFQNLSVMGL RILLKLVAGF NLLMTLRLWS SRAKRSGSGA TNFSLLKQAG DVEENPGPMG 300 TRLLFWAFC LLGADHTGAG VSQSPSNKVT EKGKDVELRC DPISGHTALY WYRQSLGQGL 360 EFLIYFQGNS APDKSGLPSD RFSAERTGGS VSTLTIQRTQ QEDSAVYLCA SIRTGPFFSG 420 NTIYFGECSW LTVVEDLRNV TPPKVSLFEP SKAEIANKQK ATLVLCLARGF FPDHVELSWW 480 VNGKEVHSGV STDPQAYKES NYSYCLSSRL RVSATFWHNP RNHFRQVQF HGLSEEDKWP 540 EGSPKPVTON ISAEAWGRAD CGITSASYHQ GVLSATILYE ILLGKATLYA VLVSLGLVMA 600 MVKRKNS 607
3-154	Sequences	
3-154-1	Sequence Number [ID]	154
3-154-2	Molecule Type	DNA
3-154-3	Length	1437
3-154-4	Features	misc_feature 1..1437
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1437 mol_type=other DNA organism=synthetic construct
3-154-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttgccat tgctcctgca cgccgcacgc 60 ccgcaggtcc aactgcaaga aagcggaccc ggactgggtga agccttctga gacacttagt 120 ctgacgtgca cggtcagtgg cggtccatc tcctcctatt attggtcatg gatacgacaa 180 ccccaggta agggcctgga atggattggc tatacttact attcaggaag cactgaactac 240 aatcccagcc tgaagtcccg agtgacaatt tcagtagata ccagtaaaaa ccagttcagt 300 cttaaaactgt caagcgtgac agctgccgac accgctgtgt attactgcgt ctcactgggtg 360 tattgtggag gggattgtta tagcgggttc gattattggg gacaggaac cctggtgact 420 gtatcttcg gcggcggcg ctcagggggg ggcggtagtg gcgggtgggg ttccgatatt 480 caactgacac aatccccag ctcactcagc gccagcgtgg gggacagggt tagctttacc 540 tgtcaagcct ctcaggatat aaataacttt ctgaactggt atcaacagaa gcctgggaag 600 gcgccaac tcctgatcta tgatgcgtcc aacctggaaa ctggcggtgc ttacgccttt 660 agcggctctg gcagtggtac agacttcact ttaccatct cttcacttca gccggaggac 720 atcgccacat attactgtca acagtacgga aacttgccct ttacttttgg aggcggcacc 780 aaagtggaaa taaaagggc cgctgccctg gataacgaaa agagcaatgg gactataata 840 catgttaaag gaaaacacct gtgtccatct ccctgttcc ctggaccgtc aaagccattt 900 tgggtgctcg tggttgtcgg tggcgttctc gcctgttata gcttgctggt gacagtagcc 960 ttcattatct ttgggtgag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020 atgactcac gccgcctgg cccacaagg aaacactacc agccttacgc accacctaga 1080 gatttcgctg cctatcggag ccgagtgaat ttttctagat cagctgatgc tcccgcctat 1140 cagcagggac agaataact ttacaatgag ctgaacctgg gtcgcagaga agagtacgac 1200 gttttgaca aacgccggg ccgagatcct gagatgggg ggaagccgag aaggaagaat 1260 cctcaagaag gcctgtacaa cgagcttcaa aaagacaaaa tggctgaggc gtactctgag 1320 atcggcatga agggcgagcg gagacgaggc aagggtcacg atggcttcta tcagggcctg 1380 agtacagcca caaaggacac ctatgacgcc ctccacatgc aggcactgcc cccacgc 1437
3-155	Sequences	
3-155-1	Sequence Number [ID]	155
3-155-2	Molecule Type	AA
3-155-3	Length	479
3-155-4	Features	REGION 1..479
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..479 mol_type=protein organism=synthetic construct
3-155-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SSYYWSWIRQ 60 PPKGLEWIG YIYSGSTNY NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYVCVSLV 120 YCGGDCYSGF DWGQGLT VTSSGGGSGG GSGGGGSDI QLTQSPSSLS ASVGDRVSFT 180 CQASQDINN LNYYQKPGK APKLLIYDAS NLETGVPSRF SSGSGGTDFT FTISLQPED 240 IATYYCQYQ NLPFTFGGT KVEIKRAAL DNEKSGTII HVKKGHLCP PLFPGPSKPF 300 WVLVVVGVL ACYSLLVTV FIFWVRSKR SLLHSDYMN MTPRRPGPTR KHYQPYAPPR 360 DFAAYRSRVK FRSADAPAY QGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRN 420 PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHGDLVQGL STATKDTYDA LHMQLPPR 479
3-156	Sequences	
3-156-1	Sequence Number [ID]	156

3-156-2	Molecule Type	DNA
3-156-3	Length	1449
3-156-4	Features	misc_feature 1..1449
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1449 mol_type=other DNA organism=synthetic construct
3-156-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccgcagggtgc agctgggtgga gtctggggga ggcgtgggtcc agcctgggag gtcccctgaga 120 ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag 180 gtccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatc 240 tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300 tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgtcaagggg 360 ccgttgcagg agccgccata cgattatgga atggacgtat ggggccaggg aacaactgtc 420 accgtctcct cagggtctac atccggctcc gggaagcccg gaagtggcga aggtagtaca 480 aagggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540 gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600 aaacctggcc aggcctccag gtcctcatc tatagcgcat ccaccagggc cactgggtac 660 ccagccaggt tcagtggcag tgggtctggg acagagttca ctctccaccat cagcgcctg 720 cagctgaag attttgcagt ttattactgt cagcagcacc acgtctggcc tctactttt 780 ggcggaggga ccaaggttga gatcaaacgg gccgtgccc ttgataatga aaagtcaaac 840 ggaacaatca ttcacgtgaa ggcgaagcac ctctgtccgt cacccttgtt ccctggtcca 900 tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgta ctctctgctc 960 gtcaccgtgg cttttataat cttctgggtt agatccaaaa gaagccgcct gtcctatagc 1020 gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac 1080 gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140 gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200 gaagagtatg acgttttggg caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260 agacgaaaaa acccccagga ggtctctat aatgagctgc agaaggataa gatggctgaa 1320 gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380 taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440 ccacctagg 1449
3-157	Sequences	
3-157-1	Sequence Number [ID]	157
3-157-2	Molecule Type	AA
3-157-3	Length	483
3-157-4	Features	REGION 1..483
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..483 mol_type=protein organism=synthetic construct
3-157-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ 60 APKGLEWVA VISYDGSNKY YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCVKG 120 PLQEPPYDYG MDVWQGQTTV TVSSGSTSGS GKPGSGEGST KGEIVMTQSP ATLSVSPGER 180 ATLSCRASQS VSSNLAWYQQ KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL 240 QSEDAVYYC QQHVVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP 300 SKPFWVLVVV GGLVACYSLL VTVAFIIFWV RSKRSRLLS DYMNMTPRRP GPTRKHYQPY 360 APPRDFAAYR SRVKFSRSAD APAYQQGQNG LYNELNLGRR EEYDVLDKRR GRDPEMGKGP 420 RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL 480 PPR 483
3-158	Sequences	
3-158-1	Sequence Number [ID]	158
3-158-2	Molecule Type	DNA
3-158-3	Length	1900
3-158-4	Features	misc_feature 1..1900
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..1900 mol_type=other DNA organism=synthetic construct
3-158-5	NonEnglishQualifier Value Residues	atgggcacca gactgttctt ttatgtggcc ctgtgtctgc tgtggaccgg ccacatggat 60 gccggaatta cacagagccc cagacacaaa gtgaccgaga caggcaccctt tgtgacactg 120 agatgccacc agaccgagaa ccaccgtac atgtactggt acagacagga tccaggccac 180 ggcctgagac tgatccacta cagctacggc gtgaaggaca ccgacaaggg cgaagtgtct 240 gacggctaca gcgtgtccag aagcaagacc gaggatttcc tgctgaccct ggaagcgcc 300 acaagcagcc agaccagcgt gtacttttgt gccatcagcg gctacaagaa caccgaggcc 360 tttttcggcc aaggcaccag gctgacagtg gtggaagatc tgaagaacgt gttcccacct 420 gaggtggccg tgtttgagcc ttctgaggcc gagatcagcc acacacagaa agccacactc 480 gtgtgcctgg ccaccggctt ttatcccgat cacgtggaac tgtcttggtg ggtcaacggc 540 aaagagggtgc acagcggcgt tagcacagac cctcagcctc tgaaagagca gcccgcctctg 600

		aacgacagca gatactgtct gagcagcaga ctgagagtgt ccgccacctt ctggcagaac 660 cccagaaacc acttcagatg ccaggtgcag ttctacggcc tgtccgagaa tgacgagtgg 720 accagagata gagccaagcc agtgacacag attgtgtctg ccgaagcctg gggcagagcc 780 gattgtggct ttacaagcga gagctaccag cagggcgctgc tgtctgccac aatcctgtat 840 gagatcctgc tgggcaaagc cactctgtac gctgtgtctg tgtctgccct ggtgtctgatg 900 gccatggtca agagaaagga cagcagaggc agagccaaga gatctggcag cggcgccaca 960 aacttttagcc tgctgaaaca ggccggcgac gtggaagaga accctggacc tatgaagtcc 1020 ctgcgggtgc tgctggttat tctgtggctg cagctgagct gggtttggag ccagggacag 1080 caagtgatgc agatccctca gtaccagcac gtgcaagaag gcgaggactt caccacctac 1140 tgcaacagca gcacaaccct gagcaacatc cagtgggtaca agcagaggcc tggcgggac 1200 cctgtgtttc tgatccagct ggtaagagc ggcaagtgga agaagcagaa gcggctgacc 1260 tttcagttcg gcgaggccaa gaagaacagc agcctgcaca ttaccgccac acagaccacc 1320 gacgtgggca catatTTTTg cgctggcaga gaaggcgga gcgagaagct ggtttttggc 1380 aagggcacca aactgaccgt gaatcccgac attcagaacc ccgatccagc cgtgtaccag 1440 ctgagagaca gcaagagcag cgacaagagc gtgtgtctgt tcaccgactt cgactccag 1500 accaatgtgt ccagagcaa ggactccgac gtgtacatca ccgataagac cgtgtcggac 1560 atgcggagca tggacttcaa gagcaatagc gccgtggctt ggagcaacaa gagcgacttt 1620 gctctgcgca acgcttcaa caacagcatc atccccgagg acacattctt cccaagtcc 1680 gagagcagct gcgacgtgaa gctgggtgaa aagagcttcg agacagacac caacctgaac 1740 ttccagaacc tgagcgtgat cggcttcaga atcctgtctg tgaaggtggc cggcttcaac 1800 ctgctgatga ctctgagact gtgggtccagc tgaattcgga tccaagctta ggcctgtctg 1860 ctttcttgct gtcccatttc tattaaggt tcctttgttc 1900
3-159 3-159-1 3-159-2 3-159-3 3-159-4 3-159-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	159 AA 610 REGION 1..610 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..610 mol_type=protein organism=synthetic construct MGTRLFFYVA LCLLWTGHMD AGITQSPRHK VTETGTPVTL RCHQTENHRY MYWYRQDPGH 60 GLRLIHYSYG VKDSDKGEVS DGYSVSRSKT EDFLLTLESA TSSQTSVYFC AISGYKNTEA 120 FFGQGTRLTV VEDLKNVFPF EVAVFEPSEA EISHTQKATL VCLATGFYPD HVELSWVNG 180 KEVHSGVSTD PQPLKEQPAL NDSRYCLSSR LRVSATFWQN PRNHFRQVQ FYGLSENDEW 240 TQDRAKPVTQ IVSAEAWGRA DCGFTSESYQ QGVLSATILY EILLGKATLY AVLVSALVLM 300 AMVKRKDSRG RAKRSGSGAT NFSLLKQAGD VEENPGPMKS LRVLLVILWL QLSWVWSQGQ 360 QVMQIPQYQH VQEGEDFTTY CNSSTLSNI QWYKQRPGGH PVFLIQLVKS GEVKKQKRLT 420 FQFGEAKKNS SLHITATQTT DVGTYFCAGR EGGSEKLVEG KGTKLTVNPD IQNPDPVAVYQ 480 LRDSKSSDKS VCLFTDFDSQ TNVSQSKDSD VYITDKTVLD MRSMDFKSNS AVAWSNKSDF 540 ACANAFNNSI IPEDTFFPSP ESSCDVKLVE KSFETDTNLN FQNLVIGFR ILLLVKAGFN 600 LLMTLRLWSS 610
3-160 3-160-1 3-160-2 3-160-3 3-160-4 3-160-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	160 DNA 1906 misc_feature 1..1906 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..1906 mol_type=other DNA organism=synthetic construct atgggacctg gattgctttg ttggggccctg ctgtgtctgc ttggagctgg acttgtggat 60 gccggcgtag cacagtctcc cacacacctg atcaagacca gaggccagca agtgaccctg 120 agatgtagcc ctaagagcgg ccacgacacc gtgtcttggg atcagcaggc tcttgccag 180 ggacctcagt tcatcttcca gtactacgag gaagaggaac ggcagcgggg caacttcct 240 gatagattct ctggccatca gttccccaac tacagcagcg agctgaacgt gaacgctctg 300 ctgctgggag atagcgccct gtatctgtgt gccagttctc ttggttggag aggcggcaga 360 tacaacgagc agttctttgg ccctggcacc agactgaccg tgctggaaga tctgaagaac 420 gtgttccac ctgaggtggc cgtgtttgag ccttctgagg ccgagatcag ccacacacag 480 aaagccacac tcgtgtgctt ggcaccggc ttttatccc atcactgga actgtcttgg 540 tggttcaacg gcaagaggtt gcacagcggc gttagcacag accctgagcc tctgaagag 600 cagcccgctc tgaacgacag cagatactgt ctgagcagca gactgagagt gtccgccacc 660 ttctggcaga accccagaaa ccacttcaga tgccaggtgc agttctacgg cctgtccag 720 aatgacgagt ggaccagga tagagccaag ccagtgcac agattgtgtc tgccgaagcc 780 tggggcagag ccgattgtgg ctttacaagc gagagctacc agcaggcgct gctgtctgcc 840 acaatcctgt atgagatcct gctgggcaaa gccactctgt acgctgtgtt ggtgtctgcc 900 ctggtgctga tggccatggt caagagaaag gacagcagag gcagagccaa gagatctggc 960 agcggcgcca caaactttag cctgtgaaa caggccggcg acgtggaaga gaacctgga 1020 cctatgaagt ccctgcggtt gctgtgtgtt attctgtggc tgcagctgag ctgggtttgg 1080 agccagggac agaacatcga ccagcctacc gagatgacag ccaccgaagg cgccatcgtg 1140 cagatcaatt gcacctacca gaccagcggc ttcaacggcc tgttctggta tcaacagcat 1200

		gccggcgagg ccctacctt cctgagctat aatgtgctgg acggcctgga agaaaagggc 1260 agattcagca gcttcctgtc cagaagcaag ggctacagct acctgctgct gaaagaactc 1320 cagatgaagg acagcgctc ctacctgtgt gcctccgtgg atggaaacaa cagactggcc 1380 ttcggcaagg gcaaccaggt ggtggtcatc cccgacattc agaaccccga tccagccgtg 1440 taccagctga gagacagcaa gagcagcgac aagagcgtgt gtctgttcac cgacttcgac 1500 tcccagacca atgtgtccca gagcaaggac tccgacgtgt acatcaccga taagaccgtg 1560 ctggacatgc ggagcatgga cttcaagagc aatagcgccg tggcttggag caacaagagc 1620 gactttgcct gcgccaacgc cttcaacaac agcatcatcc ccgaggacac attcttccca 1680 agtcttgaga gcagctgcga cgtgaagctg gtggaaaaga gcttcgagac agacaccaac 1740 ctgaacttcc agaacctgag cgtgacggc ttcagaatcc tgcgtctgaa ggtggccggc 1800 ttcaacctgc tgatgactct gagactgtgg tccagctgaa ttcggatcca agcttaggcc 1860 tgctcgcttt cttgctgtcc catttctatt aaaggttctt ttgttc 1906
3-161 3-161-1 3-161-2 3-161-3 3-161-4 3-161-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	161 AA 612 REGION 1..612 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..612 mol_type=protein organism=synthetic construct MGPGLLCWAL LCLLGAGLVD AGVTQSPHTL IKTRGQQVTL RCSPKSGHDT VSWYQQALGQ 60 GPQFIFQYYE EEERQRGNFP DRFSGHQFPN YSSELNVNAL LLGDSALYLC ASSLGWRGGR 120 YNEQFFGPGT RLTVLEDLKN VFPPEVAVFE PSEAEISHTQ KATLVCLATG FYPDHVELSW 180 WVNGKEVHSG VSTDPQPLKE QPALNDSRYC LSSRLRVSAT FWQNP RNHFR CQVQFYGLSE 240 NDEWTDRAK PVTQIVSAEA WGRADCGFTS ESYQQGVLSA TILYEILLGK ATLYAVLVSA 300 LVLAMAVK RK DSRGRAKRSG SGATNFSLK QAGDVEENPG PMKSLRVLLV ILWLQLSWVW 360 SQGQNIDQPT EMTATEGAIV QINCTYQTSG FNGLFWYQQH AGEAPTFLSY NVLDGLEEK 420 RFSSFLSRK GSYLLLLKEL QMKDSASYLC ASVDGNNRLA FGKGNQVVI PDIQNPDPAV 480 YQLRDSKSSD KSVCLFTDFD SQTNVSQSKD SDVYITDKTV LDMRSMDFKS NSAVAWSNKS 540 DFACANAFNN SIIPEDTFFP SPESSCDVKL VEKSFETDTN LNFQNL SVIG FRILLKLVAG 600 FNLLMTLR LW SS 612
3-162 3-162-1 3-162-2 3-162-3 3-162-4 3-162-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	162 DNA 66 misc_feature 1..66 note=source = /note="Description of Artificial Sequence: Synthetic oligonucleotide" source 1..66 mol_type=other DNA organism=synthetic construct atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacaccgacg attcctcctg 60 atccca 66
3-163 3-163-1 3-163-2 3-163-3 3-163-4 3-163-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	163 AA 22 REGION 1..22 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..22 mol_type=protein organism=synthetic construct MLLLVTSLLL CELPHPAFL IP 22
3-164 3-164-1 3-164-2 3-164-3 3-164-4 3-164-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	164 DNA 321 misc_feature 1..321 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..321 mol_type=other DNA organism=synthetic construct gacatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60 atcagttgca gggcaagtca ggacattagt aaatatattaa attggtatca gcagaacca 120 gatggaactg ttaaactcct gatctaccat acatcaagat tacactcagg agtcccatca 180 aggttcagt gcagtgggtc tggacagat tattctctca ccattagcaa cctggagcaa 240 gaagatatg ccacttactt ttgccacag ggtaatacgc ttccgtacac gttcggaggg 300

		gggactaagt tggaataac a	321
3-165	Sequences		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	AA	
3-165-3	Length	107	
3-165-4	Features	REGION 1..107	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..107	
		mol_type=protein	
		organism=synthetic construct	
3-165-5	NonEnglishQualifier Value Residues	DIQMTQTTSS LSASLGDRVT ISCRASQDIS KYLNWYQQKP DGTVKLLIYH TSRLHSGVPS 60 RFSGSGSGTD YSLTISNLEQ EDIATYFCQQ GNTLPYTFGG GTKLEIT 107	
3-166	Sequences		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	DNA	
3-166-3	Length	54	
3-166-4	Features	misc_feature 1..54	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic oligonucleotide"	
		source 1..54	
		mol_type=other DNA	
		organism=synthetic construct	
3-166-5	NonEnglishQualifier Value Residues	ggctccacct ctggatccgg caagcccgga tctggcgagg gatccaccaa gggc 54	
3-167	Sequences		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	AA	
3-167-3	Length	18	
3-167-4	Features	REGION 1..18	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide"	
		source 1..18	
		mol_type=protein	
		organism=synthetic construct	
3-167-5	NonEnglishQualifier Value Residues	GSTSGSGKPG SGEGSTKG 18	
3-168	Sequences		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	DNA	
3-168-3	Length	360	
3-168-4	Features	misc_feature 1..360	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"	
		source 1..360	
		mol_type=other DNA	
		organism=synthetic construct	
3-168-5	NonEnglishQualifier Value Residues	gaggtgaaac tgcaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccgtc 60 acatgcactg ttcagggggt ctcatcacc gactatggtg taagctggat tcgccagcct 120 ccacgaaagg gtctggagtg gctgggagta atatggggta gtgaaaccac atactataat 180 tcagctctca aatccagact gaccatcatc aaggacaact ccaagagcca agttttctta 240 aaaatgaaca gtctgcaaac tgatgacaca gccatttact actgtgcca acattattac 300 tacggtggta gctatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360	
3-169	Sequences		
3-169-1	Sequence Number [ID]	169	
3-169-2	Molecule Type	AA	
3-169-3	Length	120	
3-169-4	Features	REGION 1..120	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..120	
		mol_type=protein	
		organism=synthetic construct	
3-169-5	NonEnglishQualifier Value Residues	EVKLQESGPG LVAPSQSLSV TCTVSGVSLP DYGVSWIRQP PRKGLEWLGW IWGSETTYYN 60 SALKSRLTII KDNSKSQVFL KMNSLQDDT AIYYCAKHYY YGGSYAMDYW GQGTSVTVSS 120	
3-170	Sequences		
3-170-1	Sequence Number [ID]	170	
3-170-2	Molecule Type		
3-170-3	Length		
3-170-4	Features		
	Location/Qualifiers		

3-170-5	NonEnglishQualifier Value Residues	000	3
3-171	Sequences		
3-171-1	Sequence Number [ID]	171	
3-171-2	Molecule Type		
3-171-3	Length		
3-171-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-171-5	Residues	000	3
3-172	Sequences		
3-172-1	Sequence Number [ID]	172	
3-172-2	Molecule Type	DNA	
3-172-3	Length	198	
3-172-4	Features	misc_feature 1..198	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..198	
		mol_type=other DNA	
		organism=synthetic construct	
3-172-5	Residues	attgaagtta tgtatcctcc tccttaccta gacaatgaga agagcaatgg aaccattatc 60 catgtgaaag ggaaacacct ttgtccaagt cccctatttc ccggaccttc taagcccttt 120 tgggtgctgg tgggtggttg gggagtcctg gcttgctata gcttgctagt aacagtggcc 180 tttattattt tctgggtg 198	
3-173	Sequences		
3-173-1	Sequence Number [ID]	173	
3-173-2	Molecule Type	AA	
3-173-3	Length	66	
3-173-4	Features	REGION 1..66	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..66	
		mol_type=protein	
		organism=synthetic construct	
3-173-5	Residues	IEVMYPPPYL DNEKSNGTII HVKGKHLCPs PLFPGPSKPF WLVVVGGLV ACYSLLVTV 60 FIIFWV 66	
3-174	Sequences		
3-174-1	Sequence Number [ID]	174	
3-174-2	Molecule Type	DNA	
3-174-3	Length	123	
3-174-4	Features	misc_feature 1..123	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..123	
		mol_type=other DNA	
		organism=synthetic construct	
3-174-5	Residues	aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60 gggccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120 tcc 123	
3-175	Sequences		
3-175-1	Sequence Number [ID]	175	
3-175-2	Molecule Type	AA	
3-175-3	Length	41	
3-175-4	Features	REGION 1..41	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"	
		source 1..41	
		mol_type=protein	
		organism=synthetic construct	
3-175-5	Residues	RSKRSRLHS DYMNMTPRRP GPTRKHYQPY APPRDFAAAYR S 41	
3-176	Sequences		
3-176-1	Sequence Number [ID]	176	
3-176-2	Molecule Type	DNA	
3-176-3	Length	336	
3-176-4	Features	misc_feature 1..336	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..336	
		mol_type=other DNA	
		organism=synthetic construct	

3-176-5	NonEnglishQualifier Value Residues	agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60 tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120 cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180 gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240 cggaggggca aggggcacga tggcctttac cagggctcga gtacagccac caaggacacc 300 tacgacgccc ttcacatgca ggccttgccc cctcgc 336
3-177	Sequences	
3-177-1	Sequence Number [ID]	177
3-177-2	Molecule Type	AA
3-177-3	Length	112
3-177-4	Features	REGION 1..112
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..112 mol_type=protein organism=synthetic construct
3-177-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112
3-178	Sequences	
3-178-1	Sequence Number [ID]	178
3-178-2	Molecule Type	AA
3-178-3	Length	11
3-178-4	Features	REGION 1..11
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..11 mol_type=protein organism=synthetic construct
3-178-5	NonEnglishQualifier Value Residues	RASQDISKYL N 11
3-179	Sequences	
3-179-1	Sequence Number [ID]	179
3-179-2	Molecule Type	AA
3-179-3	Length	7
3-179-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..7 mol_type=protein organism=synthetic construct
3-179-5	NonEnglishQualifier Value Residues	HTSRLHS 7
3-180	Sequences	
3-180-1	Sequence Number [ID]	180
3-180-2	Molecule Type	AA
3-180-3	Length	9
3-180-4	Features	REGION 1..9
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..9 mol_type=protein organism=synthetic construct
3-180-5	NonEnglishQualifier Value Residues	QQGNTLPYT 9
3-181	Sequences	
3-181-1	Sequence Number [ID]	181
3-181-2	Molecule Type	AA
3-181-3	Length	7
3-181-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..7 mol_type=protein organism=synthetic construct
3-181-5	NonEnglishQualifier Value Residues	GVSLPDY 7
3-182	Sequences	
3-182-1	Sequence Number [ID]	182
3-182-2	Molecule Type	AA
3-182-3	Length	5
3-182-4	Features	REGION 1..5
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide"

3-182-5	NonEnglishQualifier Value Residues	source 1..5 mol_type=protein organism=synthetic construct WGSET	5
3-183 3-183-1 3-183-2 3-183-3 3-183-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	183 AA 12 REGION 1..12 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..12 mol_type=protein organism=synthetic construct	
3-183-5	NonEnglishQualifier Value Residues	HYYYGGSYAM DY	12
3-184 3-184-1 3-184-2 3-184-3 3-184-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	184 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-184-5	NonEnglishQualifier Value Residues	RASQDISKYL N	11
3-185 3-185-1 3-185-2 3-185-3 3-185-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	185 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct	
3-185-5	NonEnglishQualifier Value Residues	HTSRLHS	7
3-186 3-186-1 3-186-2 3-186-3 3-186-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	186 AA 9 REGION 1..9 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..9 mol_type=protein organism=synthetic construct	
3-186-5	NonEnglishQualifier Value Residues	QQGNTLPYT	9
3-187 3-187-1 3-187-2 3-187-3 3-187-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	187 AA 5 REGION 1..5 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..5 mol_type=protein organism=synthetic construct	
3-187-5	NonEnglishQualifier Value Residues	DYGVS	5
3-188 3-188-1 3-188-2 3-188-3 3-188-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	188 AA 16 REGION 1..16 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..16 mol_type=protein	

3-188-5	NonEnglishQualifier Value Residues	organism=synthetic construct VIWGSETTY NSALKS	16
3-189	Sequences		
3-189-1	Sequence Number [ID]	189	
3-189-2	Molecule Type	AA	
3-189-3	Length	12	
3-189-4	Features	REGION 1..12	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..12 mol_type=protein organism=synthetic construct	
3-189-5	NonEnglishQualifier Value Residues	HYYYGGSYAM DY	12
3-190	Sequences		
3-190-1	Sequence Number [ID]	190	
3-190-2	Molecule Type	DNA	
3-190-3	Length	63	
3-190-4	Features	misc_feature 1..63	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..63 mol_type=other DNA organism=synthetic construct	
3-190-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttgccat tgctcctgca cgccgcacgc ccg	60 63
3-191	Sequences		
3-191-1	Sequence Number [ID]	191	
3-191-2	Molecule Type	AA	
3-191-3	Length	21	
3-191-4	Features	REGION 1..21	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..21 mol_type=protein organism=synthetic construct	
3-191-5	NonEnglishQualifier Value Residues	MALPVTALL PLALLHAAR P	21
3-192	Sequences		
3-192-1	Sequence Number [ID]	192	
3-192-2	Molecule Type	DNA	
3-192-3	Length	321	
3-192-4	Features	misc_feature 1..321	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..321 mol_type=other DNA organism=synthetic construct	
3-192-5	NonEnglishQualifier Value Residues	gatattcaaa tgaccagtc cccgtcctcc ctgagtgctt ccgtcgggtga ccgtgttacg attacctgcc gtgcgagcca agacatctct aaatactga actggtatca gcaaaaaccg gatcaggcac cgaaactgct gatcaaacat acctcacgct tgactcggg tgtgccgagc cgcttttagtg gttccggctc aggtaccgat tacaccctga cgatcagctc tctgcagccg gaagactttg ccacgtatta ctgccagcaa ggtaataccc tgccgtatac gttcggccaa ggtaccaaac tggaaatcaa a	60 120 180 240 300 321
3-193	Sequences		
3-193-1	Sequence Number [ID]	193	
3-193-2	Molecule Type	AA	
3-193-3	Length	107	
3-193-4	Features	REGION 1..107	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..107 mol_type=protein organism=synthetic construct	
3-193-5	NonEnglishQualifier Value Residues	DIQMTQSPSS LSASVGDRV ITCRASQDIS KYLNWYQKP DQAPKLLIKH TSRLHSGVPS RFSGSGSGTD YLTISLQP EDFATYYCQQ GNTLPYTFGQ GTKLEIK	60 107
3-194	Sequences		
3-194-1	Sequence Number [ID]	194	
3-194-2	Molecule Type	DNA	
3-194-3	Length	54	

3-194-4	Features Location/Qualifiers	misc_feature 1..54 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..54 mol_type=other DNA organism=synthetic construct
3-194-5	NonEnglishQualifier Value Residues	ggctcgacga gcggctctgg taaaccgggc tctggtgaag gcagtaccaa aggt 54
3-195	Sequences	
3-195-1	Sequence Number [ID]	195
3-195-2	Molecule Type	AA
3-195-3	Length	18
3-195-4	Features Location/Qualifiers	REGION 1..18 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..18 mol_type=protein organism=synthetic construct
3-195-5	NonEnglishQualifier Value Residues	GSTSGSGKPG SGEGSTKG 18
3-196	Sequences	
3-196-1	Sequence Number [ID]	196
3-196-2	Molecule Type	DNA
3-196-3	Length	360
3-196-4	Features Location/Qualifiers	misc_feature 1..360 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..360 mol_type=other DNA organism=synthetic construct
3-196-5	NonEnglishQualifier Value Residues	gaagtgcagc tggttgaaag cgggtggtgt ctggttcaac cgggtcgcttc cctgcgtctg 60 tcatgtacgg cgagtgggtg ctccctgccg gactatggcg tgtcctggat tcgtcagccg 120 ccgggtaaag gcctggaatg gattggtgtc atctggggca gtgaaaccac gtattacaac 180 tcggccctga aaagccgttt caccatctct cgcgataaca gtaaaaatac gctgtacctg 240 cagatgaata gcctgcgcgc ggaagacacc gccgtttact actgcgcaaa acattactac 300 tacggtggca gctatgctat ggattactgg ggtcaaggca cgctgggtcac cgtttcgtca 360
3-197	Sequences	
3-197-1	Sequence Number [ID]	197
3-197-2	Molecule Type	AA
3-197-3	Length	120
3-197-4	Features Location/Qualifiers	REGION 1..120 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..120 mol_type=protein organism=synthetic construct
3-197-5	NonEnglishQualifier Value Residues	EVQLVESGGG LVQPGRSLRL SCTASGVSLP DYGVSWIRQP PGKGLEWIGV IWGSETTYYN 60 SALKSRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCAKHYY YGGSYAMDYW GQGTLVTVSS 120
3-198	Sequences	
3-198-1	Sequence Number [ID]	198
3-198-2	Molecule Type	
3-198-3	Length	
3-198-4	Features Location/Qualifiers NonEnglishQualifier Value	
3-198-5	Residues	000 3
3-199	Sequences	
3-199-1	Sequence Number [ID]	199
3-199-2	Molecule Type	
3-199-3	Length	
3-199-4	Features Location/Qualifiers NonEnglishQualifier Value	
3-199-5	Residues	000 3
3-200	Sequences	
3-200-1	Sequence Number [ID]	200
3-200-2	Molecule Type	DNA
3-200-3	Length	171
3-200-4	Features Location/Qualifiers	misc_feature 1..171 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..171

3-200-5	NonEnglishQualifier Value Residues	mol_type=other DNA organism=synthetic construct cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60 tcacccttgt tccctgggcc atccaagcca ttctgggtgt tggctcgtagt ggggtggagtc 120 ctcgcttggt actctctgct cgtcaccgtg gcttttataa tcttctgggt t 171
3-201 3-201-1 3-201-2 3-201-3 3-201-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	201 AA 57 REGION 1..57 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..57 mol_type=protein organism=synthetic construct
3-201-5	NonEnglishQualifier Value Residues	LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP FWLVVVGGV LACYSLLVTV AFIIIFW 57
3-202 3-202-1 3-202-2 3-202-3 3-202-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	202 DNA 123 misc_feature 1..123 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..123 mol_type=other DNA organism=synthetic construct
3-202-5	NonEnglishQualifier Value Residues	agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 60 ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120 agc 123
3-203 3-203-1 3-203-2 3-203-3 3-203-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	203 AA 41 REGION 1..41 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..41 mol_type=protein organism=synthetic construct
3-203-5	NonEnglishQualifier Value Residues	RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY APPRDFAA YR S 41
3-204 3-204-1 3-204-2 3-204-3 3-204-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	204 DNA 336 misc_feature 1..336 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..336 mol_type=other DNA organism=synthetic construct
3-204-5	NonEnglishQualifier Value Residues	aggggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 60 tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggaaca ggcagagga 120 cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180 gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240 agaaggggaa aagggcacga cggtttttac cagggactca gcactgctac gaaggatact 300 tatgacgctc tccacatgca agccctgcc a cctagg 336
3-205 3-205-1 3-205-2 3-205-3 3-205-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	205 AA 112 REGION 1..112 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..112 mol_type=protein organism=synthetic construct
3-205-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGDGLY QGLSTATKDT YDALHMQALP PR 112

3-206	Sequences	
3-206-1	Sequence Number [ID]	206
3-206-2	Molecule Type	AA
3-206-3	Length	12
3-206-4	Features	REGION 1..12
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..12
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-206-5	Residues	RASQSVSSSY LA 12
3-207	Sequences	
3-207-1	Sequence Number [ID]	207
3-207-2	Molecule Type	AA
3-207-3	Length	7
3-207-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-207-5	Residues	GASSRAT 7
3-208	Sequences	
3-208-1	Sequence Number [ID]	208
3-208-2	Molecule Type	AA
3-208-3	Length	9
3-208-4	Features	REGION 1..9
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..9
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-208-5	Residues	QQYGSSRFT 9
3-209	Sequences	
3-209-1	Sequence Number [ID]	209
3-209-2	Molecule Type	AA
3-209-3	Length	7
3-209-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-209-5	Residues	GGTFSSY 7
3-210	Sequences	
3-210-1	Sequence Number [ID]	210
3-210-2	Molecule Type	AA
3-210-3	Length	6
3-210-4	Features	REGION 1..6
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..6
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-210-5	Residues	IPIFGT 6
3-211	Sequences	
3-211-1	Sequence Number [ID]	211
3-211-2	Molecule Type	AA
3-211-3	Length	10
3-211-4	Features	REGION 1..10
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..10
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-211-5	Residues	EAVAADWLDP 10
3-212	Sequences	
3-212-1	Sequence Number [ID]	212

3-212-2	Molecule Type	AA	
3-212-3	Length	12	
3-212-4	Features	REGION 1..12	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-212-5	Residues	RASQSVSSSY LA	12
3-213	Sequences		
3-213-1	Sequence Number [ID]	213	
3-213-2	Molecule Type	AA	
3-213-3	Length	7	
3-213-4	Features	REGION 1..7	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-213-5	Residues	GASSRAT	7
3-214	Sequences		
3-214-1	Sequence Number [ID]	214	
3-214-2	Molecule Type	AA	
3-214-3	Length	9	
3-214-4	Features	REGION 1..9	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-214-5	Residues	QQYGSSRFT	9
3-215	Sequences		
3-215-1	Sequence Number [ID]	215	
3-215-2	Molecule Type	AA	
3-215-3	Length	5	
3-215-4	Features	REGION 1..5	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-215-5	Residues	SYAIS	5
3-216	Sequences		
3-216-1	Sequence Number [ID]	216	
3-216-2	Molecule Type	AA	
3-216-3	Length	17	
3-216-4	Features	REGION 1..17	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-216-5	Residues	GIIPIFGTTN YAQFQG	17
3-217	Sequences		
3-217-1	Sequence Number [ID]	217	
3-217-2	Molecule Type	AA	
3-217-3	Length	10	
3-217-4	Features	REGION 1..10	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-217-5	Residues	EAVAADWLDP	10
3-218	Sequences		
3-218-1	Sequence Number [ID]	218	
3-218-2	Molecule Type	DNA	
3-218-3	Length	63	

3-218-4	Features Location/Qualifiers	misc_feature 1..63 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..63 mol_type=other DNA organism=synthetic construct
3-218-5	NonEnglishQualifier Value Residues	atggccctgc ctgtgacagc tctgctgctg cccctggccc tgctgctgca tgccgccaga 60 cct 63
3-219	Sequences	
3-219-1	Sequence Number [ID]	219
3-219-2	Molecule Type	AA
3-219-3	Length	21
3-219-4	Features Location/Qualifiers	REGION 1..21 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..21 mol_type=protein organism=synthetic construct
3-219-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR P 21
3-220	Sequences	
3-220-1	Sequence Number [ID]	220
3-220-2	Molecule Type	DNA
3-220-3	Length	324
3-220-4	Features Location/Qualifiers	misc_feature 1..324 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..324 mol_type=other DNA organism=synthetic construct
3-220-5	NonEnglishQualifier Value Residues	gagatcgtgc tgaccacgtc tcccggcacc ctgtctctca gcccaggaga gagagccacc 60 ctgagctgca gagccagcca gagcgtgtcc agcagctacc tggcctggta tcagcagaag 120 cccgacagg ccccgagact gctgatctac ggcgccagct ctagagccac cggcatcccc 180 gacagattca gcggcagcgg cagtggcacc gacttcacc tgaccatcag cagactggaa 240 cccgaggact tcgccgtgta ctactgccag cagtacggca gcagccggtt caccttcggc 300 cctggcacca aggtggacat caag 324
3-221	Sequences	
3-221-1	Sequence Number [ID]	221
3-221-2	Molecule Type	AA
3-221-3	Length	108
3-221-4	Features Location/Qualifiers	REGION 1..108 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..108 mol_type=protein organism=synthetic construct
3-221-5	NonEnglishQualifier Value Residues	EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQK PGQAPRLLIY GASSRATGIP 60 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSRFTFG PGTKVDIK 108
3-222	Sequences	
3-222-1	Sequence Number [ID]	222
3-222-2	Molecule Type	DNA
3-222-3	Length	54
3-222-4	Features Location/Qualifiers	misc_feature 1..54 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..54 mol_type=other DNA organism=synthetic construct
3-222-5	NonEnglishQualifier Value Residues	ggcagcacct ccggcagcgg caagcctggc tctggcgagg gctctaccaa gggc 54
3-223	Sequences	
3-223-1	Sequence Number [ID]	223
3-223-2	Molecule Type	AA
3-223-3	Length	18
3-223-4	Features Location/Qualifiers	REGION 1..18 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..18 mol_type=protein organism=synthetic construct
3-223-5	NonEnglishQualifier Value Residues	GSTSGSGKPG SGEGSTKG 18

3-224	Sequences	
3-224-1	Sequence Number [ID]	224
3-224-2	Molecule Type	DNA
3-224-3	Length	357
3-224-4	Features	misc_feature 1..357
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..357
		mol_type=other DNA
		organism=synthetic construct
3-224-5	NonEnglishQualifier Value Residues	cagggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggctctag cgtgaagggtg 60 tccttgcaagg acagcggcgg caccttcagc agctacgccca tcagctgggt ggcgcaggcc 120 ccaggacagg ggctggaatg gatgggcggc atcatcccca tcttcggcac caccaactac 180 gcccagcagt tccagggcag agtgaccatc accgccgacg agagcaccag caccgcctac 240 atggaactga gcagcctcg gagcgaggac acagccgtgt attactgtgc ccgcgaggcc 300 gtggccgccc actggctgga tccttgggga cagggcaccc tggtgacagt gtccagc 357
3-225	Sequences	
3-225-1	Sequence Number [ID]	225
3-225-2	Molecule Type	AA
3-225-3	Length	119
3-225-4	Features	REGION 1..119
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..119
		mol_type=protein
		organism=synthetic construct
3-225-5	NonEnglishQualifier Value Residues	QVQLVQSGAE VKKPGSSVKV SCKDSGGTFS SYAISWVRQA PGQGLEWMGG IIPFGTTNY 60 AQQFQGRVTI TADESTSTAY MELSSLRSED TAVYYCAREA VAADWLDPWG QGTLVTYSS 119
3-226	Sequences	
3-226-1	Sequence Number [ID]	226
3-226-2	Molecule Type	DNA
3-226-3	Length	249
3-226-4	Features	misc_feature 1..249
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..249
		mol_type=other DNA
		organism=synthetic construct
3-226-5	NonEnglishQualifier Value Residues	ttcgtgcccg tgttcctgcc cgccaagcct accaccaccc ctgcccttag acctcccacc 60 ccagcccca caatgccag ccagcctctg tccctgcggc ccgaagcctg tagacctgct 120 gccggcggag ccgtgcacac cagaggcctg gacttcgcct gcgatatcta catctgggcc 180 cctctggccg gcacctgtgg cgtgctgctg ctgagcctgg tgatcacct gtactgcaac 240 caccggaac 249
3-227	Sequences	
3-227-1	Sequence Number [ID]	227
3-227-2	Molecule Type	AA
3-227-3	Length	83
3-227-4	Features	REGION 1..83
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..83
		mol_type=protein
		organism=synthetic construct
3-227-5	NonEnglishQualifier Value Residues	FVPVFLPAKP TTPAPRPPT PAPTIASQPL SLRPEACRPA AGGAVHTRGL DFACDIYIWA 60 PLAGTCGVLL LSLVITLYCN HRN 83
3-228	Sequences	
3-228-1	Sequence Number [ID]	228
3-228-2	Molecule Type	DNA
3-228-3	Length	123
3-228-4	Features	misc_feature 1..123
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..123
		mol_type=other DNA
		organism=synthetic construct
3-228-5	NonEnglishQualifier Value Residues	agaagcaagc ggagccggct gctgcacagc gactacatga acatgacccc aagacggcct 60 ggccccaccc ggaagcacta ccagccttac gccctccca gagacttcgc cgcctaccgg 120 tcc 123
3-229	Sequences	
3-229-1	Sequence Number [ID]	229

3-229-2	Molecule Type	AA
3-229-3	Length	41
3-229-4	Features	REGION 1..41
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..41 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-229-5	Residues	RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY APPRDFAAAYR S 41
3-230	Sequences	
3-230-1	Sequence Number [ID]	230
3-230-2	Molecule Type	DNA
3-230-3	Length	336
3-230-4	Features	misc_feature 1..336
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..336 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-230-5	Residues	agagtgaagt tcagcagatc cgccgacgcc cctgcctacc agcagggaca gaaccagctg 60 tacaacgagc tgaacctggg cagacgggaa gagtacgacg tgctggacaa gcggagaggg 120 cgggaccccg agatgggcgg aaagcccaga cggaagaacc cccaggaagg cctgtataac 180 gaactgcaga aagacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagcgg 240 aggcgcgcca agggccacga tggcctgtac cagggcctga gcaccgccac caaggacacc 300 tacgacgccc tgcacatgca ggccctgccc cccaga 336
3-231	Sequences	
3-231-1	Sequence Number [ID]	231
3-231-2	Molecule Type	AA
3-231-3	Length	112
3-231-4	Features	REGION 1..112
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..112 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-231-5	Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112
3-232	Sequences	
3-232-1	Sequence Number [ID]	232
3-232-2	Molecule Type	DNA
3-232-3	Length	339
3-232-4	Features	misc_feature 1..339
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..339 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-232-5	Residues	atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga atttagcatg 60 gctcagacag tactcagtc tcaaccagag atgtctgtgc aggaggcaga gaccgtgacc 120 ctgagctgca catatgacac cagtgaagat gattattatt tattctggtg caagcagcct 180 cccagcaggc agatgattct cgttattcgc caagaagcct ataagcaaca gaatgcaaca 240 gagaatcgtt tctctgtgaa cttccagaaa gcagccaaat ccttcagtct caagatctca 300 gactcacagc tgggggatgc cgcgatgtat ttctgtgct 339
3-233	Sequences	
3-233-1	Sequence Number [ID]	233
3-233-2	Molecule Type	AA
3-233-3	Length	135
3-233-4	Features	REGION 1..135
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..135 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-233-5	Residues	MACPGFLWAL VISTCLEFSM AQTVTQSQPE MSVQEAETVT LSCTYDTSES DYFLFWYKQP 60 PSRQMILVIR QEAYKQQNAT ENRFSVNFQK AAKSFSLKIS DSQLGDAAMY FCALRSSGT Y 120 KYIFGTGTRL KVLAN 135
3-234	Sequences	
3-234-1	Sequence Number [ID]	234
3-234-2	Molecule Type	DNA
3-234-3	Length	66

3-234-4	Features Location/Qualifiers	misc_feature 1..66 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..66 mol_type=other DNA organism=synthetic construct
3-234-5	NonEnglishQualifier Value Residues	ctccggagct caggaacct caaatacatc ttggaacag gcaccaggct gaaggtttta 60 gcaaat 66
3-235	Sequences	
3-235-1	Sequence Number [ID]	235
3-235-2	Molecule Type	DNA
3-235-3	Length	408
3-235-4	Features Location/Qualifiers	misc_feature 1..408 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..408 mol_type=other DNA organism=synthetic construct
3-235-5	NonEnglishQualifier Value Residues	atccagaacc ctgaacctgc tgtgtaccag ttaaaagatc ctcggtctca ggacagcacc 60 ctctgcctgt tcaccgactt tgactcccaa atcaatgtgc cgaaaacat ggaatctgga 120 acgttcatca ctgacaaaac tgtgtggac atgaaagcta tggattccaa gagcaatggg 180 gccattgcct ggagcaacca gacaagcttc acctgccaag atatcttcaa agagaccaac 240 gccacctacc ccagttcaga cgttcctgt gatgccagt tgactgagaa aagctttgaa 300 acagatatga acctaaactt tcaaaacctg tcagttatgg gactccgaat cctcctgctg 360 aaagtagccg gatttaacct gtcattgacg ctgaggctgt ggtccagt 408
3-236	Sequences	
3-236-1	Sequence Number [ID]	236
3-236-2	Molecule Type	AA
3-236-3	Length	136
3-236-4	Features Location/Qualifiers	REGION 1..136 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..136 mol_type=protein organism=synthetic construct
3-236-5	NonEnglishQualifier Value Residues	IQNPEPAVYQ LKDPRSQDST LCLFTDFDSQ INVPKTMESG TFITDKTVLD MKAMDSKSNQ 60 AIAWSNQTSF TCQDIFKETN ATYPSSDVPC DATLTEKSFE TDMNLNFQNL SVMGLRILL 120 KVAGFNLLMT LRLWSS 136
3-237	Sequences	
3-237-1	Sequence Number [ID]	237
3-237-2	Molecule Type	DNA
3-237-3	Length	81
3-237-4	Features Location/Qualifiers	misc_feature 1..81 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..81 mol_type=other DNA organism=synthetic construct
3-237-5	NonEnglishQualifier Value Residues	cgggccaagc ggtccggatc cggagccacc aacttcagcc tgctgaagca ggccggcgac 60 gtggaggaga acccggccc c 81
3-238	Sequences	
3-238-1	Sequence Number [ID]	238
3-238-2	Molecule Type	AA
3-238-3	Length	27
3-238-4	Features Location/Qualifiers	REGION 1..27 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..27 mol_type=protein organism=synthetic construct
3-238-5	NonEnglishQualifier Value Residues	RAKRSGSGAT NFSLLKQAGD VEENPGP 27
3-239	Sequences	
3-239-1	Sequence Number [ID]	239
3-239-2	Molecule Type	DNA
3-239-3	Length	340
3-239-4	Features Location/Qualifiers	misc_feature 1..340 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..340 mol_type=other DNA

3-239-5	NonEnglishQualifier Value Residues	organism=synthetic construct atggggcacca ggctcctctt ctgggtggcc ttctgtctcc tgggggcaga tcacacagga 60 gctggagtct cccagtcccc cagtaacaag gtcacagaga agggaaagga tgtagagctc 120 aggtgtgata caatttcagg tcatactgcc ctttactggt accgacagag cctggggcag 180 ggcctggagt ttttaattta ctccaaggc aacagtgcac cagacaaatc agggctgccc 240 agtgatcgct tctctgcaga gaggactggg ggatccgtct ccactctgac gatccagcgc 300 acacagcagg aggactcggc cgtgtatctc tgtgccagca 340
3-240 3-240-1 3-240-2 3-240-3 3-240-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	240 AA 137 REGION 1..137 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..137 mol_type=protein organism=synthetic construct
3-240-5	NonEnglishQualifier Value Residues	MGTRLLFWVA FCLLGADHTG AGVSQSPSNK VTEKGKDVEL RCDPISGHTA LYWYRQSLGQ 60 GLEFLIYFQG NSAPDKSGLP SDRFSAERTG GSVSTLTIQR TQQEDSAVYL CASIRTGPF 120 SGNTIYFGEQ SWLTVVE 137
3-241 3-241-1 3-241-2 3-241-3 3-241-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	241 DNA 71 misc_feature 1..71 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..71 mol_type=other DNA organism=synthetic construct
3-241-5	NonEnglishQualifier Value Residues	tccggacagg gccttttttc tctggaaaca ccatatattt tggagaggga agttggctca 60 ctgttgtaga g 71
3-242 3-242-1 3-242-2 3-242-3 3-242-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	242 DNA 519 misc_feature 1..519 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..519 mol_type=other DNA organism=synthetic construct
3-242-5	NonEnglishQualifier Value Residues	gacctgagaa acgtgacccc acccaaggtc tccttgtttg agccatcaaa agcagagatt 60 gcaaacaac aaaaggctac cctcgtgtgc ttggccaggg gcttcttccc tgaccacgtg 120 gagctgagct ggtgggtgaa tggcaaggag gtccacagtg gggtcagcac ggaccctcag 180 gcctacaagg agagcaatta tagctactgc ctgagcagcc gcctgagggt ctctgctacc 240 ttctggcaca atcctcgaaa ccacttccgc tgccaagtgc agttccatgg gctttcagag 300 gaggacaagt ggccagaggg ctcacccaaa cctgtcacac agaacatcag tgcagaggcc 360 tggggccgag cagactgtgg aatcacttca gcatcctatc atcagggggt tctgtctgca 420 accatcctct atgagatcct actggggaag gccaccctat atgctgtgct ggtcagtggc 480 ctggtgctga tggctatggt caaaagaaag aactcatga 519
3-243 3-243-1 3-243-2 3-243-3 3-243-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	243 AA 172 REGION 1..172 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..172 mol_type=protein organism=synthetic construct
3-243-5	NonEnglishQualifier Value Residues	DLRNVTPPKV SLFEPSKAEI ANKQKATLVC LARGFFPDHV ELSWVNGKE VHSGVSTDPQ 60 AYKESNYSYC LSSRLRVSAT FWHNPRNHFR CQVQFHGLSE EDKWPEGSPK PVTQNISAEA 120 WGRADCGITS ASYHQGVLSA TILYEILLGK ATLYAVLVSG LVLAMVKRK NS 172
3-244 3-244-1 3-244-2 3-244-3 3-244-4	Sequences Sequence Number [ID] Molecule Type Length Features	244 AA 12 REGION 1..12

3-244-5	Location/Qualifiers NonEnglishQualifier Value Residues	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..12 mol_type=protein organism=synthetic construct TYDTSESDYY LF	12
3-245 3-245-1 3-245-2 3-245-3 3-245-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	245 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct	
3-245-5	NonEnglishQualifier Value Residues	QEAYKQQ	7
3-246 3-246-1 3-246-2 3-246-3 3-246-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	246 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-246-5	NonEnglishQualifier Value Residues	ALRSSGTYKY I	11
3-247 3-247-1 3-247-2 3-247-3 3-247-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	247 AA 10 REGION 1..10 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..10 mol_type=protein organism=synthetic construct	
3-247-5	NonEnglishQualifier Value Residues	DPISGHTALY	10
3-248 3-248-1 3-248-2 3-248-3 3-248-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	248 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-248-5	NonEnglishQualifier Value Residues	FQGNSAPDKS G	11
3-249 3-249-1 3-249-2 3-249-3 3-249-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	249 AA 15 REGION 1..15 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..15 mol_type=protein organism=synthetic construct	
3-249-5	NonEnglishQualifier Value Residues	ASIRTGPFFS GNTIY	15
3-250 3-250-1 3-250-2 3-250-3 3-250-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	250 DNA 63 misc_feature 1..63 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..63	

3-250-5	NonEnglishQualifier Value Residues	mol_type=other DNA organism=synthetic construct atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60 ccg 63
3-251	Sequences	
3-251-1	Sequence Number [ID]	251
3-251-2	Molecule Type	AA
3-251-3	Length	21
3-251-4	Features	REGION 1..21
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..21 mol_type=protein organism=synthetic construct
3-251-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR P 21
3-252	Sequences	
3-252-1	Sequence Number [ID]	252
3-252-2	Molecule Type	DNA
3-252-3	Length	366
3-252-4	Features	misc_feature 1..366
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..366 mol_type=other DNA organism=synthetic construct
3-252-5	NonEnglishQualifier Value Residues	cagggtccaac tgcaagaaag cggacccgga ctggtgaagc cttctgagac acttagtctg 60 acgtgcacgg tcagtggcgg ctccatctcc tcctattatt ggtcatggat acgacaaccc 120 ccaggtaagg gcctggaatg gattggctat atctactatt caggaagcac gaactacaat 180 cccagcctga agtcccgagt gacaatttca gtagatacca gtaaaaacca gttcagtctt 240 aaactgtcaa gcgtgacagc tgccgacacc gctgtgtatt actgctctc actggtgtat 300 tgtggagggg attgttatag cgggttcgat tattggggac agggaaacct ggtgactgta 360 tcttcc 366
3-253	Sequences	
3-253-1	Sequence Number [ID]	253
3-253-2	Molecule Type	AA
3-253-3	Length	122
3-253-4	Features	REGION 1..122
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..122 mol_type=protein organism=synthetic construct
3-253-5	NonEnglishQualifier Value Residues	QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYWWSWIRQP PGKGLEWIGY IYYSGSTNYN 60 PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCVSLVY CGGDCYSGFD YWQGTLVTV 120 SS 122
3-254	Sequences	
3-254-1	Sequence Number [ID]	254
3-254-2	Molecule Type	DNA
3-254-3	Length	45
3-254-4	Features	misc_feature 1..45
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..45 mol_type=other DNA organism=synthetic construct
3-254-5	NonEnglishQualifier Value Residues	ggcggcggcg gctcaggggg tggcggtagt ggcggtgggg gttcc 45
3-255	Sequences	
3-255-1	Sequence Number [ID]	255
3-255-2	Molecule Type	AA
3-255-3	Length	15
3-255-4	Features	REGION 1..15
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..15 mol_type=protein organism=synthetic construct
3-255-5	NonEnglishQualifier Value Residues	GGGSGGGGS GGGGS 15
3-256	Sequences	

3-256-1	Sequence Number [ID]	256
3-256-2	Molecule Type	DNA
3-256-3	Length	324
3-256-4	Features	misc_feature 1..324
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..324
		mol_type=other DNA
		organism=synthetic construct
3-256-5	NonEnglishQualifier Value Residues	gatattcaac tgacacaatc ccccagctca ctcagcgcca gcgtggggga cagggttagc 60 tttacctgtc aagcctctca ggatataaat aactttctga actggtatca acagaagcct 120 gggaaggcgc ccaaactcct gatctatgat gcgtccaacc tggaaactgg cgtgccttca 180 cgcttttagcg gctctggcag tggtagacac ttcactttta ccatctcttc acttcagccg 240 gaggacatcg ccacatatta ctgtcaacag tacggaaact tgccctttac ttttggaggc 300 ggcaccaaag ttgaaatcaa aagg 324
3-257	Sequences	
3-257-1	Sequence Number [ID]	257
3-257-2	Molecule Type	AA
3-257-3	Length	108
3-257-4	Features	REGION 1..108
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..108
		mol_type=protein
		organism=synthetic construct
3-257-5	NonEnglishQualifier Value Residues	DIQLTQSPSS LSASVGDRVS FTCQASQDIN NFLNWWYQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YGNLPFTFGG GTKVEIKR 108
3-258	Sequences	
3-258-1	Sequence Number [ID]	258
3-258-2	Molecule Type	
3-258-3	Length	
3-258-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-258-5	Residues	000 3
3-259	Sequences	
3-259-1	Sequence Number [ID]	259
3-259-2	Molecule Type	
3-259-3	Length	
3-259-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-259-5	Residues	000 3
3-260	Sequences	
3-260-1	Sequence Number [ID]	260
3-260-2	Molecule Type	DNA
3-260-3	Length	171
3-260-4	Features	misc_feature 1..171
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..171
		mol_type=other DNA
		organism=synthetic construct
3-260-5	NonEnglishQualifier Value Residues	ctggataacg aaaagagcaa tgggactata atacatgtta aaggaaaaca cctgtgtcca 60 tctcccctgt tccttgacc gtcaaagcca ttttgggtgc tcgtggttgt cggtagcggtt 120 ctcgcctgtt atagcttgct ggtgacagta gccttcatta tcttttgggt g 171
3-261	Sequences	
3-261-1	Sequence Number [ID]	261
3-261-2	Molecule Type	AA
3-261-3	Length	57
3-261-4	Features	REGION 1..57
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..57
		mol_type=protein
		organism=synthetic construct
3-261-5	NonEnglishQualifier Value Residues	LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP FWLVVVGGV LACYSLLVTV AFIIFWV 57
3-262	Sequences	
3-262-1	Sequence Number [ID]	262

3-262-2	Molecule Type	DNA
3-262-3	Length	123
3-262-4	Features	misc_feature 1..123
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..123 mol_type=other DNA organism=synthetic construct
3-262-5	NonEnglishQualifier Value Residues	agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 60 ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120 agc 123
3-263	Sequences	
3-263-1	Sequence Number [ID]	263
3-263-2	Molecule Type	AA
3-263-3	Length	41
3-263-4	Features	REGION 1..41
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..41 mol_type=protein organism=synthetic construct
3-263-5	NonEnglishQualifier Value Residues	RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR S 41
3-264	Sequences	
3-264-1	Sequence Number [ID]	264
3-264-2	Molecule Type	DNA
3-264-3	Length	336
3-264-4	Features	misc_feature 1..336
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..336 mol_type=other DNA organism=synthetic construct
3-264-5	NonEnglishQualifier Value Residues	cgagtgaat tttctagatc agctgatgct cccgcctatc agcagggaca gaatcaactt 60 tacaatgagc tgaacctggg tcgcagagaa gactacgacg ttttggacaa acgccggggc 120 cgagatcctg agatgggggg gaagccgaga aggaagaatc ctcaagaagg cctgtacaac 180 gagcttcaa aagacaaaat ggctgaggcg tactctgaga tcggcatgaa gggcgagcgg 240 agacgaggca agggtcacga tggcttgat cagggcctga gtacagccac aaaggacacc 300 tatgacgccc tccacatgca ggcactgccc ccacgc 336
3-265	Sequences	
3-265-1	Sequence Number [ID]	265
3-265-2	Molecule Type	AA
3-265-3	Length	112
3-265-4	Features	REGION 1..112
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..112 mol_type=protein organism=synthetic construct
3-265-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYQQGQNL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112
3-266	Sequences	
3-266-1	Sequence Number [ID]	266
3-266-2	Molecule Type	AA
3-266-3	Length	11
3-266-4	Features	REGION 1..11
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct
3-266-5	NonEnglishQualifier Value Residues	QASQDINNFL N 11
3-267	Sequences	
3-267-1	Sequence Number [ID]	267
3-267-2	Molecule Type	AA
3-267-3	Length	7
3-267-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein

3-267-5	NonEnglishQualifier Value Residues	organism=synthetic construct DASNLET	7
3-268 3-268-1 3-268-2 3-268-3 3-268-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	268 AA 9 REGION 1..9 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..9 mol_type=protein organism=synthetic construct	
3-268-5	NonEnglishQualifier Value Residues	QQYGNLPFT	9
3-269 3-269-1 3-269-2 3-269-3 3-269-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	269 AA 7 REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..7 mol_type=protein organism=synthetic construct	
3-269-5	NonEnglishQualifier Value Residues	GGSISSY	7
3-270 3-270-1 3-270-2 3-270-3 3-270-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	270 AA 5 REGION 1..5 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..5 mol_type=protein organism=synthetic construct	
3-270-5	NonEnglishQualifier Value Residues	YYSGS	5
3-271 3-271-1 3-271-2 3-271-3 3-271-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	271 AA 14 REGION 1..14 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..14 mol_type=protein organism=synthetic construct	
3-271-5	NonEnglishQualifier Value Residues	LVYCGGDCYS GFDY	14
3-272 3-272-1 3-272-2 3-272-3 3-272-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	272 DNA 63 misc_feature 1..63 note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..63 mol_type=other DNA organism=synthetic construct	
3-272-5	NonEnglishQualifier Value Residues	atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc ccg	60 63
3-273 3-273-1 3-273-2 3-273-3 3-273-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	273 AA 21 REGION 1..21 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..21 mol_type=protein organism=synthetic construct	

3-273-5	NonEnglishQualifier Value Residues	MALPVTALLL PLALLLHAAR P	21
3-274	Sequences		
3-274-1	Sequence Number [ID]	274	
3-274-2	Molecule Type	DNA	
3-274-3	Length	369	
3-274-4	Features	misc_feature 1..369	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..369 mol_type=other DNA organism=synthetic construct	
3-274-5	NonEnglishQualifier Value Residues	cagggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60 tcctgtgcag cgtctggatt cacccttcagt agctatggca tgcactgggt ccgccaggct 120 ccaggcaagg ggctggagtg ggtggcagtt atatcgtagt atggaagtaa taaatactat 180 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240 ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300 ttgcaggagc cgccatacga ttatggaatg gacgtatggg gccagggaac aactgtcacc 360 gtctcctca 369	
3-275	Sequences		
3-275-1	Sequence Number [ID]	275	
3-275-2	Molecule Type	AA	
3-275-3	Length	123	
3-275-4	Features	REGION 1..123	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..123 mol_type=protein organism=synthetic construct	
3-275-5	NonEnglishQualifier Value Residues	QVQLVESGGG VVQGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV ISYDGSNKYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP LQEPYDYGM DVWGQGTTVT 120 VSS 123	
3-276	Sequences		
3-276-1	Sequence Number [ID]	276	
3-276-2	Molecule Type	DNA	
3-276-3	Length	54	
3-276-4	Features	misc_feature 1..54	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..54 mol_type=other DNA organism=synthetic construct	
3-276-5	NonEnglishQualifier Value Residues	gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggg 54	
3-277	Sequences		
3-277-1	Sequence Number [ID]	277	
3-277-2	Molecule Type	AA	
3-277-3	Length	18	
3-277-4	Features	REGION 1..18	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..18 mol_type=protein organism=synthetic construct	
3-277-5	NonEnglishQualifier Value Residues	GSTSGSGKPG SGEGSTKG 18	
3-278	Sequences		
3-278-1	Sequence Number [ID]	278	
3-278-2	Molecule Type	DNA	
3-278-3	Length	324	
3-278-4	Features	misc_feature 1..324	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..324 mol_type=other DNA organism=synthetic construct	
3-278-5	NonEnglishQualifier Value Residues	gaaatagtgta tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60 ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120 ggccaggctc ccaggctcct catctatagc gcatccacca gggccactgg tatcccagcc 180 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240 gaagattttg cagtttatta ctgtcagcag caccacgtct ggcctctcac ttttggcgga 300	

		gggaccaagg ttgagatcaa acgg	324
3-279	Sequences		
3-279-1	Sequence Number [ID]	279	
3-279-2	Molecule Type	AA	
3-279-3	Length	108	
3-279-4	Features	REGION 1..108	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..108	
		mol_type=protein	
		organism=synthetic construct	
3-279-5	NonEnglishQualifier Value Residues	EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS ASTRATGIPA 60 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR 108	
3-280	Sequences		
3-280-1	Sequence Number [ID]	280	
3-280-2	Molecule Type		
3-280-3	Length		
3-280-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-280-5	Residues	000	3
3-281	Sequences		
3-281-1	Sequence Number [ID]	281	
3-281-2	Molecule Type		
3-281-3	Length		
3-281-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-281-5	Residues	000	3
3-282	Sequences		
3-282-1	Sequence Number [ID]	282	
3-282-2	Molecule Type	DNA	
3-282-3	Length	171	
3-282-4	Features	misc_feature 1..171	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"	
		source 1..171	
		mol_type=other DNA	
		organism=synthetic construct	
3-282-5	NonEnglishQualifier Value Residues	cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60 tcacccttgt tccctggtcc atccaagcca ttctgggtgt tggtcgtagt gggaggagtc 120 ctcgttgtt actctctgct cgtcaccgtg gcttttataa tcttctgggt t 171	
3-283	Sequences		
3-283-1	Sequence Number [ID]	283	
3-283-2	Molecule Type	AA	
3-283-3	Length	57	
3-283-4	Features	REGION 1..57	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..57	
		mol_type=protein	
		organism=synthetic construct	
3-283-5	NonEnglishQualifier Value Residues	LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP FWLVVVGGV LACYSLLVTV AFIIFW 57	
3-284	Sequences		
3-284-1	Sequence Number [ID]	284	
3-284-2	Molecule Type	DNA	
3-284-3	Length	123	
3-284-4	Features	misc_feature 1..123	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"	
		source 1..123	
		mol_type=other DNA	
		organism=synthetic construct	
3-284-5	NonEnglishQualifier Value Residues	agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgcct 60 ggccccacaa ggaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120 agc 123	
3-285	Sequences		
3-285-1	Sequence Number [ID]	285	
3-285-2	Molecule Type	AA	

3-285-3	Length	41
3-285-4	Features Location/Qualifiers	REGION 1..41 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..41 mol_type=protein organism=synthetic construct
3-285-5	NonEnglishQualifier Value Residues	RSKRSRL LHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR S 41
3-286	Sequences	
3-286-1	Sequence Number [ID]	286
3-286-2	Molecule Type	DNA
3-286-3	Length	336
3-286-4	Features Location/Qualifiers	misc_feature 1..336 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..336 mol_type=other DNA organism=synthetic construct
3-286-5	NonEnglishQualifier Value Residues	agggtgaagt ttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 60 tataacgagc tcaacctggg acgcaggga gagtatgacg ttttggacaa gcgcagagga 120 cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180 gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240 agaaggggaa aagggcacga cggttgtac cagggactca gcactgctac gaaggatact 300 tatgacgctc tccacatgca agccctgccca cctagg 336
3-287	Sequences	
3-287-1	Sequence Number [ID]	287
3-287-2	Molecule Type	AA
3-287-3	Length	112
3-287-4	Features Location/Qualifiers	REGION 1..112 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..112 mol_type=protein organism=synthetic construct
3-287-5	NonEnglishQualifier Value Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGDGLY QGLSTATKDT YDALHMQALP PR 112
3-288	Sequences	
3-288-1	Sequence Number [ID]	288
3-288-2	Molecule Type	AA
3-288-3	Length	11
3-288-4	Features Location/Qualifiers	REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..11 mol_type=protein organism=synthetic construct
3-288-5	NonEnglishQualifier Value Residues	RASQSVSSNL A 11
3-289	Sequences	
3-289-1	Sequence Number [ID]	289
3-289-2	Molecule Type	AA
3-289-3	Length	7
3-289-4	Features Location/Qualifiers	REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..7 mol_type=protein organism=synthetic construct
3-289-5	NonEnglishQualifier Value Residues	SASTRAT 7
3-290	Sequences	
3-290-1	Sequence Number [ID]	290
3-290-2	Molecule Type	AA
3-290-3	Length	10
3-290-4	Features Location/Qualifiers	REGION 1..10 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..10 mol_type=protein organism=synthetic construct
3-290-5	NonEnglishQualifier Value Residues	QQHHVWPLTF 10

3-291	Sequences	
3-291-1	Sequence Number [ID]	291
3-291-2	Molecule Type	AA
3-291-3	Length	7
3-291-4	Features	REGION 1..7
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-291-5	Residues	GFTFSSY 7
3-292	Sequences	
3-292-1	Sequence Number [ID]	292
3-292-2	Molecule Type	AA
3-292-3	Length	17
3-292-4	Features	REGION 1..17
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..17
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-292-5	Residues	VISYDGSNKY YADSVKG 17
3-293	Sequences	
3-293-1	Sequence Number [ID]	293
3-293-2	Molecule Type	AA
3-293-3	Length	16
3-293-4	Features	REGION 1..16
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..16
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-293-5	Residues	VKGPLQEPPY DYGM DV 16
3-294	Sequences	
3-294-1	Sequence Number [ID]	294
3-294-2	Molecule Type	DNA
3-294-3	Length	393
3-294-4	Features	misc_feature 1..393
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..393
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-294-5	Residues	atgggcacca gactgttctt ttatgtggcc ctgtgtctgc tgtggaccgg ccacatggat 60 gccggaatta cacagagccc cagacacaaa gtgaccgaga caggcaccac tgtgacactg 120 agatgccacc agaccgagaa ccaccgtac atgtactggt acagacagga tccaggccac 180 ggcctgagac tgatccacta cagctacggc gtgaaggaca ccgacaaggg cgaagtgtct 240 gacggctaca gcgtgtccag aagcaagacc gaggatttcc tgctgaccct ggaaagcgcc 300 acaagcagcc agaccagcgt gtacttttgt gccatcagcg gctacaagaa caccgaggcc 360 tttttcggcc aaggcaccag gctgacagtg gtg 393
3-295	Sequences	
3-295-1	Sequence Number [ID]	295
3-295-2	Molecule Type	AA
3-295-3	Length	131
3-295-4	Features	REGION 1..131
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide"
		source 1..131
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-295-5	Residues	MGTRLFFYVA LCLLWTGHMD AGITQSPRHK VTETGTPVTL RCHQTENHRY MYWYRQDPGH 60 GLRLIHYSYG VKDSDKGEVS DGYSVSRSKT EDLLTLESA TSSQTSVYFC AISGYKNTEA 120 FFQGQTRLTV V 131
3-296	Sequences	
3-296-1	Sequence Number [ID]	296
3-296-2	Molecule Type	DNA
3-296-3	Length	537
3-296-4	Features	misc_feature 1..537
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"

3-296-5	NonEnglishQualifier Value Residues	source 1..537 mol_type=other DNA organism=synthetic construct gaagatctga agaacgtgtt cccacctgag gtggccgtgt ttgagccttc tgaggccgag 60 atcagccaca cacagaaagc cacactcgtg tgcctggcca cgggctttta tcccgatcac 120 gtggaactgt cttggtgggt caacggcaaa gaggtgcaca gcggcgttag cacagaccct 180 cagcctctga aagagcagcc gcgtctgaac gacagcagat actgtctgag cagcagactg 240 agagtgtccg ccaccttctg gcagaacccc agaaaccact tcagatgcc a ggtgcagttc 300 tacggcctgt ccgagaatga cgagtggacc caggatagag ccaagccagt gacacagatt 360 gtgtctgccg aagcctgggg cagagccgat tgtggcttta caagcgagag ctaccagcag 420 ggcgtgctgt ctgccacaat cctgtatgag atcctgctgg gcaaagccac tctgtacgct 480 gtgctgggtgt ctgccctggt gctgatggcc atggtcaaga gaaaggacag cagaggc 537
3-297 3-297-1 3-297-2 3-297-3 3-297-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	297 AA 179 REGION 1..179 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..179 mol_type=protein organism=synthetic construct
3-297-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWVWNGK EVHSGVSTDP 60 QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNHFRCVQVF YGLSENDEWT QDRAKPVTTI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMV MVKRKDSRG 179
3-298 3-298-1 3-298-2 3-298-3 3-298-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	298 DNA 81 misc_feature 1..81 note=source = /note="Description of Artificial Sequence: Synthetic oligonucleotide" source 1..81 mol_type=other DNA organism=synthetic construct
3-298-5	NonEnglishQualifier Value Residues	agagccaaga gatctggcag cggcgccaca aactttagcc tgctgaaaca ggccggcgac 60 gtggaagaga accctggacc t 81
3-299 3-299-1 3-299-2 3-299-3 3-299-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	299 AA 27 REGION 1..27 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..27 mol_type=protein organism=synthetic construct
3-299-5	NonEnglishQualifier Value Residues	RAKRSGSGAT NFSLLKQAGD VEENPGP 27
3-300 3-300-1 3-300-2 3-300-3 3-300-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	300 DNA 396 misc_feature 1..396 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..396 mol_type=other DNA organism=synthetic construct
3-300-5	NonEnglishQualifier Value Residues	atgaagtccc tgcgggtgct gctggttatt ctgtggctgc agctgagctg ggtttgagac 60 cagggacagc aagtgatgca gatccctcag taccagcacg tgcaagaagg cgaggacttc 120 accacctact gcaacagcag cacaaccctg agcaacatcc agtggtagaa gcagaggcct 180 ggcgggcacc ctgtgtttct gatccagctg gttaagagcg gcgaagtga gaagcagaag 240 cggtgacct ttcagttcgg cgaggccaag aagaacagca gcctgcacat taccgccaca 300 cagaccaccg acgtgggcac atatttttgc gctggcagag aaggcggcag cgagaagctg 360 gtttttggca agggcaccaa actgaccgtg aatccc 396
3-301 3-301-1 3-301-2 3-301-3	Sequences Sequence Number [ID] Molecule Type Length	301 AA 132

3-301-4	Features Location/Qualifiers	REGION 1..132 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..132 mol_type=protein organism=synthetic construct
3-301-5	NonEnglishQualifier Value Residues	MKSLRVLLVI LWLQLSWVWS QGQVMQIPQ YQHVQEGEDF TTYCNSSTTL SNIQWYKQRP 60 GGHPVFLIQL VKSGEVKKQK RLTFQFGEAK KNSSLHITAT QTDTVGTYFC AGREGGSEKL 120 VFGKGTKLTV NP 132
3-302	Sequences	
3-302-1	Sequence Number [ID]	302
3-302-2	Molecule Type	DNA
3-302-3	Length	493
3-302-4	Features Location/Qualifiers	misc_feature 1..493 note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide" source 1..493 mol_type=other DNA organism=synthetic construct
3-302-5	NonEnglishQualifier Value Residues	gacattcaga accccgatcc agccgtgtac cagctgagag acagcaagag cagcgacaag 60 agcgtgtgtc tgttcaccga cttcgactcc cagaccaatg tgtcccagag caaggactcc 120 gacgtgtaca tcaccgataa gaccgtgctg gacatgcgga gcatggactt caagagcaat 180 agcgccgtgg cttggagcaa caagagcgac ttgacctgcg ccaacgcctt caacaacagc 240 atcatccccg aggacacatt cttcccaagt cctgagagca gctgcgacgt gaagctggtg 300 gaaaagagct tcgagacaga caccaacctg aacttccaga acctgagcgt gatcggcttc 360 agaatcctgc tgctgaagggt ggccggcttc aacctgctga tgactctgag actgtggtcc 420 agctgaattc ggatccaagc ttaggcctgc tcgctttctt gctgtcccat ttctattaaa 480 ggttcctttg ttc 493
3-303	Sequences	
3-303-1	Sequence Number [ID]	303
3-303-2	Molecule Type	AA
3-303-3	Length	141
3-303-4	Features Location/Qualifiers	REGION 1..141 note=source = /note="Description of Artificial Sequence: Synthetic polypeptide" source 1..141 mol_type=protein organism=synthetic construct
3-303-5	NonEnglishQualifier Value Residues	DIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RIILLKVAGF NLLMTLRLWS S 141
3-304	Sequences	
3-304-1	Sequence Number [ID]	304
3-304-2	Molecule Type	AA
3-304-3	Length	5
3-304-4	Features Location/Qualifiers	REGION 1..5 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..5 mol_type=protein organism=synthetic construct
3-304-5	NonEnglishQualifier Value Residues	TTLSN 5
3-305	Sequences	
3-305-1	Sequence Number [ID]	305
3-305-2	Molecule Type	AA
3-305-3	Length	7
3-305-4	Features Location/Qualifiers	REGION 1..7 note=source = /note="Description of Artificial Sequence: Synthetic peptide" source 1..7 mol_type=protein organism=synthetic construct
3-305-5	NonEnglishQualifier Value Residues	LVKSGEV 7
3-306	Sequences	
3-306-1	Sequence Number [ID]	306
3-306-2	Molecule Type	AA
3-306-3	Length	11
3-306-4	Features Location/Qualifiers	REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic peptide"

3-306-5	NonEnglishQualifier Value Residues	source 1..11 mol_type=protein organism=synthetic construct AGREGGSEKL V	11
3-307 3-307-1 3-307-2 3-307-3 3-307-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	307 AA 5 REGION 1..5 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..5 mol_type=protein organism=synthetic construct	
3-307-5	NonEnglishQualifier Value Residues	ENHRY	5
3-308 3-308-1 3-308-2 3-308-3 3-308-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	308 AA 6 REGION 1..6 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..6 mol_type=protein organism=synthetic construct	
3-308-5	NonEnglishQualifier Value Residues	SYGVKD	6
3-309 3-309-1 3-309-2 3-309-3 3-309-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	309 AA 11 REGION 1..11 note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..11 mol_type=protein organism=synthetic construct	
3-309-5	NonEnglishQualifier Value Residues	AISGYKNTEA F	11
3-310 3-310-1 3-310-2 3-310-3 3-310-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	310 DNA 405 misc_feature 1..405 note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..405 mol_type=other DNA organism=synthetic construct	
3-310-5	NonEnglishQualifier Value Residues	atgggacctg gattgctttg ttgggccctg ctgtgtctgc ttggagctgg acttgtggat 60 gccggcgtga cacagtctcc cacacacctg atcaagacca gaggccagca agtgaccctg 120 agatgtagcc ctaagagcgg ccacgacacc gtgtcttggg atcagcaggc tcttgccag 180 ggacctcagt tcatcttcca gtactacgag gaagaggaaac ggcagcgggg caacttcct 240 gatagattct ctggccatca gttccccaac tacagcagcg agctgaacgt gaacgctctg 300 ctgctgggcg atagcgccct gtatctgtgt gccagttctc ttggttggag aggcggcaga 360 tacaacgagc agttcttttg ccctggcacc agactgaccg tgctg 405	
3-311 3-311-1 3-311-2 3-311-3 3-311-4	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers	311 AA 135 REGION 1..135 note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..135 mol_type=protein organism=synthetic construct	
3-311-5	NonEnglishQualifier Value Residues	MGPGLLCWAL LCLLGAGLVD AGVTQSPTHL IKTRGQQVTL RCSPKSGHDT VSWYQQALGQ 60 GPQFIFQYYE EERQRGNFP DRFSGHQFPN YSSELNVNAL LLGDSALYLC ASSLGWRGGR 120 YNEQFFPGPT RLTVL 135	
3-312	Sequences		

3-312-1	Sequence Number [ID]	312
3-312-2	Molecule Type	DNA
3-312-3	Length	537
3-312-4	Features	misc_feature 1..537
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..537 mol_type=other DNA organism=synthetic construct
3-312-5	NonEnglishQualifier Value Residues	gaagatctga agaactgtt cccacctgag gtggccgtgt ttgagccttc tgaggccgag 60 atcagccaca cacagaaagc cacactcgtg tgcctggcca ccggctttta tcccgatcac 120 gtggaactgt cttggtgggt caacggcaaa gaggtgcaca gcggcgtag cacagaccct 180 cagcctctga aagagcagcc cgctctgaac gacagcagat actgtctgag cagcagactg 240 agagtgtccg ccaccttctg gcagaacccc agaaaccact tcagatgccca ggtgcagttc 300 tacggcctgt ccgagaatga cgagtggacc caggatagag ccaagccagt gacacagatt 360 gtgtctgccg aagcctgggg cagagccgat tgtggcttta caagcgagag ctaccagcag 420 ggcgtgctgt ctgccacaat cctgtatgag atcctgctgg gcaaagccac tctgtacgct 480 gtgctggtgt ctgccctggt gctgatggcc atgggtcaaga gaaaggacag cagagggc 537
3-313	Sequences	
3-313-1	Sequence Number [ID]	313
3-313-2	Molecule Type	AA
3-313-3	Length	179
3-313-4	Features	REGION 1..179
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lypeptide" source 1..179 mol_type=protein organism=synthetic construct
3-313-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMA MVKRKDSRG 179
3-314	Sequences	
3-314-1	Sequence Number [ID]	314
3-314-2	Molecule Type	DNA
3-314-3	Length	81
3-314-4	Features	misc_feature 1..81
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide" source 1..81 mol_type=other DNA organism=synthetic construct
3-314-5	NonEnglishQualifier Value Residues	agagccaaga gatctggcag cggcgccaca aactttagcc tgctgaaaca ggccggcgac 60 gtggaagaga accctggacc t 81
3-315	Sequences	
3-315-1	Sequence Number [ID]	315
3-315-2	Molecule Type	AA
3-315-3	Length	27
3-315-4	Features	REGION 1..27
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide" source 1..27 mol_type=protein organism=synthetic construct
3-315-5	NonEnglishQualifier Value Residues	RAKRSGSGAT NFSLLKQAGD VEENPGP 27
3-316	Sequences	
3-316-1	Sequence Number [ID]	316
3-316-2	Molecule Type	DNA
3-316-3	Length	390
3-316-4	Features	misc_feature 1..390
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide" source 1..390 mol_type=other DNA organism=synthetic construct
3-316-5	NonEnglishQualifier Value Residues	atgaagtccc tgcgggtgct gctggttatt ctgtggctgc agctgagctg ggttttggagc 60 cagggacaga acatcgacca gcctaccgag atgacagcca ccgaaggcgc catcgtgcag 120 atcaattgca cctaccagac cagcggcttc aacggcctgt tctggtatca acagcatgcc 180 ggcgaggccc ctaccttctt gagctataat gtgctggacg gcctggaaga aaagggcaga 240 ttcagcagct tctgtccag aagcaagggc tacagctacc tgctgctgaa agaactccag 300 atgaaggaca ggcctccta cctgtgtgcc tccgtggatg gaaacaacag actggccttc 360

		ggcaagggca accaggtggt ggtcatcccc	390
3-317	Sequences		
3-317-1	Sequence Number [ID]	317	
3-317-2	Molecule Type	AA	
3-317-3	Length	130	
3-317-4	Features	REGION 1..130	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..130	
		mol_type=protein	
		organism=synthetic construct	
3-317-5	NonEnglishQualifier Value Residues	MKSLRVLLVI LWLQLSWWS QGQNIDQPT MTATEGAIVQ INCTYQTSGF NGLFWYQQA 60 GEAPTFLSYN VLDGLEEKGR FSSFLSRSGK YSYLLKELQ MKDSASYLCA SVDGNNRLAF 120 GKGNQVVVIP	130
3-318	Sequences		
3-318-1	Sequence Number [ID]	318	
3-318-2	Molecule Type	DNA	
3-318-3	Length	493	
3-318-4	Features	misc_feature 1..493	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polynucleotide"	
		source 1..493	
		mol_type=other DNA	
		organism=synthetic construct	
3-318-5	NonEnglishQualifier Value Residues	gacattcaga accccgatcc agccgtgtac cagctgagag acagcaagag cagcgacaag 60 agcgtgtgtc tgttcaccga cttcgactcc cagaccaatg tgtcccagag caaggactcc 120 gacgtgtaca tcaccgataa gaccgtgctg gacatgcgga gcatggactt caagagcaat 180 agcgccgtgg cttggagcaa caagagcgac ttgacctgcg ccaacgcctt caacaacagc 240 atcatccccg aggacacatt cttcccaagt cctgagagag gctgcgacgt gaagctgggtg 300 gaaaagagct tcgagacaga caccaacctg aacttccaga acctgagcgt gatcggtctc 360 agaatcctgc tgctgaagggt gcccggttc aacctgctga tgactctgag actgtggtcc 420 agctgaattc ggatccaagc ttaggcctgc tcgctttcct gctgtcccat ttctattaaa 480 ggttcctttg ttc	493
3-319	Sequences		
3-319-1	Sequence Number [ID]	319	
3-319-2	Molecule Type	AA	
3-319-3	Length	141	
3-319-4	Features	REGION 1..141	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic polypeptide"	
		source 1..141	
		mol_type=protein	
		organism=synthetic construct	
3-319-5	NonEnglishQualifier Value Residues	DIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLVIGF 120 RILLKLVAGF NLLMTLRLWS S	141
3-320	Sequences		
3-320-1	Sequence Number [ID]	320	
3-320-2	Molecule Type	AA	
3-320-3	Length	6	
3-320-4	Features	REGION 1..6	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide"	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
3-320-5	NonEnglishQualifier Value Residues	TSGFNG	6
3-321	Sequences		
3-321-1	Sequence Number [ID]	321	
3-321-2	Molecule Type	AA	
3-321-3	Length	6	
3-321-4	Features	REGION 1..6	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic peptide"	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
3-321-5	NonEnglishQualifier Value Residues	NVLDGL	6
3-322	Sequences		
3-322-1	Sequence Number [ID]	322	

3-322-2	Molecule Type	AA
3-322-3	Length	10
3-322-4	Features	REGION 1..10
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..10
		mol_type=protein
		organism=synthetic construct
3-322-5	NonEnglishQualifier Value	
3-322-5	Residues	ASVDGNNRLA 10
3-323	Sequences	
3-323-1	Sequence Number [ID]	323
3-323-2	Molecule Type	AA
3-323-3	Length	5
3-323-4	Features	REGION 1..5
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..5
		mol_type=protein
		organism=synthetic construct
3-323-5	NonEnglishQualifier Value	
3-323-5	Residues	SGHDT 5
3-324	Sequences	
3-324-1	Sequence Number [ID]	324
3-324-2	Molecule Type	AA
3-324-3	Length	6
3-324-4	Features	REGION 1..6
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		mol_type=protein
		organism=synthetic construct
3-324-5	NonEnglishQualifier Value	
3-324-5	Residues	YYEEEE 6
3-325	Sequences	
3-325-1	Sequence Number [ID]	325
3-325-2	Molecule Type	AA
3-325-3	Length	15
3-325-4	Features	REGION 1..15
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..15
		mol_type=protein
		organism=synthetic construct
3-325-5	NonEnglishQualifier Value	
3-325-5	Residues	ASSLGWRGGR YNEQF 15
3-326	Sequences	
3-326-1	Sequence Number [ID]	326
3-326-2	Molecule Type	DNA
3-326-3	Length	6762
3-326-4	Features	misc_feature 1..6762
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..6762
		mol_type=other DNA
		organism=synthetic construct
3-326-5	NonEnglishQualifier Value	
3-326-5	Residues	ctgacgcgcc ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga 60 ccgctacact tgcacgcgcc ctacgcgccg ctcttttcgc tttcttccct tcctttctcg 120 ccacgttcgc cgcttttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat 180 ttagtgcctt acggcacctc gaccccaaaa aacttgatta gggatgaggt tcacgtagtg 240 ggccatcgcc ctgatatagc gtttttcgcc ctttgacgtt ggagtccacg ttccttaata 300 gtggactctt gttccaaact ggaacaacac tcaaccttat ctcggtctat tcttttgatt 360 tataagggat tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat 420 ttaacgcgaa ttttaacaaa atattaacgc ttacaatttg ccattcgcca ttcaggtctg 480 gcaactgttg ggaagggcga tcggtgcggg cctcttcgct attacgccag ctggcgaaag 540 ggggatgtgc tgcaaggcga ttaagttggg taacgccagg gttttcccag tcacgacgtt 600 gtaaaacgac ggccagtga ttgtaatac actcactata gggcgaccg gggatggcg 660 gccagtaatc aattacgggg tcattagttc atagcccata tatggagttc cgcgttacat 720 aacttacggt aaatggcccg cctggctgac cgcccaacga ccccgccca ttgacgtcaa 780 taatgacgta tgttcccata gtaacgcaa tagggacttt ccattgacgt caatgggtg 840 agtattttac gtaaaactgcc cacttgccag tacatcaagt gtatcatatg ccaagtacgc 900 cccctattga cgtcaatgac ggtaaatggc ccgcctggca ttatgcccag tacatgacct 960 tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt accatgctga 1020 tgcggttttg gcagtacatc aatgggcgtg gatagcgggt tgactcacgg ggatttccaa 1080

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