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NOVEL T CELL RECEPTORS AND IMMUNE THERAPY USING THE SAME

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ABSTRACT

The present invention pertains to antigen recognizing constructs against tumor associated antigens (MAGEA1). The Invention in particular provides novel T cell receptor (TCR) based molecules which are selective and specific for the tumor expressed antigen of the invention. The TCR of the invention, and TAA binding fragments derived therefrom, are of use for the diagnosis, treatment and prevention of TAA expressing cancerous diseases. Further provided are nucleic acids encoding the antigen recognizing constructs of the invention, vectors comprising these nucleic acids, recombinant cells expressing the antigen recognizing constructs and pharmaceutical compositions comprising the compounds of the invention.

NOVEL T CELL RECEPTORS AND IMMUNE THERAPY USING THE SAME**FIELD OF THE INVENTION**

The present application is a divisional application from Australian patent application number 2021203099, which itself is a divisional application from Australian patent application number 2017373740, the entire disclosure of each application is incorporated herein by way of this reference.

The present invention pertains to antigen recognizing constructs against the tumor associated antigen (TAA) derived peptide MAGEA1-003. The invention in particular provides novel T cell receptor (TCR) based molecules which are selective and specific for the TAA of the invention. The TCR of the invention, and TAA binding fragments derived therefrom, are of use for the diagnosis, treatment and prevention of TAA expressing cancerous diseases. Further provided are nucleic acids encoding the antigen recognizing constructs of the invention, vectors comprising these nucleic acids, recombinant cells expressing the antigen recognizing constructs and pharmaceutical compositions comprising the compounds of the invention.

DESCRIPTION

The melanoma antigen genes (MAGE-A) were found to be expressed in a variety of tumors of different histological origin. Proteins encoded by the MAGE genes are tumor rejection anti-gens, which can induce specific cytotoxic T-lymphocytes (CTL) having the ability to recognize and kill cancerous cells. MAGE genes and proteins are thus a preferential target for the development of novel drugs to fight cancer by immunotherapy. MAGE-A proteins constitute a sub-family of Cancer-Testis Antigens which are expressed mainly, but not exclusively, in the germ line. They are however also expressed in various human cancers where they are associated with, and may drive, malignancy. This specific expression of MAGE antigens in tumors and not the normal surrounding healthy tissue makes this family of antigens very interesting for targeted adoptive T cell transfer. However, to date no satisfactory immune therapy is known due to the lack of specific and highly avid antibodies or T cell receptors targeting the MAGE antigen.

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T-cell based immunotherapy targets represent peptide epitopes derived from tumor-associated or tumor-specific proteins, which are presented by molecules of the major histocompatibility complex (MHC). These tumor associated antigens (TAAs) can be peptides derived from all protein classes, such as enzymes, receptors, transcription factors, etc. which are expressed and, as compared to unaltered cells of the same origin, usually up-regulated in cells of the respective tumor.

Specific elements of the cellular immune response are capable of selectively recognizing and destroying tumor cells. The isolation of T-cells from tumor-infiltrating cell populations or from peripheral blood suggests that such cells play an important role in natural immune defense against cancer. CD8-positive T-cells in particular, which recognize class I molecules of the major histocompatibility complex (MHC)-bearing peptides of usually 8 to 10 amino acid residues derived from proteins or defective ribosomal products (DRiPs) located in the cytosol, play an important role in this response. The MHC-molecules of the human are also designated as human leukocyte-antigens (HLA).

There are two classes of MHC-molecules, MHC class I and MHC class II. Complexes of peptide and MHC class I are recognized by CD8-positive T-cells bearing the appropriate T-cell receptor (TCR), whereas complexes of peptide and MHC class II molecules are recognized by CD4-positive-helper-T-cells bearing the appropriate TCR. Since both types of response, CD8 and CD4 dependent, contribute jointly and synergistically to the anti-tumor effect, the identification and characterization of tumor-associated antigens and corresponding T cell receptors is important in the development of cancer immunotherapies such as vaccines and cell therapies.

In the MHC class I dependent immune reaction, peptides not only have to be able to bind to certain MHC class I molecules expressed by tumor cells, they subsequently also have to be recognized by T-cells bearing specific T-cell

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receptors (TCR). There-fore, TAAs are a starting point for the development of a T-cell based therapy including but not limited to tumor vaccines and cell therapies.

Approximately 90 percent of peripheral blood T cells express a TCR consisting of an α polypeptide and a β polypeptide. Beside $\alpha\beta$ T cells, a small percentage of T cells (about 5% of total T cells) have been shown to express a TCR consisting of a γ polypeptide and a δ polypeptide. $\gamma\delta$ T cells are found at their highest abundance in the gut mucosa, within a population of lymphocytes known as intraepithelial lymphocytes (IELs). The antigenic molecules that activate $\gamma\delta$ T cells are still widely unknown. However, $\gamma\delta$ T cells are not MHC restricted and seem to be able to recognize whole proteins rather than requiring peptides to be presented by MHC molecules on antigen presenting cells, although some recognize MHC class IB molecules. Human V γ 9/V δ 2 T cells, which constitute the major $\gamma\delta$ T cell population in peripheral blood, are unique in that they specifically and rapidly respond to a small non-peptidic microbial metabolite, HMB-PP, an isopentenyl pyrophosphate precursor.

The chains of the T cell antigen receptor of a T cell clone are each composed of a unique combination of domains designated variable (V), [diversity (D),] joining (J), and constant (C). In each T cell clone, the combination of V, D and J domains of both the alpha and the beta chains or of both the delta and gamma chains participates in antigen recognition in a manner which is uniquely characteristic of that T cell clone and defines a unique binding site, also known as the idotype of the T cell clone. In contrast, the C domain does not participate in antigen binding.

A TCR is a heterodimeric cell surface protein of the immunoglobulin super-family, which is associated with invariant proteins of the CD3 complex involved in mediating signal transduction. TCRs exist in $\alpha\beta$ and $\gamma\delta$ forms, which are structurally similar but have quite distinct anatomical locations and probably functions. The extracellular portion of native heterodimeric $\alpha\beta$ TCR and $\gamma\delta$ TCR each contain two polypeptides, each of which has a membrane-proximal

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constant domain, and a membrane-distal variable domain. Each of the constant and variable domains includes an intra-chain disulfide bond. The variable domains contain the highly polymorphic loops analogous to the complementarity determining regions (CDRs) of antibodies. The use of TCR gene therapy overcomes a number of current hurdles. It allows equipping patients' own T cells with desired specificities and generation of sufficient numbers of T cells in a short period of time, avoiding their exhaustion. The TCR will be transduced into central memory T cells or T cells with stem cell characteristics, which may ensure better persistence and function upon transfer. TCR-engineered T cells will be infused into cancer patients rendered lymphopenic by chemotherapy or irradiation, allowing efficient engraftment but inhibiting immune suppression.

While advances have been made in the development of molecular-targeting drugs for cancer therapy, there remains a need in the art to develop new anti-cancer agents that specifically target molecules highly specific to cancer cells. The present description addresses that need by providing novel MAGEA1 TCRs, respective recombinant TCR constructs, nucleic acids, vectors and host cells that specifically bind TAA epitope(s) as disclosed; and methods of using such molecules in the treatment of cancer. The term TAA in context of the invention relates in particular to the following preferred proteins, namely MAGEA1 proteins, fragments thereof, in particular antigenic peptides presented by HLA, and preferably associated with a proliferative disorder. The preferred antigenic peptide of the invention is the peptide MAGEA1-003, having the amino acid sequence set forth in any of the SEQ ID NO: 133 to 142 and 154 to 162 in table 2 below. A TAA peptide preferably is a peptide as set forth in any of SEQ ID NO: 133 to 142 and 154 to 162.

Antigen Recognizing Constructs

The object of the invention is solved in a first aspect by an antigen recognizing construct comprising at least one complementary determining region (CDR) 3 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or preferably

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100% sequence identity to an amino acid sequence selected from SEQ ID NOs. 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111 and 117.

In some embodiments the antigen recognizing construct of the invention specifically binds to a TAA-peptide-HLA molecule complex, wherein the TAA peptide comprises, or alternatively consists of, a variant of the TAA which is at least 66%, preferably at least 77%, and more preferably at least 88% homologous (preferably at least 77% or at least 88% identical) to the amino acid sequence of the TAA of the invention, wherein said variant binds to an HLA class I or class II molecule and/or induces T-cells cross-reacting with said peptide, or a pharmaceutically acceptable salt thereof, wherein said peptide is not the underlying full-length polypeptide.

As used herein, the terms "identical" or percent "identity", when used anywhere herein in the context of two or more nucleic acid or protein/polypeptide sequences, refer to two or more sequences or subsequences that are the same or have (or have at least) a specified percentage of amino acid residues or nucleotides that are the same (i.e., at, or at least, about 60% identity, preferably at, or at least, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93% or 94%, identity, and more preferably at, or at least, about 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region - preferably over their full length sequences - , when compared and aligned for maximum correspondence over the comparison window or designated region) as measured using a sequence comparison algorithms, or by manual alignment and visual inspection (see, e.g., NCBI web site). In a particular embodiment, for example when comparing the protein or nucleic acid sequence of an antigen recognizing construct of the invention to another protein/gene, the percentage identity can be determined by the Blast searches supported at the Human Olfactory Data Explorer (e.g., <https://genome.weizmann.ac.il/cgi-bin/horde/blastHorde.pl>); in particular for amino acid identity, those using BLASTP 2.2.28+ with the following parameters: Matrix: BLOSUM62; Gap Penalties: Existence: 11, Extension: 1; Neighboring words threshold: 11; Window for multiple hits: 40.

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In the context of the present invention it shall be understood that any embodiments referred to as “comprising” certain features of the invention, shall be understood to include in some more preferred embodiments the more restricted description of “consisting of” or “consisting essentially of” the very same features of the present invention.

In another additional or alternative embodiment, the antigen recognizing construct may further comprise a CDR1 and/or a CDR2 domain sequence. Within the variable domain, CDR1 and CDR2 are found in the variable (V) region of a polypeptide chain, and CDR3 includes some of V, all of diversity (D) and joining (J) regions. CDR3 is the most variable and is the main CDR responsible for specifically and selectively recognizing an antigen. CDR1 and CDR2 sequences may be selected from a CDR sequence of a human variable chain allele.

Native alpha-beta heterodimeric TCRs have an alpha chain and a beta chain. Each chain comprises variable, joining and constant regions, and the beta chain also usually contains a short diversity region between the variable and joining regions, but this diversity region is often considered as part of the joining region. Each variable region comprises three CDRs (Complementarity Determining Regions) embedded in a framework sequence, one being the hypervariable region named CDR3. There are several types of alpha chain variable ($V\alpha$) regions and several types of beta chain variable ($V\beta$) regions distinguished by their framework, CDR1 and CDR2 sequences, and by a partly defined CDR3 sequence. The $V\alpha$ types are referred to in IMGT nomenclature by a unique TRAV number, $V\beta$ types are referred to by a unique TRBV number. For more information on immunoglobulin antibody and TCR genes see the international ImMunoGeneTics information system®, Lefranc M-P et al (Nucleic Acids Res. 2015 Jan;43(Database issue):D413-22; and <http://www.imgt.org/>).

Therefore, in one additional or alternative embodiment the antigen recognizing construct of the invention comprises CDR1, CDR2 and CDR3 sequences in a combination as provided in table 1 herein below, which display the respective

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variable chain allele together with the CDR3 sequence. Therefore, preferred are antigen recognizing constructs of the invention which comprise at least one, preferably, all three CDR sequences CDR1, CDR2 and CDR3. Preferably, an antigen recognizing construct of the invention comprises the respective CDR1 to CDR3 of one individual herein disclosed TCR variable region of the invention (see table 1 herein below and the example section).

The term “specificity” or “antigen specificity” or “specific for” a given antigen, as used herein means that the antigen recognizing construct can specifically bind to said antigen, preferably a TAA antigen, more preferably with high avidity, when said antigen is presented by HLA, preferably by HLA A2. For example, a TCR, as antigen recognizing construct, may be considered to have “antigenic specificity” for the TAA, if T cells expressing the TCR secrete at least 200 pg/ml or more (e.g., 250 pg/ml or more, 300 pg/ml or more, 400 pg/ml or more, 500 pg/ml or more, 600 pg/ml or more, 700 pg/ml or more, 1000 pg/ml or more, 2,000 pg/ml or more, 2,500 pg/ml or more, 5,000 pg/ml or more) of interferon γ (IFN- γ) upon co-culture with HLA A2-positive target cells pulsed with a low concentration of a TAA antigen, such as the TAA epitopes and antigens provided herein below (e.g., about 10^{-11} mol/l, 10^{-10} mol/l, 10^{-9} mol/l, 10^{-8} mol/l, 10^{-7} mol/l, 10^{-6} mol/l, 10^{-5} mol/l). Alternatively, or additionally, a TCR may be considered to have “antigenic specificity” for the TAA, if T cells expressing the TCR secrete at least twice as much IFN- γ as the untransduced background level of IFN- γ upon co-culture with target cells pulsed with a low concentration of the TAA antigens. Such a “specificity” as described above can – for example – be analyzed with an ELISA.

In one alternative or additional embodiment of the invention, the antigen recognizing construct selectively binds to a TAA derived antigenic peptide; preferably wherein the TAA antigenic peptide is a protein epitope or peptide having an amino acid sequence shown in SEQ ID NO: 133, or a variant thereof, wherein the variant is an amino acid deletion, addition, insertion or substitution of not more than three, preferably two and most preferably not more than one amino acid position. In some embodiments, the antigen recognizing construct of

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the invention selectively binds any of the modified MAGEA1-003 peptides set forth in SEQ ID NO: 132 to 142 and 154 to 162. In some preferred embodiments, the antigen recognizing construct of the invention does not selectively bind any of the modified MAGEA1-003 peptides set forth in SEQ ID NO: 143 to 152.

The term "selectivity" or "selective recognizing/binding" is understood to refer to the property of an antigen recognizing construct, such as a TCR or antibody, to selectively recognize or bind to preferably only one specific epitope and preferably shows no or substantially no cross-reactivity to another epitope. Preferably "selectivity" or "selective recognizing/binding" means that the antigen recognizing construct (e.g. a TCR) selectively recognizes or binds to preferably only one specific epitope and preferably shows no or substantially no cross-reactivity to another epitope, wherein said epitope is unique for one protein, such that the antigen recognizing construct shows no or substantially no cross-reactivity to another epitope and another protein.

The antigen recognizing construct according to the invention is preferably selected from an antibody, or derivative or fragment thereof, or a T cell receptor (TCR), or derivative or fragment thereof. A derivative or fragment of an antibody or TCR of the invention shall preferably retain the antigen binding/recognizing ability of the parent molecule, in particular its specificity and/or selectivity as explained above. Such binding functionality may be retained by the presence of a CDR3 region as defined herein.

In an embodiment of the invention, the inventive TCRs are able to recognize TAA antigens in a major histocompatibility complex (MHC) class I-dependent manner. "MHC class I-dependent manner," as used herein, means that the TCR elicits an immune response upon binding to TAA antigens within the context of an MHC class I molecule. The MHC class I molecule can be any MHC class I molecule known in the art, e.g., HLA-A molecules. In a preferred embodiment of the invention, the MHC class I molecule is an HLA-A2 molecule.

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The invention provides both single chain antigen recognizing construct and double chain recognizing constructs.

In an embodiment, the TCR alpha variable domain has at least one mutation relative to a TCR alpha domain shown in Table 1; and/or the TCR beta variable domain has at least one mutation relative to a TCR alpha domain shown in Table 1. In an embodiment, a TCR comprising at least one mutation in the TCR alpha variable domain and/or TCR beta variable domain has a binding affinity for, and/or a binding half-life for, a TAA peptide-HLA molecule complex, which is at least double that of a TCR comprising the unmutated TCR alpha domain and/or unmutated TCR beta variable domain.

The TCR alpha chains of the present description may further comprise a TCR alpha transmembrane domain and/or a TCR alpha intracellular domain. The TCR beta chains of the present description may further comprise a TCR beta transmembrane domain and/or a TCR beta intracellular domain.

The invention in particular provides a TCR as antigen recognizing construct, or fragment or derivative thereof. The TCR preferably is of human, which is understood as being generated from a human TCR locus and therefore comprising human TCR sequences. Furthermore, the TCR of the invention may be characterized in that it is of human origin and specifically recognizes a TAA antigen of the invention.

Another embodiment of the invention additionally or alternatively provides the antigen recognizing construct described above, which induces an immune response, preferably wherein the immune response is characterized by an increase in interferon (IFN) γ levels.

TCRs of the invention may be provided as single chain α or β , or γ and δ , molecules, or alternatively as double chain constructs composed of both the α and β chain, or γ and δ chain.

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The antigen recognizing construct of the invention may comprise a TCR α or γ chain; and/or a TCR β or δ chain; wherein the TCR α or γ chain comprises a CDR3 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 3, 15, 27, 39, 51, 63, 75, 87, 99 and 111, and/or wherein the TCR β or δ chain comprises a CDR3 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 9, 21, 33, 45, 57, 69, 81, 93, 105 and 117.

Most preferably, in some additional embodiments, wherein the disclosure refers to antigen recognizing constructs comprising any one, two or all of the CDR1 to CDR3 regions of the herein disclosed TCR chains (see Table 1), such antigen recognizing constructs may be preferred, which comprise the respective CDR sequence of the invention with not more than three, two, and preferably only one, modified amino acid residues. A modified amino acid residue may be selected from an amino acid insertion, deletion or substitution. Most preferred is that the three, two, preferably only one modified amino acid residue is the first or last amino acid residue of the respective CDR sequence. If the modification is a substitution then it is preferable in some embodiments that the substitution is a conservative amino acid substitution.

If the antigen recognizing construct of the invention is composed of at least two amino acid chains, such as a double chain TCR, or antigen binding fragment thereof, the antigen recognizing construct may comprise in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 3, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 9; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 15, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 21; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 27, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 33; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 39, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 45; or in a first polypeptide

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chain the amino acid sequence according to SEQ ID NO: 51, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 57; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 63, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 69; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 75, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 81; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 87, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 93; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 99, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 105; or in a first polypeptide chain the amino acid sequence according to SEQ ID NO: 111, and in a second polypeptide chain the amino acid sequence according to SEQ ID NO: 117. Any one of the aforementioned double chain TCR, or antigen binding fragments thereof, are preferred TCR of the present invention. In some embodiments, the CDR3 of the double chain TCR of the invention may be mutated. Mutations of the CDR3 sequences of SEQ ID NOs. 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111 and 117, as provided above preferably include a substitution, deletion, addition, or insertion of not more than three, preferably not more than two, and most preferably not more than one amino acid residue. In some embodiments, the first polypeptide chain may be a TCR α or γ chain, and the second polypeptide chain may be a TCR β or δ chain. Preferred is the combination of an $\alpha\beta$ or $\gamma\delta$ TCR.

The TCR, or the antigen binding fragment thereof, is in some embodiments composed of a TCR α and a TCR β chain, or γ and δ chain. Such a double chain TCR comprises within each chain variable regions, and the variable regions each comprise one CDR1, one CDR2 and one CDR3 sequence. The TCRs comprises the CDR1 to CDR3 sequences as comprised in the variable chain amino acid sequence of SEQ ID NO: 4 and SEQ ID NO: 10 (R26P1A9), or SEQ ID NO: 16 and SEQ ID NO: 22 (R26P2A6); or SEQ ID NO: 28 and SEQ ID NO: 34 (R26P3H1) or SEQ ID NO: 40 and SEQ ID NO: 46 (R35P3A4), or SEQ ID NO: 52 and SEQ ID NO: 58 (R37P1C9), or SEQ ID NO: 64 and SEQ ID

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NO: 70 (R37P1H1), or SEQ ID NO: 76 and SEQ ID NO: 82 (R42P3A9), or SEQ ID NO: 88 and SEQ ID NO: 94 (R43P3F2), or SEQ ID NO: 100 and SEQ ID NO: 106 (R43P3G5), or SEQ ID NO: 112 and SEQ ID NO: 118 (R59P2E7).

Some embodiments of the invention pertain to a TCR, or a fragment thereof, composed of a TCR α and a TCR β chain, wherein said TCR comprises the variable region sequences having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or preferably 100% sequence identity to the amino acid sequence selected from the α and β chain according to SEQ ID NO: 4 and 10 respectively, or 16 and 22 respectively; or 28 and 34 respectively or 40 and 46 respectively, or 52 and 58 respectively, or 64 and 70 respectively, or 76 and 82 respectively, or 88 and 94 respectively, or 100 and 106 respectively or 112 and 118 respectively.

The inventive TCRs may further comprise a constant region derived from any suitable species, such as any mammal, e.g., human, rat, monkey, rabbit, donkey, or mouse. In an embodiment of the invention, the inventive TCRs further comprise a human constant region. In some preferred embodiments, the constant region of the TCR of the invention may be slightly modified, for example, by the introduction of heterologous sequences, preferably mouse sequences, which may increase TCR expression and stability.

Some embodiments of the invention pertain to a TCR, or a fragment thereof, composed of a TCR α and a TCR β chain, wherein said TCR comprises the constant region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or preferably 100% sequence identity to an amino acid sequence selected from of the α and β chain according to SEQ ID NO: 5 and 11 respectively, or 17 and 23 respectively; or 29 and 35 respectively; or 41 and 47 respectively; or 53 and 59 respectively; or 65 and 71 respectively; or 77 and 83 respectively; or 89 and 95 respectively; or 101 and 107 respectively; or 113 and 119 respectively.

The TCR α or γ chain of the invention may further comprise a CDR1 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity

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to an amino acid sequence selected from SEQ ID Nos. 1, 13, 25, 37, 49, 61, 73, 85, 97, and 109; and/or a CDR2 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 2, 14, 26, 38, 50, 62, 74, 86, 98, and 110.

According to the invention the TCR β or δ chain may further comprise a CDR1 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 7, 19, 31, 43, 55, 67, 79, 91, 103 and 115; and/or a CDR2 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 8, 20, 32, 44, 56, 68, 80, 92, 104 and 116.

The antigen recognizing construct may in a further embodiment comprise a binding fragment of a TCR, and wherein said binding fragment comprises CDR1 to CDR3, optionally selected from the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID Nos. 1, 2, 3, or 7, 8, 9 or 13, 14, 15, or 19, 20, 21, or 25, 26, 27 or 31, 32, 33 or 37, 38, 39 or 43, 44, 45 or 49, 50, 51 or 55, 56, 57 or 61, 62, 63 or 67, 68, 69 or 73, 74, 75 or 79, 80, 81 or 85, 86, 87 or 91, 92, 93 or 97, 98, 99 or 103, 104, 105 or 109, 110, 111 or 115, 116, 117.

In further embodiments of the invention the antigen recognizing construct as described herein elsewhere is a TCR, or a fragment thereof, composed of at least one TCR α and one TCR β chain sequence, wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 1 to 3, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 7 to 9; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 13 to 15, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 19 to 21; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 25 to 27, and said TCR β chain sequence

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comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 31 to 33; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 37 to 39, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 43 to 45; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 49 to 51, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 55 to 57; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 61 to 63, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 67 to 69; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 73 to 75, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 79 to 81; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 85 to 87, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 91 to 93; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 97 to 99, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 103 to 105; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 109 to 111, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 115 to 117.

In further embodiments of the invention the antigen recognizing construct as described herein before is a TCR, or a fragment thereof, comprising at least one TCR α and one TCR β chain sequence, wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 4, and wherein said TCR β chain sequence comprises a variable region

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sequence having the amino acid sequence of SEQ ID No. 10; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 16, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 22; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 28, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 34; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 40, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 46; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 52, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 58; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 64, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 70; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 76, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 82; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 88, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 94; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 100, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 106; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 112, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 118.

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In further embodiments of the invention the antigen recognizing construct as described herein before is a TCR, or a fragment thereof, further comprising a TCR constant region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113 and 119, preferably wherein the TCR is composed of at least one TCR α and one TCR β chain sequence, wherein the TCR α chain sequence comprises a constant region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 5, 17, 29, 41, 53, 65, 77, 89, 101 and 113.

Also disclosed are antigen recognizing constructs as described herein before comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 6, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 12. The invention also provides TCRs comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 18, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 24. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 30, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 36. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 42, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 48. In further embodiments the invention provides antigen recognizing constructs

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which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 54, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 60. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 66, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 72. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 78, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 84. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 90, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 96. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 102, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 108. In further embodiments the invention provides antigen recognizing constructs which are TCR and comprise a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 114, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 120.

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As used herein, the term “murine” or “human,” when referring to an antigen recognizing construct, or a TCR, or any component of a TCR described herein (e.g., complementarity determining region (CDR), variable region, constant region, α chain, and/or β chain), means a TCR (or component thereof), which is derived from a mouse or a human unrearranged TCR locus, respectively.

In an embodiment of the invention, chimeric TCR are provided, wherein the TCR chains comprise sequences from multiple species. Preferably, a TCR of the invention may comprise an α chain comprising a human variable region of an α chain and, for example, a murine constant region of a murine TCR α chain.

In one embodiment, the TCR of the invention is a human TCR comprising human variable regions according to the above embodiments and human constant regions.

In some embodiments the antigen recognizing construct is murinized or humanized. These terms are used when amino acid sequences from a foreign species are introduced into a construct of the invention.

The TCR of the invention may be provided as a single chain TCR (scTCR). A scTCR can comprise a polypeptide of a variable region of a first TCR chain (e.g., an alpha chain) and a polypeptide of an entire (full-length) second TCR chain (e.g., a beta chain), or vice versa. Furthermore, the scTCR can optionally comprise one or more linkers which join the two or more polypeptides together. The linker can be, for instance, a peptide, which joins together two single chains, as described herein. Also provided is such a scTCR of the invention, which is fused to a human cytokine, such as IL-2, IL-7 or IL-15.

The antigen recognizing construct according to the invention can also be provided in the form of a multimeric complex, comprising at least two scTCR molecules, wherein said scTCR molecules are each fused to at least one biotin moiety, or other interconnecting molecule/linker, and wherein said scTCRs are interconnected by biotin-streptavidin interaction to allow the formation of said

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multimeric complex. Similar approaches known in the art for the generation of multimeric TCR are also possible and included in this disclosure. Also provided are multimeric complexes of a higher order, comprising more than two scTCR of the invention.

For the purposes of the present invention, a TCR is a moiety having at least one TCR alpha or gamma and/or TCR beta or delta variable domain. Generally, they comprise both a TCR alpha variable domain and a TCR beta variable domain, alternatively both a TCR gamma variable domain and a TCR delta variable domain. They may be $\alpha\beta/\gamma\delta$ heterodimers or may be in single chain format. For use in adoptive therapy, an $\alpha\beta$ or $\gamma\delta$ heterodimeric TCR may, for example, be transfected as full length chains having both cytoplasmic and transmembrane domains. If desired, an introduced disulfide bond between residues of the respective constant domains may be present.

In a preferred embodiment, the antigen recognizing construct is a human TCR, or fragment or derivative thereof. A human TCR or fragment or derivative thereof is a TCR, which comprises over 50% of the corresponding human TCR sequence. Preferably, only a small part of the TCR sequence is of artificial origin or derived from other species. It is known, however, that chimeric TCRs, e.g. derived from human origin with murine sequences in the constant domains, are advantageous. Particularly preferred are, therefore, TCRs in accordance with the present invention, which contains murine sequences in the extracellular part of their constant domains.

Thus, it is also preferred that the inventive antigen recognizing construct is able to recognize its antigen in a human leucocyte antigen (HLA) dependent manner, preferably in a HLA-A02 dependent manner. The term "HLA dependent manner" in the context of the present invention means that the antigen recognizing construct binds to the antigen only in the event that the antigenic peptide is presented by said HLA.

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The antigen recognizing construct in accordance with the invention in one embodiment preferably induces an immune response, preferably wherein the immune response is characterized by the increase in interferon (IFN) γ levels.

Also provided by the invention is a polypeptide comprising a functional portion of any of the TCRs (or functional variants thereof) described herein, for examples, of any one of the TCRs selected from R26P1A9, R26P2A6, R26P3H1, R35P3A4, R37P1C9, R37P1H1, R42P3A9, R43P3F2, R43P3G5 and R59P2E7, as provided in the example section and table 1. The term "polypeptide" as used herein includes oligopeptides and refers to a single chain of amino acids connected by one or more peptide bonds. With respect to the inventive polypeptides, the functional portion can be any portion comprising contiguous amino acids of the TCR (or functional variant thereof), of which it is a part, provided that the functional portion specifically binds to the TAA antigen, preferably as disclosed herein in Table 2, and peptides MAGEA1-003_A1 to A9 (SEQ ID NOs: 134-142) and MAGEA1-003_T1 to T9 (SEQ ID NOs: 154-162). The term "functional portion" when used in reference to a TCR (or functional variant thereof) refers to any part or fragment of the TCR (or functional variant thereof) of the invention, which part or fragment retains the biological activity of the TCR (or functional variant thereof), of which it is a part (the parent TCR or parent functional variant thereof). Functional portions encompass, for example, those parts of a TCR (or functional variant thereof) that retain the ability to specifically bind to the TAA antigen (in an HLA dependent manner), or detect, treat, or prevent cancer, to a similar extent, the same extent, or to a higher extent, as the parent TCR (or functional variant thereof). In reference to the parent TCR (or functional variant thereof), the functional portion can comprise, for instance, about 10%, 25%, 30%, 50%, 68%, 80%, 90%, 95%, or more, of the parent TCR variable sequences (or functional variant thereof).

The functional portion can comprise additional amino acids at the amino or carboxy terminus of the portion, or at both termini, in which additional amino acids are not found in the amino acid sequence of the parent TCR or functional variant thereof. Desirably, the additional amino acids do not interfere with the

biological function of the functional portion, e.g., specifically binding to the TAA antigens; and/or having the ability to detect cancer, treat or prevent cancer, etc. More desirably, the additional amino acids enhance the biological activity, as compared to the biological activity of the parent TCR or functional variant thereof.

The polypeptide can comprise a functional portion of either or both of the α and β chains of the TCRs or functional variant thereof of the invention, such as a functional portion comprising one or more of CDR1, CDR2, and (preferably) CDR3 of the variable region(s) of the α chain and/or β chain of a TCR or functional variant thereof of the invention. In an embodiment of the invention, the polypeptide can comprise a functional portion comprising the amino acid sequence of SEQ ID NO: 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111 and 117 (CDR3 of the variable regions of the TCR of the invention), or a combination thereof. In an embodiment of the invention, the inventive polypeptide can comprise, for instance, the variable region of the inventive TCR or functional variant thereof comprising a combination of the CDR regions set forth above. In this regard, the polypeptide can comprise the amino acid sequence of any of SEQ ID NO: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112 and 118 (the variable regions of an α or β chain of the TCR of the invention).

In some instances, the construct of the invention may comprise one or two polypeptide chains comprising sequences according to any of the SEQ ID NO: 1 to 120 (CDR sequences, constant and variable regions and full-length sequences), or functional fragments thereof, and further comprise(s) other amino acid sequences, e.g., an amino acid sequence encoding an immunoglobulin or a portion thereof, then the inventive protein can be a fusion protein. In this regard, the invention also provides a fusion protein comprising at least one of the inventive polypeptides described herein along with at least one other polypeptide. The other polypeptide can exist as a separate polypeptide of the fusion protein, or can exist as a polypeptide, which is expressed in frame (in tandem) with one of the inventive polypeptides described herein. The other

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polypeptide may include any peptidic or proteinaceous molecule, or a portion thereof, including, but not limited to an immunoglobulin, CD3, CD4, CD8, an MHC molecule, a CD1 molecule, e.g., CD1a, CD1b, CD1c, CD1d, etc.

The fusion protein can comprise one or more copies of the inventive polypeptide and/or one or more copies of the other polypeptide. For instance, the fusion protein can comprise 1, 2, 3, 4, 5, or more, copies of the inventive polypeptide and/or of the other polypeptide. Suitable methods of making fusion proteins are known in the art, and include, for example, recombinant methods. In some embodiments of the invention, the TCRs (and functional portions and functional variants thereof), polypeptides, and proteins of the invention may be expressed as a single protein comprising a linker peptide linking the α chain and the β chain, and linking the γ chain and the δ chain. In this regard, the TCRs (and functional variants and functional portions thereof), polypeptides, and proteins of the invention comprising the amino acid sequences of the variable regions of the TCR of the invention and may further comprise a linker peptide. The linker peptide may advantageously facilitate the expression of a recombinant TCR (including functional portions and functional variants thereof), polypeptide, and/or protein in a host cell. The linker peptide may comprise any suitable amino acid sequence. Linker sequences for single chain TCR constructs are well known in the art. Such a single chain construct may further comprise one, or two, constant domain sequences. Upon expression of the construct including the linker peptide by a host cell, the linker peptide may also be cleaved, resulting in separated α and β chains, and separated γ and δ chain.

The TCR of the invention may be modified in order to avoid mispairing of the TCR chains. The term "mispairing" shall relate to the incorrect pairing between a TCR chain of a TCR α/γ or β/δ transgene of the invention and an endogenous TCR α/γ or β/δ chain, respectively, and results in diluted cell surface expression of the transgenic TCR $\alpha\beta/\gamma\delta$ heterodimer, which reduces the functional avidity of the modified T cells. Preferably, Q at position 44 in the TCR variable domain according to the IMGT numbering is substituted by another amino acid in one or

both chains of the TCR of the invention. The substitution is preferably selected from the group consisting of R, D, E, K, I, W and V.

As already mentioned above, the binding functionality of the TCR of the invention may be provided in the framework of an antibody. For example, CDR sequences of the TCR of the invention, possibly including additional 3, 2 or 1 N and/or C terminal framework residues, may be directly grafted into an antibody variable heavy/light chain sequence. The term “antibody” in its various grammatical forms is used herein to refer to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen-binding site or a paratope. Such molecules are also referred to as “antigen binding fragments” of immunoglobulin molecules. The invention further provides an antibody, or antigen binding portion thereof, which specifically binds to the antigens described herein. The antibody can be any type of immunoglobulin that is known in the art. For instance, the antibody can be of any isotype, e.g., IgA, IgD, IgE, IgG, IgM, etc. The antibody can be monoclonal or polyclonal. The antibody can be a naturally-occurring antibody, e.g., an antibody isolated and/or purified from a mammal, e.g., mouse, rabbit, goat, horse, chicken, hamster, human, etc. Alternatively, the antibody can be a genetically-engineered antibody, e.g., a humanized antibody or a chimeric antibody. The antibody can be in monomeric or polymeric form.

The term “antibody” includes, but is not limited to, genetically engineered or otherwise modified forms of immunoglobulins, such as intrabodies, chimeric antibodies, fully human antibodies, humanized antibodies (e.g. generated by “CDR-grafting”), antibody fragments, and heteroconjugate antibodies (e.g., bispecific antibodies, diabodies, triabodies, tetra-bodies, etc.). The term “antibody” includes cys-diabodies and minibodies. Thus, each and every embodiment provided herein in regard to “antibodies”, or “antibody like constructs” is also envisioned as, bi-specific antibodies, diabodies, scFv fragments, chimeric antibody receptor (CAR) constructs, diabody and/or minibody embodiments, unless explicitly denoted otherwise. The term “antibody” includes a polypeptide of the immunoglobulin family or a polypeptide

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comprising fragments of an immunoglobulin that is capable of non-covalently, reversibly, and in a specific manner binding a corresponding antigen, preferably the TAA of the invention, as disclosed herein. An exemplary antibody structural unit comprises a tetramer. In some embodiments, a full length antibody can be composed of two identical pairs of polypeptide chains, each pair having one "light" and one "heavy" chain (connected through a disulfide bond). Antibody structure and isotypes are well known to the skilled artisan (for example from Janeway's Immunobiology, 9th edition, 2016).

The recognized immunoglobulin genes of mammals include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes (for more information on immunoglobulin genes see the international Im-MunoGeneTics information system®, Lefranc M-P et al, Nucleic Acids Res. 2015 Jan;43(Database issue):D413-22; and <http://www.imgt.org/>). For full-length chains, the light chains are classified as either kappa or lambda. For full-length chains, the heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these regions of light and heavy chains respectively. As used in this invention, an "antibody" encompasses all variations of antibody and fragments thereof. Thus, within the scope of this concept are full length antibodies, chimeric antibodies, humanized antibodies, single chain antibodies (scFv), Fab, Fab', and multimeric versions of these fragments (e.g., F(ab')₂) with the same, essentially the same or similar binding specificity. In some embodiments, the anti-body binds specifically to a peptide TAA of the invention. Preferred antigen recognizing constructs according to the invention include an antibody heavy chain, preferably the variable domain thereof, or an antigen binding fragment thereof, and/or an antibody light chain, preferably the variable domain thereof, or an antigen binding fragment thereof. Similarly, disulfide-stabilized variable region fragments (dsFv) can be prepared by recombinant DNA technology, antibody

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fragments of the invention, however, are not limited to these exemplary types of antibody fragments. Also, the antibody, or antigen binding portion thereof, can be modified to comprise a detectable label, such as, for instance, a radioisotope, a fluorophore (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE)), an enzyme (e.g., alkaline phosphatase, horseradish peroxidase), and element particles (e.g., gold particles). In some instances, the TCR CDR3 sequence may be slightly modified, but preferably by not more than 3 amino acid residues, preferably only two and most preferably only one amino acid position, as compared to the CDR3 sequences provided in SEQ ID Nos: 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111 and 117. Preferably, the antibodies comprise the CDR3, preferably all of CDR1 to CDR3 regions in the combination, as indicated for the TCR of the invention in table 1, in each case independently, optionally with not more than three or two, preferably one, amino acid substitution(s), insertion(s) and/or deletion(s) compared to these sequences.

Suitable methods of making antibodies are known in the art. For instance, standard hybridoma methods are described in, e.g., Kohler and Milstein, *Eur. J. Immunol.*, 5, 51 1-519 (1976), Harlow and Lane (eds.), *Antibodies: A Laboratory Manual*, CSH Press (1988), and C.A. Janeway et al. (eds.), *Immunobiology*, 8 Ed., Garland Publishing, New York, NY (201 1)). Alternatively, other methods, such as EBV-hybridoma methods (Haskard and Archer, *J. Immunol. Methods*, 74(2), 361-67 (1984), and Roder et al, *Methods Enzymol.*, 121, 140-67 (1986)), and bacteriophage vector expression systems (see, e.g., Huse et al., *Science*, 246, 1275-81 (1989)) are known in the art. Further, methods of producing antibodies in non-human animals are described in, e.g., U.S. Patents 5,545,806, 5,569,825, and 5,714,352, and U.S. Patent Application Publication No. 2002/0197266.

Some embodiments of the invention also pertain to TCRs, or functional fragments and polypeptides thereof, which are soluble TCRs. As used herein, the term "soluble T-cell receptor" refers to heterodimeric truncated variants of native TCRs, which comprise extracellular portions of the TCR α -chain and β -

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chain, for example linked by a disulfide bond, but which lack the transmembrane and cytosolic domains of the native protein. The terms "soluble T-cell receptor α -chain sequence and soluble T-cell receptor β -chain sequence" refer to TCR α -chain and β -chain sequences that lack the transmembrane and cytosolic domains. The sequence (amino acid or nucleic acid) of the soluble TCR α -chain and β -chains may be identical to the corresponding sequences in a native TCR or may comprise variant soluble TCR α -chain and β -chain sequences, as compared to the corresponding native TCR sequences. The term "soluble T-cell receptor" as used herein encompasses soluble TCRs with variant or non-variant soluble TCR α -chain and β -chain sequences. The variations may be in the variable or constant regions of the soluble TCR α -chain and β -chain sequences and can include, but are not limited to, amino acid deletion, insertion, substitution mutations as well as changes to the nucleic acid sequence, which do not alter the amino acid sequence. Soluble TCR of the invention in any case retain the binding functionality of their parent molecules.

The above problem is further solved by a nucleic acid encoding for an antigen recognizing construct of the invention, or any of the aforementioned protein or polypeptide constructs. The nucleic acid preferably (a) has a strand encoding for an antigen recognizing construct according to the invention; (b) has a strand complementary to the strand in (a); or (c) has a strand that hybridizes under stringent conditions with a molecule as described in (a) or (b). Stringent conditions are known to the person of skill in the art, specifically from Sambrook et al, "Molecular Cloning". In addition to that, the nucleic acid optionally has further sequences, which are necessary for expressing the nucleic acid sequence corresponding to the protein, specifically for expression in a mammalian/human cell. The nucleic acid used can be contained in a vector suitable for allowing expression of the nucleic acid sequence corresponding to the peptide in a cell. However, the nucleic acids can also be used to transform an antigen-presenting cell, which may not be restricted to classical antigen-presenting cells, such as dendritic cells, in such a way that they themselves produce the corresponding proteins on their cellular surface.

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In some embodiments, the polypeptides of the antigen recognizing constructs can be encoded by nucleic acids and expressed *in vivo* or *in vitro*. Thus, in some embodiments, a nucleic acid encoding an antigen recognizing construct is provided. In some embodiments, the nucleic acid encodes one part or monomer of an antigen recognizing construct of the invention (for example one of two chains of a TCR of the invention), and/or another nucleic acid encodes another part or monomer of an antigen recognizing construct of the invention (for example the other of two chains of the TCR). In some embodiments, the nucleic acid encodes two or more antigen recognizing construct polypeptide chains, for example, at least 2 TCR chains. Nucleic acids encoding multiple antigen recognizing construct chains can include nucleic acid cleavage sites between at least two chain sequences, can encode transcription or translation start site between two or more chains sequences, and/or can encode proteolytic target sites between two or more antigen recognizing construct chains.

By “nucleic acid” as used herein includes “polynucleotide,” “oligonucleotide,” and “nucleic acid molecule,” and generally means a polymer of DNA or RNA, which can be single-stranded or double-stranded, synthesized or obtained (e.g., isolated and/or purified) from natural sources, which can contain natural, non-natural or altered nucleotides, and can contain a natural, non-natural or altered internucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified oligonucleotide.

Preferably, the nucleic acids of the invention are recombinant. As used herein, the term “recombinant” refers to (i) molecules that are constructed outside living cells by joining natural or synthetic nucleic acid segments to nucleic acid molecules that can replicate in a living cell, or (ii) molecules that result from the replication of those described in (i) above. For purposes herein, the replication can be *in vitro* replication or *in vivo* replication. The nucleic acid can comprise any nucleotide sequence, which encodes any of the TCRs, polypeptides, or proteins, or functional portions or functional variants thereof described herein.

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Furthermore, the invention provides a vector comprising a nucleic acid in accordance to the invention as described above. Desirably, the vector is an expression vector or a recombinant expression vector. The term “recombinant expression vector” refers in context of the present invention to a nucleic acid construct that allows for the expression of an mRNA, protein or polypeptide in a suitable host cell. The recombinant expression vector of the invention can be any suitable recombinant expression vector, and can be used to transform or transfect any suitable host. Suitable vectors include those designed for propagation and expansion or for expression or both, such as plasmids and viruses. Examples of animal expression vectors include pEUK-CI, pMAM, and pMAMneo. Preferably, the recombinant expression vector is a viral vector, e.g., a retroviral vector. The recombinant expression vector comprises regulatory sequences, such as transcription and translation initiation and termination codons, which are specific to the type of host cell (e.g., bacterium, fungus, plant, or animal), into which the vector is to be introduced and in which the expression of the nucleic acid of the invention may be performed. Furthermore, the vector of the invention may include one or more marker genes, which allow for selection of transformed or transfected hosts. The recombinant expression vector can comprise a native or normative promoter operably linked to the nucleotide sequence encoding the constructs of the invention, or to the nucleotide sequence, which is complementary to or which hybridizes to the nucleotide sequence encoding the constructs of the invention. The selections of promoters include, e.g., strong, weak, inducible, tissue-specific and developmental-specific promoters. The promoter can be a non-viral promoter or a viral promoter. The inventive recombinant expression vectors can be designed for either transient expression, for stable expression, or for both. Also, the recombinant expression vectors can be made for constitutive expression or for inducible expression.

The invention also pertains to a host cell comprising an antigen recognizing construct in accordance with the invention. Specifically, the host cell of the invention comprises a nucleic acid, or a vector as described herein above. The host cell can be a eukaryotic cell, e.g., plant, animal, fungi, or algae, or can be a

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prokaryotic cell, e.g., bacteria or protozoa. The host cell can be a cultured cell or a primary cell, i.e., isolated directly from an organism, e.g., a human. The host cell can be an adherent cell or a suspended cell, i.e., a cell that grows in suspension. For purposes of producing a recombinant TCR, polypeptide, or protein, the host cell is preferably a mammalian cell. Most preferably, the host cell is a human cell. While the host cell can be of any cell type, can originate from any type of tissue, and can be of any developmental stage, the host cell preferably is a peripheral blood leukocyte (PBL) or a peripheral blood mononuclear cell (PBMC). More preferably, the host cell is a T cell. The T cell can be any T cell, such as a cultured T cell, e.g., a primary T cell, or a T cell from a cultured T cell line, e.g., Jurkat, SupT1, etc., or a T cell obtained from a mammal, preferably a T cell or T cell precursor from a human patient. If obtained from a mammal, the T cell can be obtained from numerous sources, including but not limited to blood, bone marrow, lymph node, the thymus, or other tissues or fluids. T cells can also be enriched for or purified. Preferably, the T cell is a human T cell. More preferably, the T cell is a T cell isolated from a human. The T cell can be any type of T cell and can be of any developmental stage, including but not limited to, CD4-positive and/or CD8-positive, CD4-positive helper T cells, e.g., Th1 and Th2 cells, CD8-positive T cells (e.g., cytotoxic T cells), tumor infiltrating cells (TILs), memory T cells, naive T cells, and the like. Preferably, the T cell is a CD8-positive T cell or a CD4-positive T cell.

Preferably, the host cell of the invention is a lymphocyte, preferably, a T lymphocyte, such as a CD4-positive or CD8-positive T-cell. The host cell furthermore preferably is a tumor reactive T cell specific for TAA expressing tumor cells.

The objective of the invention is also solved by a method of manufacturing a TAA specific antigen recognizing construct, or of a TAA specific antigen recognizing construct expressing cell line, comprising

a. Providing a suitable host cell,

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- b. Providing a genetic construct comprising a coding sequence encoding for an antigen recognizing construct according to the herein disclosed invention,
- c. Introducing into said suitable host cell said genetic construct, and
- d. Expressing said genetic construct by said suitable host cell.

The method may further comprise a step of cell surface presentation of said antigen recognizing construct on said suitable host cell.

In other preferred embodiments, the genetic construct is an expression construct comprising a promoter sequence operably linked to said coding sequence.

Preferably, said antigen recognizing construct is of mammalian origin, preferably of human origin. The preferred suitable host cell for use in the method of the invention is a mammalian cell, such as a human cell, in particular a human T lymphocyte. T cells for use in the invention are described in detail herein above.

Also encompassed by the invention are embodiments, wherein said antigen recognizing construct is a modified TCR, wherein said modification is the addition of functional domains, such as a label or a therapeutically active substance. Furthermore, encompassed are TCR having alternative domains, such as an alternative membrane anchor domain instead of the endogenous transmembrane region.

Desirably, the transfection system for introducing the genetic construct into said suitable host cell is a retroviral vector system. Such systems are well known to the skilled artisan.

Also comprised by the present invention is in one embodiment the additional method step of isolation and purification of the antigen recognizing construct

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from the cell and, optionally, the reconstitution of the translated antigen recognizing construct-fragments in a T-cell.

In an alternative aspect of the invention a T-cell is provided obtained or obtainable by a method for the production of a T cell receptor (TCR), which is specific for tumorous cells and has high avidity as described herein above. Such a T cell is depending on the host cell used in the method of the invention, for example, a human or non-human T-cell, preferably a human TCR.

The term "isolated" as used herein in the context of a polypeptide, such as an antigen recognizing construct (an example of which could be an antibody), refers to a polypeptide that is purified from proteins or polypeptides or other contaminants that would interfere with its therapeutic, diagnostic, prophylactic, research or other use. An antigen recognizing construct according to the invention may be a recombinant, synthetic or modified (non-natural) antigen binding construct. The term "isolated" as used herein in the context of a nucleic acid or cells refers to a nucleic acid or cells that is/are purified from DNA, RNA, proteins or polypeptides or other contaminants (such as other cells) that would interfere with its therapeutic, diagnostic, prophylactic, research or other use, or it refers to a recombinant, synthetic or modified (non-natural) nucleic acid. In this context, a "recombinant" protein/polypeptide or nucleic acid is one made using recombinant techniques. Methods and techniques for the production of recombinant nucleic acids and proteins are well known in the art.

Treatment Methods and Diseases

One further aspect of the present invention relates to the herein disclosed antigen recognizing constructs, nucleic acids, vectors, pharmaceutical compositions and/or host cell for use in medicine. The use in medicine in one preferred embodiment includes the use in the diagnosis, prevention and/or treatment of a tumor disease, such as a malignant or benign tumor disease. The tumor disease is, for example, a tumor disease characterized by the expression of the TAA, in a cancer or tumor cell of said tumor disease.

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With respect to the above mentioned medical applications of the antigen recognizing constructs and other materials derived therefrom, pertaining thereto or encoding the same, in accordance of the present disclosure, the to be treated and/or to be diagnosed diseases can be any proliferative disorder, preferably characterized by the expression of the TAA or TAA epitope sequence of the invention, for example any cancer, including any of acute lymphocytic cancer, acute myeloid leukemia, alveolar rhabdomyosarcoma, bone cancer, brain cancer, breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct, cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vagina, cancer of the vulva, chronic lymphocytic leukemia, chronic myeloid cancer, colon cancer, esophageal cancer, cervical cancer, gastrointestinal carcinoid tumor, glioma, Hodgkin lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer, lung cancer, malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin lymphoma, cancer of the oropharynx, ovarian cancer, cancer of the penis, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal cancer, skin cancer, small intestine cancer, soft tissue cancer, stomach cancer, testicular cancer, thyroid cancer, cancer of the uterus, ureter cancer, and urinary bladder cancer. A preferred cancer is cancer is cancer of the uterine cervix, oropharynx, anus, anal canal, anorectum, vagina, vulva, or penis. A particularly preferred cancer is a TAA positive cancer, including preferably, melanoma, gastrointestinal and gastric cancer.

The constructs, proteins, TCRs antibodies, polypeptides and nucleic acids of the invention are in particular for use in immune therapy, preferably, in adoptive T cell therapy. The administration of the compounds of the invention can, for example, involve the infusion of T cells of the invention into said patient. Preferably, such T cells are autologous T cells of the patient and *in vitro* transduced with a nucleic acid or antigen recognizing construct of the present invention.

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The inventive antigen recognizing constructs, TCRs, polypeptides, proteins (including functional variants thereof), nucleic acids, recombinant expression vectors, host cells (including populations thereof), and antibodies (including antigen binding portions thereof), all of which are collectively referred to as "inventive TCR materials" hereinafter, can be formulated into a composition, such as a pharmaceutical composition. In this regard, the invention provides a pharmaceutical composition comprising any of the antigen recognizing constructs, TCRs, polypeptides, proteins, functional portions, functional variants, nucleic acids, expression vectors, host cells (including populations thereof), and antibodies (including antigen binding portions thereof) described herein, and a pharmaceutically acceptable carrier, excipient and/or stabilizer. The inventive pharmaceutical compositions containing any of the inventive TCR materials can comprise more than one inventive TCR material, e.g., a polypeptide and a nucleic acid, or two or more different TCRs (including functional portions and functional variants thereof). Alternatively, the pharmaceutical composition can comprise an inventive TCR material in combination with another pharmaceutically active agent(s) or drug(s), such as chemotherapeutic agents, e.g., asparaginase, busulfan, carboplatin, cisplatin, daunorubicin, doxorubicin, fluorouracil, gemcitabine, hydroxyurea, methotrexate, paclitaxel, rituximab, vinblastine, vincristine, etc. Preferably, the carrier is a pharmaceutically acceptable carrier. With respect to pharmaceutical compositions, the carrier can be any of those conventionally used for the particular inventive TCR material under consideration. Such pharmaceutically acceptable carriers are well-known to those skilled in the art and are readily available to the public. It is preferred that the pharmaceutically acceptable carrier be one, which has no detrimental side effects or toxicity under the conditions of use.

Thus also provided is a pharmaceutical composition, comprising any of the herein described products of the invention and TCR materials of the invention, specifically any proteins, nucleic acids or host cells. In a preferred embodiment the pharmaceutical composition is for immune therapy, preferably adoptive cell therapy.

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Preferably, the inventive TCR material is administered by injection, e.g., intravenously. When the inventive TCR material is a host cell expressing the inventive TCR (or functional variant thereof), the pharmaceutically acceptable carrier for the cells for injection may include any isotonic carrier such as, for example, normal saline (about 0.90% w/v of NaCl in water, about 300 mOsm/L NaCl in water, or about 9.0 g NaCl per liter of water), NORMOSOL R electrolyte solution (Abbott, Chicago, IL), PLASMA-LYTE A (Baxter, Deerfield, IL), about 5% dextrose in water, or Ringer's lactate. In an embodiment, the pharmaceutically acceptable carrier is supplemented with human serum albumen.

For purposes of the invention, the amount or dose (e.g., numbers of cells when the inventive TCR material is one or more cells) of the inventive TCR material administered may be sufficient to affect, e.g., a therapeutic or prophylactic response, in the subject or animal over a reasonable time frame. For example, the dose of the inventive TCR material should be sufficient to bind to a cancer antigen, or detect, treat or prevent cancer in a period of from about 2 hours or longer, e.g., 12 to 24 or more hours, from the time of administration. In certain embodiments, the time period could be even longer. The dose will be determined by the efficacy of the particular inventive TCR material and the condition of the animal (e.g., human), as well as the body weight of the animal (e.g., human) to be treated.

It is contemplated that the inventive pharmaceutical compositions, antigen recognizing constructs, TCRs (including functional variants thereof), polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, or populations of cells can be used in methods of treating or preventing cancer, or TAA-positive premalignancy. The inventive TCRs (and functional variants thereof) are believed to bind specifically to the TAA of the invention, such that the TCR (or related inventive polypeptide or protein and functional variants thereof), when expressed by or on a cell, such as a T cell, is able to mediate an immune response against a target cell expressing the TAA of the

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invention, preferably presenting TAA peptides via MHC I or II on the surface of said target cell. In this regard, the invention provides a method of treating or preventing a condition, in particular cancer, in a mammal, comprising administering to the mammal any of the pharmaceutical compositions, antigen recognizing constructs, in particular TCRs (and functional variants thereof), polypeptides, or proteins described herein, any nucleic acid or recombinant expression vector comprising a nucleotide sequence encoding any of the TCRs (and functional variants thereof), polypeptides, proteins described herein, or any host cell or population of cells comprising a nucleic acid or recombinant vector, which encodes any of the constructs of the invention (and functional variants thereof), polypeptides, or proteins described herein, in an amount effective to treat or prevent the condition in the mammal, wherein the condition is preferably cancer, such as a cancer expressing the TAA of the invention.

Examples of pharmaceutically acceptable carriers or diluents useful in the present invention include stabilizers such as SPGA, carbohydrates (e.g. sorbitol, mannitol, starch, sucrose, glucose, dextran), proteins such as albumin or casein, protein containing agents such as bovine serum or skimmed milk and buffers (e.g. phosphate buffer).

The terms “treat,” and “prevent” as well as words stemming therefrom, as used herein, do not necessarily imply 100% or complete treatment or prevention. Rather, there are varying degrees of treatment or prevention of which one of ordinary skill in the art recognizes as having a potential benefit or therapeutic effect. In this respect, the inventive methods can provide any amount of any level of treatment or prevention of a condition in a mammal. Furthermore, the treatment or prevention provided by the inventive method can include treatment or prevention of one or more conditions or symptoms of the condition, e.g., cancer, being treated or prevented. For example, treatment or prevention can include promoting the regression of a tumor. Also, for purposes herein, “prevention” can encompass delaying the onset of the condition, or a symptom or condition thereof.

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The present invention also relates to a method of treating cancer comprising administering a TCR, a nucleic acid, or a host cell of the present description in combination with at least one chemotherapeutic agent and/or radiation therapy.

Another aspect of the invention further pertains to a method for detecting a TAA protein, or a complex of MHC and the TAA protein (protein epitope of the TAA), in a (biological) sample –such as one obtained from a subject or patient - comprising contacting the sample with an antigen recognizing construct specifically binding to said TAA peptide, or to the TAA peptide/MHC complex, and detecting the binding between said antigen recognizing construct and said TAA peptide, or to the TAA peptide/MHC complex. In some embodiments, the antigen recognizing construct is a TCR or antibody, or similar constructs, or preferably the antigen recognizing construct according to the herein described invention. In some embodiments, the (biological) sample is a sample of a tumour or a cancer (such as one of those described elsewhere herein) for example a sample comprising tumour or cancer cells.

Also provided is a method of treating cancer in a subject in need thereof, comprising:

- a) isolating a cell from said subject;
- b) transforming the cell with at least one vector encoding an antigen recognizing construct of the present invention to produce a transformed cell;
- c) expanding the transformed cell to produce a plurality of transformed cells; and
- d) administering the plurality of transformed cells to said subject.

Also provided is a method of treating cancer in a subject in need thereof, comprising:

- a) isolating a cell from a healthy donor;
- b) transforming the cell with a vector encoding an antigen recognizing construct of the present invention to produce a transformed cell;
- c) expanding the transformed cell to produce a plurality of transformed cells; and

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d) administering the plurality of transformed cells to said subject.

Also provided is a method of detecting cancer in a biological sample comprising:

- a) contacting the biological sample with an antigen recognizing construct of the present description;
- b) detecting binding of the antigen recognizing construct to the biological sample.

In some embodiments, the method of detecting cancer is carried out *in vitro*, *in vivo* or *in situ*.

Also provided is a method of detecting the presence of a condition in a mammal. The method comprises (i) contacting a sample comprising one or more cells from the mammal with any of the inventive TCRs (and functional variants thereof), polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, populations of cells, antibodies, or antigen binding portions thereof, or pharmaceutical compositions described herein, thereby forming a complex, and detecting the complex, wherein detection of the complex is indicative of the presence of the condition in the mammal, wherein the condition is cancer, such as a TAA expressing malignancy.

With respect to the inventive method of detecting a condition in a mammal, the sample of cells can be a sample comprising whole cells, lysates thereof, or a fraction of the whole cell lysates, e.g., a nuclear or cytoplasmic fraction, a whole protein fraction, or a nucleic acid fraction.

For purposes of the inventive detecting method, the contacting can take place *in vitro* or *in vivo* with respect to the mammal. Preferably, the contacting is *in vitro*.

Also, detection of the complex can occur through any number of ways known in the art. For instance, the inventive antigen recognizing constructs (and functional variants thereof), polypeptides, proteins, nucleic acids, recombinant

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expression vectors, host cells, populations of cells, or antibodies or TCRs, or antigen binding portions thereof, described herein, can be labeled with a detectable label such as, for instance, a radioisotope, a fluorophore (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE)), an enzyme (e.g., alkaline phosphatase, horseradish peroxidase), and element particles (e.g., gold particles).

For purposes of the inventive methods, wherein host cells or populations of cells are administered, the cells can be cells that are allogeneic or autologous to the mammal. Preferably, the cells are autologous to the mammal.

With respect to the above mentioned medical applications of the TCR material of the invention, the to be treated and/or diagnosed cancer can be any cancer, including any of acute lymphocytic cancer, acute myeloid leukemia, alveolar rhabdomyosarcoma, bone cancer, brain cancer, breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct, cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vagina, cancer of the vulva, chronic lymphocytic leukemia, chronic myeloid cancer, colon cancer, esophageal cancer, cervical cancer, gastrointestinal carcinoid tumor, glioma, Hodgkin lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer, lung cancer, malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin lymphoma, cancer of the oropharynx, ovarian cancer, cancer of the penis, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal cancer, skin cancer, small intestine cancer, soft tissue cancer, stomach cancer, testicular cancer, thyroid cancer, cancer of the uterus, ureter cancer, and urinary bladder cancer. A preferred cancer is cancer of the uterine cervix, oropharynx, anus, anal canal, anorectum, vagina, vulva, or penis. A particularly preferred cancer is a TAA positive cancer, such as skin cancer, such as preferably melanoma, gastrointestinal or gastric cancer.

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In general, the invention provides a method for treating a subject suffering from a tumor or tumor disease comprising the administration of the antigen recognizing constructs, nucleic acids, vectors, pharmaceutical compositions and/or host cell as disclosed by the present invention. Preferably the subject is a subject in need of such a treatment. The subject in preferred embodiments is a mammalian subject, preferably a human patient, suffering from a tumor or tumor disease, which is TAA-positive.

In view of the disclosure herein it will be appreciated that the invention furthermore pertains to the following items:

Item 1: An antigen recognizing construct comprising at least one complementary determining region (CDR) 3 having at least 50% sequence identity to an amino acid sequence selected from SEQ ID NOs. 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111 and 117.

Item 2: The antigen recognizing construct according to item 1, wherein said antigen recognizing construct is capable of specifically and/or selectively binding to a TAA of the invention antigenic peptide.

Item 3: The antigen recognizing construct according to item 1 or 2, wherein the antigen recognizing construct is an antibody, or derivative or fragment thereof, or a T cell receptor (TCR), or a derivative or fragment thereof.

Item 4: The antigen recognizing construct according to any one of items 1 to 3, wherein said antigen recognizing construct binds to a human leucocyte antigen (HLA) presented TAA antigenic peptide, wherein said HLA is optionally type A2.

Item 5: The antigen recognizing construct according to any one of items 1 to 4, wherein the construct specifically and/or selectively binds to an epitope having the amino acid sequence selected from SEQ ID NO: 133 to 142, preferably to SEQ ID NO: 133.

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Item 6: The antigen recognizing construct according to any one of items 1 to 5, wherein the construct is an α/β -TCR, or fragment or derivative thereof, or the construct is a γ/δ -TCR, or a fragment or derivative thereof.

Item 7: The antigen recognizing construct according to any one of items 1 to 6, characterized in that the construct is of human origin and specifically and/or selectively recognizes a TAA antigenic peptide.

Item 8: The antigen recognizing construct according to any one of items 1 to 7, wherein said antigen recognizing construct is capable of inducing an immune response in a subject, optionally wherein the immune response is characterized by an increase in interferon (IFN) γ levels.

Item 9: The antigen recognizing construct according to any one of items 1 to 8, comprising a TCR α or γ chain; and/or a TCR β or δ chain; wherein the TCR α or γ chain comprises a CDR3 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 3, 15, 27, 39, 51, 63, 75, 87, 99 and 111, and/or wherein the TCR β or δ chain comprises a CDR3 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 9, 21, 33, 45, 57, 69, 81, 93, 105 and 117.

Item 10: The antigen recognizing construct according to item 9, wherein the TCR α or γ chain further comprises a CDR1 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 1, 13, 25, 37, 49, 61, 73, 85, 97 and 109; and/or a CDR2 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 2, 14, 26, 38, 50, 62, 74, 86, 98 and 110.

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Item 11: The antigen recognizing construct according to item 9 or 10, wherein the TCR β or δ chain further comprises a CDR1 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 7, 19, 31, 43, 55, 67, 79, 91, 103 and 115; and/or a CDR2 having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 8, 20, 32, 44, 56, 68, 80, 92, 104 and 116.

Item 12: The antigen recognizing construct according to any of items 1 to 11, comprising a TCR variable chain region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112 and 118.

Item 13: The antigen recognizing construct according to any of items 1 to 12, wherein the construct is humanized, chimerized and/or murinized.

Item 14: The antigen recognizing construct according to any of items 1 to 13, comprising a binding fragment of a TCR, and wherein said binding fragment comprises CDR1 to CDR3 optionally selected from the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID Nos. 1, 2, 3, or 7, 8, 9 or 13, 14, 15, or 19, 20, 21, or 25, 26, 27 or 31, 32, 33 or 37, 38, 39 or 43, 44, 45 or 49, 50, 51 or 55, 56, 57 or 61, 62, 63 or 67, 68, 69 or 73, 74, 75 or 79, 80, 81 or 85, 86, 87 or 91, 92, 93 or 97, 98, 99 or 103, 104, 105 or 109, 110, 111 or 115, 116, 117.

Item 15: The antigen recognizing construct according to any of items 1 to 14, wherein the construct is a TCR, or a fragment thereof, composed of at least one TCR α and one TCR β chain sequence, wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 1 to 3, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 7 to 9; or wherein said TCR α chain sequence comprises the CDR1 to

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CDR3 sequences having the amino acid sequences of SEQ ID NO: 13 to 15, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 19 to 21; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 25 to 27, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 31 to 33; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 37 to 39, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 43 to 45; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 49 to 51, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 55 to 57; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 61 to 63, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 67 to 69; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 73 to 75, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 79 to 81; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 85 to 87, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 91 to 93; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 97 to 99, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 103 to 105; or wherein said TCR α chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 109 to 111, and said TCR β chain sequence comprises the CDR1 to CDR3 sequences having the amino acid sequences of SEQ ID NO: 115 to 117.

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Item 16: The antigen recognizing construct according to any of items 1 to 15, wherein the construct is a TCR, or a fragment thereof, comprising at least one TCR α and one TCR β chain sequence, wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 4, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 10; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 16, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 22; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 28, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 34; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 40, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 46; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 52, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 58; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 64, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 70; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 76, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 82; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 88, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 94; or wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 100, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 106; or

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wherein said TCR α chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 112, and wherein said TCR β chain sequence comprises a variable region sequence having the amino acid sequence of SEQ ID No. 118..

Item 17: The antigen recognizing construct according to any of items 1 to 16, wherein the construct is a TCR, or a fragment thereof, further comprising a TCR constant region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113 and 119, preferably wherein the TCR is composed of at least one TCR α and one TCR β chain sequence, wherein the TCR α chain sequence comprises a constant region having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID Nos. 5, 17, 29, 41, 53, 65, 77, 89, 101 and 113.

Item 18: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 6, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 12.

Item 19: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 18, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 24.

Item 20: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of

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SEQ ID No. 30, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 36.

Item 21: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 42, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 48.

Item 22: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 54, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 60.

Item 23: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 66, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 72.

Item 24: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 78, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 84.

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Item 25: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 90, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 96.

Item 26: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 102, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 108.

Item 27: The antigen recognizing construct according to any of items 1 to 17, comprising a first TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 114, and a second TCR chain having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID No. 120.

Item 28: A nucleic acid encoding for an antigen recognizing construct according to any one of items 1 to 27.

Item 29: A vector comprising a nucleic acid according to item 28.

Item 30: A host cell comprising an antigen recognizing construct according to any one of items 1 to 27, or a nucleic acid according to item 28, or a vector according to item 29.

Item 31: The host cell according to item 30, wherein the cell is a lymphocyte, preferably a T lymphocyte or T lymphocyte progenitor, more preferably a CD4 or CD8 positive T-cell.

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Item 32: A pharmaceutical composition comprising the antigen recognizing construct according to any of items 1 to 27, or the nucleic acid according to item 28, or the vector according to item 29, or the host cell according to item 30 or 31, and a pharmaceutical acceptable carrier, stabilizer and/or excipient.

Item 33: The antigen recognizing construct according to any one of items 1 to 27, or a nucleic acid according to item 28, or a vector according to item 29, or a host cell according to item 30 or 31, or the pharmaceutical composition according to item 32, for use in medicine.

Item 34: The antigen recognizing construct, or the nucleic acid, or the vector, or the host cell, or the pharmaceutical composition, for use according to item 33, for use in the diagnosis, prevention, and/or treatment of a proliferative disease, wherein the disease comprises a malignant or benign tumor disease.

Item 35: The antigen recognizing construct, or the nucleic acid, or the vector, or the host cell, or the pharmaceutical composition, for use according to item 34, wherein the tumor disease is characterized by the expression of TAA in a tumor cell of the tumor disease.

Item 36: The antigen recognizing construct, or the nucleic acid, or the vector, or the host cell, or the pharmaceutical composition, for use according to any one of items 33 to 35, wherein the use in medicine is a use in immune therapy optionally comprising an adoptive cell transfer, wherein the immune therapy comprises adoptive autologous or heterologous T-cell therapy.

Item 37: A method of manufacturing a TAA specific antigen recognizing construct expressing cell line, comprising

- a. providing a suitable host cell,
- b. providing a genetic construct comprising a coding sequence encoding the antigen recognizing construct according to any of items 1 to 27,
- c. introducing into said suitable host cell said genetic construct,

d. expressing said genetic construct by said suitable host cell.

Item 38: The method according to item 37, further comprising cell surface presentation of said antigen recognizing construct.

Item 39: The method according to item 37 or 38, wherein the genetic construct is an expression construct comprising a promoter sequence operably linked to said coding sequence.

Item 40: The method according to any one of items 37 to 39, wherein said antigen recognizing construct is of mammalian origin, preferably of human origin.

Item 41: The method according to any one of items 37 to 40, wherein said suitable host cell is a mammalian cell, optionally selected from a human cell or a human T lymphocyte.

Item 42: The method according to any of items 37 to 41, wherein said antigen recognizing construct is a modified TCR, wherein said modification comprises addition of a functional domain comprising a label, or an alternative domain comprising a membrane anchor domain.

Item 43: The method according to item 42, wherein said antigen recognizing construct is an alpha/beta TCR, gamma/delta TCR, or a single chain TCR (scTCR).

Item 44: The method according to any of items 37 to 43, wherein said genetic construct is introduced into said suitable host cell by retroviral transfection.

Item 45: The method according to any of items 37 to 44, further comprising the isolation and purification of the antigen recognizing construct from the

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suitable host cell and, optionally, reconstitution of the antigen recognizing construct in a T-cell.

Item 46: A method of killing target-cells in a patient, in which target cells aberrantly express TAA, the method comprising administering to the patient an effective number of T cells expressing a TCR of any of the aforementioned items, the nucleic acid, the expression vector, the host cell, and/or the pharmaceutical composition of the aforementioned items.

Item 47: The TCR of any of the aforementioned items, wherein the alpha chain comprises a TCR alpha variable domain at least 95% identical to the amino acid sequence of SEQ ID NO: 4; and the beta chain comprises a TCR beta variable domain at least 95% identical to SEQ ID NO: 10, and wherein the TCR specifically binds to a TAA-peptide MHC molecule complex.

Item 48: The TCR of any of the aforementioned items having at least one mutation in the alpha chain relative to SEQ ID NO: 4 and/or having at least one mutation in the beta chain relative to SEQ ID NO: 10, and wherein the TCR has a binding affinity for, and/or a binding half-life for, a TAA peptide-HLA molecule complex, which is at least double that of the unmutated TCR for the same peptide.

Item 49: The TCR of any of the aforementioned items having at least one mutation in the alpha chain relative to SEQ ID NO: 4 and/or having at least one mutation in the beta chain relative to SEQ ID NO: 10, and wherein the TCR has modified glycosylation compared to the unmutated TCR.

Item 50: The method of treating of the aforementioned items, wherein the TCR, the nucleic acid, the expression vector, the host cell or the pharmaceutical composition is administered in at least two administrations separated by at least 24 hours.

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Item 51: The method of item 50, wherein the TCR, the nucleic acid, the expression vector, the host cell or the pharmaceutical composition is administered to the subject over a period of days, weeks or months, for example by local infusion, such as by an infusion pump and/or a catheter system.

Item 52: The method of item 51, wherein said local infusion is into a solid tumor, a blood vessel that feeds a solid tumor, and/or the area surrounding a solid tumor.

Item 52: The treatment method of any of the aforementioned items, wherein the TCR, the nucleic acid, the expression vector, the host cell or the pharmaceutical composition of is administered in a dose of about 10^4 to about 10^{10} cells per dose.

Item 53: A TCR comprising at least one alpha chain complementarity determining region (CDR) selected from the group consisting of an alpha chain CDR1, CDR2 and CDR3 of SEQ ID NO: 4 and/or at least one beta chain complementarity determining region (CDR) selected from the group consisting of a beta chain CDR1, CDR2 and CDR3 of SEQ ID NO: 10, and wherein the TCR specifically binds to a TAA peptide-MHC molecule complex.

The present invention will now be further described in the following examples with reference to the accompanying figures and sequences, nevertheless, without being limited thereto. For the purposes of the present invention, all references as cited herein are incorporated by reference in their entireties. In the figures and Sequences:

Figure 1: IFN γ release from CD8 $^+$ T-cells electroporated with alpha and beta chain RNA of TCR R26P1A9 (SEQ ID NO:1-12) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ

release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 2: IFN γ release from CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R26P2A6 (SEQ ID NO:13-24) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 3: IFN γ release from CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R26P3H1 (SEQ ID NO:25-36) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 4: IFN γ release from CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R35P3A4 (SEQ ID NO:37-48) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target

cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 5: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1C9 (SEQ ID NO:49-60) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 6: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1H1 (SEQ ID NO:61-72) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 7: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R42P3A9 (SEQ ID NO:73-84) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

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Figure 8: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3F2 (SEQ ID NO:85-96) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 9: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3G5 (SEQ ID NO:97-108) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 10: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R59P2E7 (SEQ ID NO:109-120) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 alanine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:134-142) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 11: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P1A9 (SEQ ID NO:1-12) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous

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but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 12: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P2A6 (SEQ ID NO:13-24) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 13: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P3H1 (SEQ ID NO:25-36) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide

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NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 14: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R35P3A4 (SEQ ID NO:37-48) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 15: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1C9 (SEQ ID NO:49-60) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

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Figure 16: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1H1 (SEQ ID NO:61-72) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 17: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R42P3A9 (SEQ ID NO:73-84) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 18: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3F2 (SEQ ID NO:85-96) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001

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(SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 19: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3G5 (SEQ ID NO:97-108) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 20: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R59P2E7 (SEQ ID NO:109-120) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or homologous but unrelated peptide TMEM175-001 (SEQ ID NO:143), EPAS-001 (SEQ ID NO:144), PTRF-001 (SEQ ID NO:145), GALNTL4-001 (SEQ ID NO:146), PSME2-001 (SEQ ID NO:147), KIAA103-002 (SEQ ID NO:148), NSD1-001 (SEQ ID NO:149), TBC1D9-002 (SEQ ID NO:150), TMTC4-001 (SEQ ID NO:151) or RASAL2-002 (SEQ ID NO:152) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-

cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0004) is shown on the left Y-axis, donor 2 (TCRA-0005) on the right Y-axis, respectively.

Figure 21: HLA-A*02/MAGEA1-003 tetramer or HLA-A*02/NYESO1-001 tetramer staining, respectively, of CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R26P2A6 and R26P3H1, respectively. CD8⁺ T-cells electroporated with RNA of 1G4 TCR that specifically binds to HLA-A*02/NYESO1-001 complex and mock electroporated CD8⁺ T-cells served as controls.

Figure 22: IFN γ release from CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R26P1A9 (SEQ ID NO:1-12) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 23: IFN γ release from CD8⁺ T-cells electroporated with alpha and beta chain RNA of TCR R26P2A6 (SEQ ID NO:13-24) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8⁺ T-cells derived from two different donors. RNA electroporated CD8⁺ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

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Figure 24: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P3H1 (SEQ ID NO:25-36) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 25: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R35P3A4 (SEQ ID NO:37-48) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 26: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1C9 (SEQ ID NO:49-60) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 27: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1H1 (SEQ ID NO:61-72) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various

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MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from one donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls.

Figure 28: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R42P3A9 (SEQ ID NO:73-84) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from one donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls.

Figure 29: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3F2 (SEQ ID NO:85-96) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 30: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3G5 (SEQ ID NO:97-108) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target

cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 31: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R59P2E7 (SEQ ID NO:109-120) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) or various MAGEA1-003 threonine-substitution variants at positions 1-9 of SEQ ID NO:1 (SEQ ID NO:154-162) or control peptide NYESO1-001 (SEQ ID NO:153). IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different donors. RNA electroporated CD8 $^{+}$ T-cells alone or in co-incubation with unloaded target cells served as controls. Donor 1 (TCRA-0006) is shown on the left Y-axis, donor 2 (TCRA-0007) on the right Y-axis, respectively.

Figure 32: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCRs R35P3A4 (SEQ ID NO:37-48), R37P1C9 (SEQ ID NO:49-60) and R43P3G5 (SEQ ID NO:97-108) after co-incubation with different tumor cell lines. U266B1 and UACC-257 present the target, KMM-1, NCI-H2023, L-1236, MCF-7 and A-375 do not present the target. T2 target cells loaded with MAGEA1-003 or control peptide NYESO1-001 (SEQ ID NO:153) and RNA electroporated CD8 $^{+}$ T-cells alone served as controls.

Figure 33: IFN γ release from T-cells after lentiviral transduction with different constructs containing alpha and beta chain of TCRs R35P3A4 (SEQ ID NO:37-48; constructs R35D, R35G), R37P1C9 (SEQ ID NO:49-60; constructs R37D, R37G) and R43P3G5 (SEQ ID NO:97-108; constructs R43A, R43H) after co-incubation with different primary cells and iPSC-derived cell types. U266B1 and UACC-257 and T-cells alone served as controls.

Cell type	Abbreviation	source
Normal Human Dermal Fibroblasts	NHDF	Primary cells
Human Coronary Artery Smooth Muscle Cells	HCASMC	Primary cells
Human Tracheal Smooth Muscle Cells	HTSMC	Primary cells

Human Renal Epithelial Cells	HREpC	Primary cells
Human Cardiomyocytes	HCM	Primary cells
Human Cardiac Microvascular Endothelial Cells	HCMEC	Primary cells
iCell Hepatocytes 2.0	-	iPSC-derived cells
iCell Astrocytes	-	iPSC-derived cells
iCell Neurons	-	iPSC-derived cells

Figure 34: IFN γ release from T-cells after lentiviral transduction with different constructs containing alpha and beta chain of TCR R37P1C9 to assess LV-R37D-mediated recognition of endogenously processed and presented MAGEA1-003. (A) T cells from three healthy donors, non-transduced (NT) or transduced with LV-R37D were co-cultured with 3 different tumor cell lines. IFN- γ production with HLA-A*02+ tumor cell lines endogenously expressing MAGEA1 (UACC257 and U266B1) or lacking surface-presented (KMM1). E:T targets are indicated. (B) IFN- γ production with serially diluted MAGEA1 peptide pulsed T2 cells. Co-cultures were set up at E:T ratio 4:1 (60,000 T cells; 15,000 T2 cells). Mean and standard deviation of IFN- γ released after 20 h from three replicates (donors) is shown as duplicate measurements by ELISA.

Figure 35: Potency assay evaluating cytolytic activity of lentivirally transduced T cells expressing TCR R37P1C9 (construct R37D) against MAGEA1+ tumor cells. Cytotoxic response of LV-R37D transduced and non-transduced (NT) T cells measured against (A) U138MG MAGEA1+ tumor cells (HLA-A*02+), (B) U138MG MAGEA1- (HLA-A*02+), or (C) U2-OS MAGEA1+ (HLA-A*02+) tumor cells. The assays were performed at various E:T ratios (A and B) or at 10:1 E:T ratio (C) in a 96 hour fluorescence microscopy based cytotoxicity assay. Results are presented as mean $\pm$ SD of 3 replicates. NT- Non-transduced. For graphs A and B, % Killing = (Area-Under-Curve of experiment sample with T cells / Area-Under-Curve tumor targets alone) * 100, where Area-Under-Curve is calculated

from the longitudinal growth measurements as shown in graph C; negative % Killing values are set to 0.

Figure 36: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P1A9 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Figure 37: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R26P2A6 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Figure 38: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R35P3A4 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM.

Figure 39: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1C9 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Figure 40: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R37P1H1 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM.

Figure 41: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R42P3A9 (Table 1) after co-incubation with T2 target

cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM.

Figure 42: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3F2 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Figure 43: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R43P3G5 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Figure 44: IFN γ release from CD8 $^{+}$ T-cells electroporated with alpha and beta chain RNA of TCR R59P2E7 (Table 1) after co-incubation with T2 target cells loaded with MAGEA1-003 peptide (SEQ ID NO:133) in various peptide loading concentrations from 10 μ M to 10pM. IFN γ release data were obtained with CD8 $^{+}$ T-cells derived from two different healthy donors.

Table 1: TCR sequences of the invention

SEQ ID NO:	TCR	Chain	Region	Sequence
1	R26P1A9	alpha	CDR1	TSINN
2	R26P1A9	alpha	CDR2	IRS
3	R26P1A9	alpha	CDR3	CLIGASGSRLTF
4	R26P1A9	alpha	variable domain	METLLGVSLVILWLQLARVNSQQGEED PQALSIQEGENATMNC SYKTSINN LQW YRQNSGRGLVHLILIRSNEREKHSGR LR VTLDTSKKSSSLLITASRAADTASYFCLI GASGSRLTFGEGTQLTVNP
5	R26P1A9	alpha	constant domain	DIQNPDPAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNN SIIP EDTFFPSP ESSCDVKLVEKSFETDTNLN

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				FQNLSVIGFRILLKLVAGFNLLMTLRLWS S
6	R26P1A9	alpha	full-length	METLLGVSLVILWLQLARVNSQQGEED PQALSIQEGENATMNC SYKTSINN LQW YRQNSGRGLVHLILIRSNEREKHSGR LR VTLDTSKKSSSLLITASRAADTASYFCL I GASGSRLTFGEGTQLTVNPD IQNPDPA VYQLRDSKSSDKSVCLFTDFDSQTNVS QSKDSDVYITDKTVLDMRSMDFKSNSA VAWSNKSDFACANAFNNSIIPEDTFFPS PESSCDVKLVEKSFETDTNLFQNL SVI GFRILLKLVAGFNLLMTLRLWSS
7	R26P1A9	beta	CDR1	SGHDY
8	R26P1A9	beta	CDR2	FNNNVP
9	R26P1A9	beta	CDR3	CASSYFGWNEKLFF
10	R26P1A9	beta	variable domain	MGSWTLCCVSLC ILVAKHTDAGVIQSP R HEVTEMGQEVTLRCKPISGHDYLFWYR QTMMRGLELLIYFNNNVPIDDSGMPED RFSAKMPNASFSTLKIQPSEPRDSAVYF CASSYFGWNEKLFFGSGTQLSVL
11	R26P1A9	beta	constant domain	EDLNKVFPPEVAVFEPSEAEISHTQKAT LVCLATGFFPDHVELSWWWNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFR CQVQFYGLSEND EWTQDRAKPVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDF
12	R26P1A9	beta	full-length	MGSWTLCCVSLC ILVAKHTDAGVIQSP R HEVTEMGQEVTLRCKPISGHDYLFWYR QTMMRGLELLIYFNNNVPIDDSGMPED RFSAKMPNASFSTLKIQPSEPRDSAVYF CASSYFGWNEKLFFGSGTQLSVLEDLN KVFPPEVAVFEPSEAEISHTQKATLVCL ATGFFPDHVELSWWWNGKEVHSGVST DPQPLKEQPALNDSRYCLSSRLRVSAT FWQNPRNHFR CQVQFYGLSENDEWTQ DRAKPVTQIVSAEAWGRADCGFTSVSY QQGVLSATILYEILLGKATLYAVLV SALV LMAMVKRKDF
13	R26P2A6	alpha	CDR1	NSAFQY
14	R26P2A6	alpha	CDR2	TY
15	R26P2A6	alpha	CDR3	CAMSDVSGGYNKLIF
16	R26P2A6	alpha	variable domain	MMKSLRVLLVILWLQLSWVWSQQKEVE QDPGPLSVPEGAI VSLNCTYSNSAFQYF MWYRQYSRKGP ELLMYTYSSGNKEDG RFTAQVDKSSKYISLFIRDSQPSDSATY LCAMSDVSGGYNKLIFGAGTRLAVHP

17	R26P2A6	alpha	constant domain	YIQNPDPVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNLVIGFRILLKLVAGFNLLMTLRLWS S
18	R26P2A6	alpha	full-length	MMKSLRVLLVILWLQLSWVWSQQKEVE QDPGPLSVPEGAIVSLNCTYSNSAFQYF MWYRQYSRKGPPELLMYTYSSGNKEDG RFTAQVDKSSKYISLFIRDSQPSDSATY LCAMSDVSGGYNKLIFGAGTRLAVHPYI QNPDPVYQLRDSKSSDKSVCLFTDFD SQTNVVSQSKDSDVYITDKTVLDMRSM FKSNSAVAWSNKSDFACANAFNNSIPE DTFFPSPESSCDVKLVEKSFETDTNLNF QNLVIGFRILLKLVAGFNLLMTLRLWSS
19	R26P2A6	beta	CDR1	MNHEY
20	R26P2A6	beta	CDR2	SMNVEV
21	R26P2A6	beta	CDR3	CASTTPDGTDEQFF
22	R26P2A6	beta	variable domain	MGPQLLGYVVLCLLGAGPLEAQVTQNP RYLITVTGKKLTVTCSQNMNHEYMSWY RQDPGLGLRQIYYSMNVEVTDKGDVPE GYKVS RKEKRNFLILESPSPNQTSLYF CASTTPDGTDEQFFGPGTRLTVL
23	R26P2A6	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRQVQFYGLSEND EWTQDRAKPVTTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
24	R26P2A6	beta	full-length	MGPQLLGYVVLCLLGAGPLEAQVTQNP RYLITVTGKKLTVTCSQNMNHEYMSWY RQDPGLGLRQIYYSMNVEVTDKGDVPE GYKVS RKEKRNFLILESPSPNQTSLYF CASTTPDGTDEQFFGPGTRLTVLEDLK NVFPPEVAVFEPSEAEISHTQKATLVCL ATGFYPDHVELSWWVNGKEVHSGVST DPQPLKEQPALNDSRYCLSSRLRVSAT FWQNPRNHFRQVQFYGLSENDEWTQ DRAKPVTTQIVSAEAWGRADCGFTSESY QQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDSRG
25	R26P3H1	alpha	CDR1	VSGNPY
26	R26P3H1	alpha	CDR2	YITG
27	R26P3H1	alpha	CDR3	CAVRDMNRDDKIIF
28	R26P3H1	alpha	variable	MASAPISMLAMLFTLSGLRAQSVAQPE

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			domain	DQVNVAEGNPLTVKCTYSVSGNPYLFW YVQYPNRGLQFLLKYITGDNLVKGSYGF EAEFNKSQTSFHLKKPSALVSDSALYFC AVRDMNRDDKIIFGKGTRLHLIP
29	R26P3H1	alpha	constant domain	NIQNPDPAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNLSVIGFRILLKLVAGFNLLMTLRLWS S
30	R26P3H1	alpha	full-length	MASAPISMLAMLFTLSGLRAQSVAQPE DQVNVAEGNPLTVKCTYSVSGNPYLFW YVQYPNRGLQFLLKYITGDNLVKGSYGF EAEFNKSQTSFHLKKPSALVSDSALYFC AVRDMNRDDKIIFGKGTRLHLIPNIQNPD PAVYQLRDSKSSDKSVCLFTDFDSQTN VSQSKDSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFACANAFNNSIIPEDTFF PSPESSCDVKLVEKSFETDTNLNFQNLS VIGFRILLKLVAGFNLLMTLRLWSS
31	R26P3H1	beta	CDR1	LNHDA
32	R26P3H1	beta	CDR2	SQIVND
33	R26P3H1	beta	CDR3	CASSRAEGGEQYF
34	R26P3H1	beta	variable domain	MSNQVLCCVVLCLGANTVDGGITQSP KYLFRKEGQNVTLSCQNLNHDAMYW YRQDPGQGLRLIYYSQIVNDFQKGDIAE GYSVSREKKESFPLTVTSAQKNPTAFYL CASSRAEGGEQYFGPGTRTLTVT
35	R26P3H1	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRCQVQFYGLSEND EWTQDRAKPVTTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
36	R26P3H1	beta	full-length	MSNQVLCCVVLCLGANTVDGGITQSP KYLFRKEGQNVTLSCQNLNHDAMYW YRQDPGQGLRLIYYSQIVNDFQKGDIAE GYSVSREKKESFPLTVTSAQKNPTAFYL CASSRAEGGEQYFGPGTRTLTVTEDLKN VFPPEVAVFEPSEAEISHTQKATLVCLA TGFPDHVELSWWVNGKEVHSGVSTD PQPLKEQPALNDSRYCLSSRLRVSATF WQNPRNHFRCQVQFYGLSENDEWTQ DRAKPVTTQIVSAEAWGRADCGFTSESY QQGVLSATILYEILLGKATLYAVLV LMAMVKRKDSRG
37	R35P3A4	alpha	CDR1	DSASNY

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38	R35P3A4	alpha	CDR2	IRS
39	R35P3A4	alpha	CDR3	CAASPTGGYNKLIF
40	R35P3A4	alpha	variable domain	MTSIRAVFIFLWLQLDLVNGENVEQHPS TLVQEGDSAVIKCTYSDSASNYFPWY KQELGKRPQLIIDIRSNVGEKKDQRIAVT LNKTAKHFSLHITETQPEDSAVYFCAAS PTGGYNKLIFGAGTRLAVHP
41	R35P3A4	alpha	constant domain	YIQNPDPVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVKESFETDTNLN FQNLVIGFRILLKLVAGFNLLMTLRLWS S
42	R35P3A4	alpha	full-length	MTSIRAVFIFLWLQLDLVNGENVEQHPS TLVQEGDSAVIKCTYSDSASNYFPWY KQELGKRPQLIIDIRSNVGEKKDQRIAVT LNKTAKHFSLHITETQPEDSAVYFCAAS PTGGYNKLIFGAGTRLAVHPYIQNPDPV YQLRDSKSSDKSVCLFTDFDSQTNVS QSKDSDVYITDKTVLDMRSMDFKSNSA VAWSNKSDFACANAFNNSIIPEDTFFPS PESSCDVKLVKESFETDTNLNFQNLVIG FRILLKLVAGFNLLMTLRLWSS
43	R35P3A4	beta	CDR1	MNHEY
44	R35P3A4	beta	CDR2	SVGAGI
45	R35P3A4	beta	CDR3	CASSLGGASQEQYF
46	R35P3A4	beta	variable domain	MSIGLLCCAALSLLWAGPVNAGVTQTP KFQVLKTGQSM TLQCAQDMNHEYMSW YRQDPGMGLRLIHYSVGAGITDQGEVP NGYNVSRSTTEDFPLRLLSAAPSQTSV YFCASSLGGASQEQYFGPGTRTLVT
47	R35P3A4	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRQVQFYGLSEND EWTQDRAKPVTTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
48	R35P3A4	beta	full-length	MSIGLLCCAALSLLWAGPVNAGVTQTP KFQVLKTGQSM TLQCAQDMNHEYMSW YRQDPGMGLRLIHYSVGAGITDQGEVP NGYNVSRSTTEDFPLRLLSAAPSQTSV YFCASSLGGASQEQYFGPGTRTLVTED LKNVFPPEVAVFEPSEAEISHTQKATLV CLATGFYPDHVELSWVNGKEVHSGV STDPQPLKEQPALNDSRYCLSSRLRVS ATFWQNPRNHFRQVQFYGLSENDEW

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				TQDRAKPVTQIVSAEAWGRADCGFTSE SYQQGVLSATILYEILLGKATLYAVLVSA LVLMAMVKRKDSRG
49	R37P1C9	alpha	CDR1	TISGTDY
50	R37P1C9	alpha	CDR2	G
51	R37P1C9	alpha	CDR3	CILFNFNKFYF
52	R37P1C9	alpha	variable domain	MKLVTSITVLLSLGIMGDAKTTQPNSME SNEEEPVHLPCNHSTISGTDYIHWYRQL PSQGPEYVIHGLTSNVNNRMASLAIAED RKSSTLILHRATLRDAAVYYCILFNFNKF YFGSGTKLNVKP
53	R37P1C9	alpha	constant domain	NIQNPDPAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNL SVIGFRILLK VAGFNLLMTLRLWS S
54	R37P1C9	alpha	full-length	MKLVTSITVLLSLGIMGDAKTTQPNSME SNEEEPVHLPCNHSTISGTDYIHWYRQL PSQGPEYVIHGLTSNVNNRMASLAIAED RKSSTLILHRATLRDAAVYYCILFNFNKF YFGSGTKLNVKPNIQNPDPAVYQLRDS KSSDKSVCLFTDFDSQTNVSQSKDSDV YITDKTVLDMRSMDFKSNSAVAWSNK DFACANAFNNSIIPEDTFFPSPESSCDV KLVEKSFETDTNLNFQNL SVIGFRILLK VAGFNLLMTLRLWSS
55	R37P1C9	beta	CDR1	LNHNV
56	R37P1C9	beta	CDR2	YYDKDF
57	R37P1C9	beta	CDR3	CATSSGETNEKLFF
58	R37P1C9	beta	variable domain	MGPGLLHWMALCCLGTGHGDAMVIQN PRYQVTQFGKPVTLSQSQTNLHNVMY WYQQKSSQAPKLLFHYYDKDFNNEADT PDNFQSRRPNTSFCFLDIRSPGLGDAA MYLCATSSGETNEKLFFGSGTQLSVL
59	R37P1C9	beta	constant domain	EDLNKVFPPEVAVFEPSEAEISHTQKAT LVCLATGFFPDHVELSWWWNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRCQVQFYGLSEND EWTQDRAKPVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDF
60	R37P1C9	beta	full-length	MGPGLLHWMALCCLGTGHGDAMVIQN PRYQVTQFGKPVTLSQSQTNLHNVMY WYQQKSSQAPKLLFHYYDKDFNNEADT PDNFQSRRPNTSFCFLDIRSPGLGDAA MYLCATSSGETNEKLFFGSGTQLSVLE

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				DLNKVFPPEVAVFEPSEAEISHTQKATL VCLATGFFPDHVELSWWWNGKEVHSG VSTDPQPLKEQPALNDSRYCLSSRLRV SATFWQNPRNHFRCQVQFYGLSENDE WTQDRAKPVTQIVSAEAWGRADCGFT SVSYQQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
61	R37P1H1	alpha	CDR1	TSESNNY
62	R37P1H1	alpha	CDR2	QEAY
63	R37P1H1	alpha	CDR3	CAFGYSGGGADGLTF
64	R37P1H1	alpha	variable domain	MTRVSLWAVVSTCLESMAQTVTQS QPEMSVQEAETVTLSCYDTSESNNYL FWYKQPPSRQMILVIRQEAYKQGNATE NRFSVNFQKAASFSLKISDSQLGDTA MYFCAFGYSGGGADGLTFGKGTHLIQ P
65	R37P1H1	alpha	constant domain	YIQNPDPVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNLVIGFRILLKLVAGFNLLMTLRLWS S
66	R37P1H1	alpha	full-length	MTRVSLWAVVSTCLESMAQTVTQS QPEMSVQEAETVTLSCYDTSESNNYL FWYKQPPSRQMILVIRQEAYKQGNATE NRFSVNFQKAASFSLKISDSQLGDTA MYFCAFGYSGGGADGLTFGKGTHLIQ PYIQNPDPVYQLRDSKSSDKSVCLFTD FDSQTNVSQSKDSDVYITDKTVLDMRS MDFKSNSAVAWSNKSDFACANAFNNSI IPEDTFFPSPESSCDVKLVEKSFETDTN LNFQNLVIGFRILLKLVAGFNLLMTLRL WSS
67	R37P1H1	beta	CDR1	SGHDT
68	R37P1H1	beta	CDR2	YEEEE
69	R37P1H1	beta	CDR3	CASSNEGQGWEAEAFF
70	R37P1H1	beta	variable domain	MGPGLLCWALLCLLGAGLVDAGVTQSP THLIKTRGQQVTLRCSPKSGHDTVSWY QQALGQQPQFIFQYEEEEERQRGNFPD RFSGHQFPNYSSELNVNALLGDSALYL CASSNEGQGWEAEAFFGQGTRLTVV
71	R37P1H1	beta	constant domain	EDLNKVPPEVAVFEPSEAEISHTQKAT LVCLATGFFPDHVELSWWWNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRCQVQFYGLSEND EWTQDRAKPVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILLGKATLYAVL

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				VSALVLMAMVKRKDF
72	R37P1H1	beta	full-length	MGPGLLCWALLCLLGAGLVDAAGVTQSP THLIKTRGQQVTLRCSPKSGHDTVSWY QQALGQGPQFIFQYEEEEERQQRGNFPD RFSGHQFPNYSSELNVNALLGDSALYL CASSNEGQGWAEAEFFGQGTRLTVVE DLNKVFPPEVAVFEPSEAEISHTQKATL VCLATGFFPDHVELSWWWVNGKEVHSG VSTDQPPLKEQPALNDSRYCLSSRLRV SATFWQNPRNHFRCCQVQFYGLSENDE WTQDRAKPVTQIVSAEAWGRADCGFT SVSYQQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
73	R42P3A9	alpha	CDR1	DSVNN
74	R42P3A9	alpha	CDR2	I
75	R42P3A9	alpha	CDR3	CAVHNFNKFYF
76	R42P3A9	alpha	variable domain	MKRILGALLGLLSAQVCCVRGIQVEQSP PDLILQEGANSTLRCNFSDSVNNLQWF HQNPWGQLINLFYIPSGTKQNGRLSATT VATERYSLLYISSSQTTDSGVYFCAVHN FNKFYFGSGTKLNVKP
77	R42P3A9	alpha	constant domain	NIQNPDPVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNLVIGFRILLKLVAGFNLLMTLRLWS S
78	R42P3A9	alpha	full-length	MKRILGALLGLLSAQVCCVRGIQVEQSP PDLILQEGANSTLRCNFSDSVNNLQWF HQNPWGQLINLFYIPSGTKQNGRLSATT VATERYSLLYISSSQTTDSGVYFCAVHN FNKFYFGSGTKLNVKPNIQNPDPVYQL RDSKSSDKSVCLFTDFDSQTNVSQSKD SDVYITDKTVLDMRSMDFKSNSAVAWS NKSDFACANAFNNSIIPEDTFFPSPESS CDVKLVEKSFETDTNLNFQNLVIGFRIL LLKVAGFNLLMTLRLWSS
79	R42P3A9	beta	CDR1	PRHDT
80	R42P3A9	beta	CDR2	FYEKM
81	R42P3A9	beta	CDR3	CASSLLGQGYNEQFF
82	R42P3A9	beta	variable domain	MLSPDLPDSAWNTRLLCHVMLCLLGAV SVAAGVIQSPRHLIKEKRETATLKCYP RHDTVYVYQQGPGQDPQFLISFYEM QSDKGSIPDRFSAQQFSDYHSELMSS LELGDSALYFCASSLLGQGYNEQFFGP GTRLTVL
83	R42P3A9	beta	constant	EDLKNVFPPEVAVFEPSEAEISHTQKAT

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			domain	LVCLATGFYPDHVLSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRQCQVQFYGLSEND EWTQDRAKPVQTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
84	R42P3A9	beta	full-length	MLSPDLPDSAWNTRLLCHVMLCCLLGAV SVAAGVIQSPRHLIKEKRETATLKCYP RHDTVYQYQQGPGQDPQFLISFYK QSDKGSIPDRFSAQQFSDYHSELNMS LELGDSALYFCASSLLGGYNEQFFGP GTRLTVLEDLKNVFPPEVAVFEPSEAEI SHTQKATLVCLATGFYPDHVLSWWVN GKEVHSGVSTDPQPLKEQPALNDSRYC LSSRLRVSATFWQNPRNHFRQCQVQFY GLSENDEWTQDRAKPVQTQIVSAEAWG RADCGFTSESYQQGVLSATILYEILLGK ATLYAVLVSALVLMAMVKRKDSRG
85	R43P3F2	alpha	CDR1	TRDTTYY
86	R43P3F2	alpha	CDR2	RNSF
87	R43P3F2	alpha	CDR3	CALSNNNAGNMLTF
88	R43P3F2	alpha	variable domain	MLTASLLRAVIASICVVSSMAQKVTQAAQ TEISVVEKEDVTLDVYETRDTTYLFW YKQPPSGELVFLIRRNSFDEQNEISGRY SWNFQKSTSSFNFTITASQVVDNAVYF CALSNNNAGNMLTFGGGTRLMVKP
89	R43P3F2	alpha	constant domain	HIQNPDAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAFAWSNKSDFAFANFNSIIP EDTFFPSPSSCDVKLVEKSFETDTNLN FQNLVIGFRILLKLVAGFNLLMTLRLWS S
90	R43P3F2	alpha	full-length	MLTASLLRAVIASICVVSSMAQKVTQAAQ TEISVVEKEDVTLDVYETRDTTYLFW YKQPPSGELVFLIRRNSFDEQNEISGRY SWNFQKSTSSFNFTITASQVVDNAVYF CALSNNNAGNMLTFGGGTRLMVKPHIQ NPDAVYQLRDSKSSDKSVCLFTDFDS QTNVSQSKDSDVYITDKTVLDMRSMDF KNSAFAWSNKSDFAFANFNSIIPED TFFPSPSSCDVKLVEKSFETDTNLNFQ NLSVIGFRILLKLVAGFNLLMTLRLWSS
91	R43P3F2	beta	CDR1	PRHDT
92	R43P3F2	beta	CDR2	FYEKM
93	R43P3F2	beta	CDR3	CASSPTGTSGYNEQFF
94	R43P3F2	beta	variable domain	MLSPDLPDSAWNTRLLCHVMLCCLLGAV SVAAGVIQSPRHLIKEKRETATLKCYP

				RHDTVYWYQQGPGQDPQFLISFYEM QSDKGSIPDRFSAQQFSDYHSELMSS LELGDSALYFCASSPTGTSGYNEQFFG PGTRLTVL
95	R43P3F2	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRQVQFYGLSEND EWTQDRAKPVTTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
96	R43P3F2	beta	full-length	MLSPDLPDSAWNTRLLCHVMLCCLGAV SVAAGVIQSPRHLIKEKRETATLKCYP RHDVTYWYQQGPGQDPQFLISFYEM QSDKGSIPDRFSAQQFSDYHSELMSS LELGDSALYFCASSPTGTSGYNEQFFG PGTRLTVLEDLKNVFPPEVAVFEPSEAE ISHTQKATLVCLATGFYPDHVELSWWV NGKEVHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSATFWQNPRNHFRQVQF YGLSENDEWTQDRAKPVTTQIVSAEAW GRADCGFTSESYQQGVLSATILYEILLG KATLYAVLVSALVLMAMVKRKDSRG
97	R43P3G5	alpha	CDR1	SSNFYA
98	R43P3G5	alpha	CDR2	MTL
99	R43P3G5	alpha	CDR3	CALNRDDKIIF
100	R43P3G5	alpha	variable domain	MEKNPLAAPLLILWFHLCVSSILNVEQ SPQSLHVQEGDSTNFTCSFPSSNFYAL HWYRWETAKSPEALFVMTLNGDEKKK GRISATLNTKEGYSYLYIKGSQPEDSAT YLCALNRDDKIIFGKGTRLHILP
101	R43P3G5	alpha	constant domain	NIQNPDPAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKSDVYITDKTVLDMRSM DFKSNSAFAWSNKSDFAFANFNSIIP EDTFFPSPSSCDVKLVEKSFETDTNLN FQNLVIGFRILLKVAGFNLLMTLRLWS S
102	R43P3G5	alpha	full-length	MEKNPLAAPLLILWFHLCVSSILNVEQ SPQSLHVQEGDSTNFTCSFPSSNFYAL HWYRWETAKSPEALFVMTLNGDEKKK GRISATLNTKEGYSYLYIKGSQPEDSAT YLCALNRDDKIIFGKGTRLHILPNIQNPD PAVYQLRDSKSSDKSVCLFTDFDSQTN VSQSKSDVYITDKTVLDMRSMDFKSN SAFAWSNKSDFAFANFNSIIPEDTFF PSPSSCDVKLVEKSFETDTNLNFQNLV VIGFRILLKVAGFNLLMTLRLWSS
103	R43P3G5	beta	CDR1	MDHEN

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104	R43P3G5	beta	CDR2	SYDVKM
105	R43P3G5	beta	CDR3	CASRLPSRTYEQYF
106	R43P3G5	beta	variable domain	MGIRLLCRVAFCLAVGLVDVKVTQSSR YLVKRTGEKVFLECVQDMDHENMFWY RQDPGLGLRLIYFSYDVKMKEKGDPIEG YSVSREKKERFSLILESASTNQTSMYLC ASRLPSRTYEQYFGPGTRLTVT
107	R43P3G5	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRCQVQFYGLSEND EWTQDRAKPVTTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
108	R43P3G5	beta	full-length	MGIRLLCRVAFCLAVGLVDVKVTQSSR YLVKRTGEKVFLECVQDMDHENMFWY RQDPGLGLRLIYFSYDVKMKEKGDPIEG YSVSREKKERFSLILESASTNQTSMYLC ASRLPSRTYEQYFGPGTRLTVT EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLA TGYPDHVELSWWVNGKEVHSGVSTD PQPLKEQPALNDSRYCLSSRLRVSATF WQNPRNHFRCQVQFYGLSENDEWTQ DRAKPVTTQIVSAEAWGRADCGFTSESY QQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDSRG
109	R59P2E7	alpha	CDR1	DSAIYN
110	R59P2E7	alpha	CDR2	IQS
111	R59P2E7	alpha	CDR3	CAVNSDYKLSF
112	R59P2E7	alpha	variable domain	METLLGLLILWLQLQWVSSKQEVQIPA ALSVPEGENLVNCSFTDSAIYNLQWFR QDPGKGLTSLLLIQSSQREQTSGRLNA SLDKSSGRSTLYIAASQPGDSATYLCV NSDYKLSFGAGTTVTVRA
113	R59P2E7	alpha	constant domain	NIQNPDPAVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSAVAWSNKSDFACANAFNNSIIP EDTFFPSPESSCDVKLVEKSFETDTNLN FQNLVIGFRILLKVAGFNLLMTLRLWS S
114	R59P2E7	alpha	full-length	METLLGLLILWLQLQWVSSKQEVQIPA ALSVPEGENLVNCSFTDSAIYNLQWFR QDPGKGLTSLLLIQSSQREQTSGRLNA SLDKSSGRSTLYIAASQPGDSATYLCV NSDYKLSFGAGTTVTVRANIQNPDPV YQLRDSKSSDKSVCLFTDFDSQTNVSQ SKDSDVYITDKTVLDMRSMDFKSNSAV

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				AWSNKSDFACANAFNNSIIPEDTFFPSP ESSCDVKLVEKSFETDTNLFQNLSVIG FRILLKLVAGFNLLMTLRLWSS
115	R59P2E7	beta	CDR1	PHRDT
116	R59P2E7	beta	CDR2	FYEKMQ
117	R59P2E7	beta	CDR3	CASSLGLGTGDYGYTF
118	R59P2E7	beta	variable domain	MLSPDLPD SAWNTRLLCHVMLC LLGAV SVAAGVIQSPRH LIKEKRETATLKC YPIP RHDTVYWYQQGPGQDPQFLISFYEKM QSDKGSIPDRFSAQQFSDYHSELNMSS LELGDSALYFCASSLGLGTGDYGYTFG SGTRLTVV
119	R59P2E7	beta	constant domain	EDLNKVFPP EVAVFEPSEAEISHTQKAT LVCLATGFFPDHVELS WWWNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFR CQVQFYGLSEND EWTQDRAK PVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILLG KATLYAVL VSALVLMAMVKRKDF
120	R59P2E7	beta	full-length	MLSPDLPD SAWNTRLLCHVMLC LLGAV SVAAGVIQSPRH LIKEKRETATLKC YPIP RHDTVYWYQQGPGQDPQFLISFYEKM QSDKGSIPDRFSAQQFSDYHSELNMSS LELGDSALYFCASSLGLGTGDYGYTFG SGTRLTVVEDLNKVFPP EVAVFEPSEAE ISHTQKATLVCLATGFFPDHVELS WWW NGKEVHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSATFWQNPRNHFR CQVQF YGLSENDEWTQDRAK PVTQIVSAEAW GRADCGFTSVSYQQGVLSATILYEILLG KATLYAVLVSALVLMAMVKRKDF
121	1G4	alpha	CDR1	DSAIYN
122	1G4	alpha	CDR2	IQS
123	1G4	alpha	CDR3	CAVRPTSGGSYIPTF
124	1G4	alpha	variable domain	METLLGLLILWLQLQWVSSKQEVTQIPA ALSVPEGENLV LNCSFTDSAIYNLQWFR QDPGKGLTSLLLIQSSQREQTSGRLNA SLDKSSGRSTLYIAASQPGDSATYLC AV RPTSGGSYIPTFGRGTSLIVHP
125	1G4	alpha	constant domain	YIQNPDP AVYQLRDSKSSDKSVCLFTDF DSQTNVSQSKDSDVYITDKTVLDMRSM DFKSNSA VAWSNKSDFACANAFNNSIIP EDTFFPSP ESSCDVKLVEKSFETDTNLF QNLSVIGFRILLKLVAGFNLLMTLRLWS S
126	1G4	alpha	full-length	METLLGLLILWLQLQWVSSKQEVTQIPA ALSVPEGENLV LNCSFTDSAIYNLQWFR

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				QDPGKGLTSLLLIQSSQREQTSGRLNA SLDKSSGRSTLYIAASQPGDSATYLCV RPTSGGSYIPTFGRGTSLIVHPYIQNP PAVYQLRDSKSSDKSVCLFTDFDSQTN VSQSKDSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFACANAFNNSIIPEDTFF PSPRESSCDVKLVEKSFETDTNLFQNL S VIGFRILLKVAGFNLLMTLRLWSS
127	1G4	beta	CDR1	MNHEY
128	1G4	beta	CDR2	SVGAGI
129	1G4	beta	CDR3	CASSYVGNTGELFF
130	1G4	beta	variable domain	MSIGLLCCAALSLLWAGPVNAGVTQTP KFQVLKTGQSMTLQCAQDMNHEYMSW YRQDPGMGLRLIHYSVGAGITDQGEVP NGYNVSRSTTEDFPLRLLSAAPSQTSV YFCASSYVGNTGELFFGEGSRLTVL
131	1G4	beta	constant domain	EDLKNVFPPEVAVFEPSEAEISHTQKAT LVCLATGFYPDHVELSWWVNGKEVHS GVSTDPQPLKEQPALNDSRYCLSSRLR VSATFWQNPRNHFRCQVQFYGLSEND EWTQDRAKPVTQIVSAEAWGRADCGF TSESYQQGVLSATILYEILLGKATLYAVL VSALVLMAMVKRKDSRG
132	1G4	beta	full-length	MSIGLLCCAALSLLWAGPVNAGVTQTP KFQVLKTGQSMTLQCAQDMNHEYMSW YRQDPGMGLRLIHYSVGAGITDQGEVP NGYNVSRSTTEDFPLRLLSAAPSQTSV YFCASSYVGNTGELFFGEGSRLTVLED LKNVFPPEVAVFEPSEAEISHTQKATLV CLATGFYPDHVELSWWVNGKEVHSGV STDPQPLKEQPALNDSRYCLSSRLRVS ATFWQNPRNHFRCQVQFYGLSENDEW TQDRAKPVTQIVSAEAWGRADCGFTSE SYQQGVLSATILYEILLGKATLYAVLVSA LVLMAMVKRKDSRG

Table 2: Peptide sequences of the invention

Peptide Code	Sequence	SEQ ID NO:
MAGEA1-003	KVLEYVIKV	133
MAGEA1-003_A1	AVLEYVIKV	134
MAGEA1-003_A2	KALEYVIKV	135
MAGEA1-003_A3	KVAEYVIKV	136

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MAGEA1-003_A4	KVLAYVIKV	137
MAGEA1-003_A5	KVLEAVIKV	138
MAGEA1-003_A6	KVLEYAIKV	139
MAGEA1-003_A7	KVLEYVAKV	140
MAGEA1-003_A8	KVLEYVIAV	141
MAGEA1-003_A9	KVLEYVIKA	142
TMEM175-001	ILLPYVSKV	143
EPAS-001	KALEGFIAV	144
PTRF-001	KLLEKVRKV	145
GALNTL4-001	KLTEYVDKV	146
PSME2-001	KVLERVNAV	147
KIAA103-002	KVLNKVITV	148
NSD1-001	KVQEQVHKV	149
TBC1D9-002	LLLPDVIKV	150
TMTC4-001	NVLEIVQKV	151
RASAL2-002	SVLEPVISV	152
NYESO1-001	SLLMWITQV	153
MAGEA1-003_T1	TVLEYVIKV	154
MAGEA1-003_T2	KTLEYVIKV	155
MAGEA1-003_T3	KVTEYVIKV	156
MAGEA1-003_T4	KVLTYYVIKV	157
MAGEA1-003_T5	KVLETVIKV	158
MAGEA1-003_T6	KVLEYTIKV	159
MAGEA1-003_T7	KVLEYVTKV	160
MAGEA1-003_T8	KVLEYVITV	161
MAGEA1-003_T9	KVLEYVIKT	162

EXAMPLES

Ten MAGEA1-003-specific TCRs (R26P1A9, R26P2A6, R26P3H1, R35P3A4, R37P1C9, R37P1H1, R42P3A9, R43P3F2, R43P3G5 and R59P2E7, see Table 1), each encoding tumor specific TCR-alpha and TCR-beta chains, were isolated and amplified from T-cells of healthy donors. Cells from healthy donors were in vitro stimulated according to a method previously described (Walter et al., 2003 J Immunol., Nov 15;171(10):4974-8) and target-specific cells were single-cell sorted using HLA-A*02 multimers and then used for subsequent TCR isolation. TCR sequences were isolated via 5' RACE by standard methods as described by e.g. Molecular Cloning a laboratory manual fourth edition by Green and Sambrook. The alpha and beta variable regions of TCRs R26P1A9, R26P2A6, R26P3H1, R42P3A9, R43P3F2, R43P3G5, R59P2E7, R35P3A4, R37P1C9 and R37P1H1 were sequenced and expression constructs were generated by gene synthesis for further functional characterization.

R26P1A9, R26P2A6, R26P3H1, R42P3A9, R43P3F2, R43P3G5 and R59P2E7 are derived from HLA-A*02 negative donor (allo-reactive setting) and R35P3A4, R37P1C9 and R37P1H1 are derived from a HLA-A*02 positive donor.

TCRs of interest were expressed in human T cells by transduction, e.g. through mRNA electroporation or lentiviral transduction. For lentiviral transduction, PBMC were thawed and rested overnight, and then activated using immobilized antibodies. Activated cells were transduced using a lentiviral vector encoding the MAGEA1-specific TCR and expanded in the presence of cytokines. T cells were harvested and concentrated by centrifugation, then cryopreserved.

The T cells were assessed for IFN- γ release after co-culture with different target cells, such as T2 cells loaded with different peptides as well as tumor cell lines and primary cells from healthy tissues. T-cell activation data are shown in absolute IFN γ levels or a background subtracted way as indicated below.

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Efficacy of CD8⁺ T cells expressing TCRs R35P3A4, R37P1C9 and R43P3G5 was determined e.g. by T cell activation studies (IFN γ release) or killing assays using different tumor cell lines as target cells. The characterization of the safety profile of TCRs of interest was approached by testing the potential activation of TCR-expressing T cells upon co-culture with isolated primary cell types from healthy tissues and induced pluripotent stem cell (iPSC)-derived cell types from HLA-A*02-positive donors (Figure 33). Cell types were selected in a manner to cover critical organs like brain, heart and liver and different cell types as epithelium, endothelium or smooth muscle. Tumor cell lines were analyzed side-by-side as positive and negative controls.

Background subtraction method for IFN γ release:

$$\text{Mean}_{\text{bg}}(\text{TCRoi}; \text{co}) = [\text{mean}_{(\text{TCRoi}; \text{co})} - \text{mean}_{(\text{TCRoi}; \text{effector only})}] - [\text{mean}_{(\text{mock}; \text{co})} - \text{mean}_{(\text{mock}; \text{effector only})}]$$

The respective SD_{bg} was calculated:

$$\text{SD}_{\text{bg}}(\text{TCRoi}; \text{co}) = [\text{SD}_{(\text{TCRoi}; \text{co})}^2 + \text{SD}_{(\text{TCRoi}; \text{effector only})}^2 + \text{SD}_{(\text{mock}; \text{co})}^2 + \text{SD}_{(\text{mock}; \text{effector only})}^2]^{1/2}$$

TCRoi = effector cells expressing TCR of interest

Mock = effector cells without exogenous TCR expression

Co = effector cells co-cultured with target cells

Effector only = effector cells not co-cultured

Mean_(bg) = mean IFN γ release (background subtracted)

SD_(bg) = standard deviation (background subtracted)

Example 1: T-cell receptor R26P1A9

TCR R26P1A9 (SEQ ID NO:1-12) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO:133) (see Figure 11). R26P1A9 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of

MAGEA1-003 (Figures 1 and 22). TCR R26P1A9 does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 11). NYESO1-001 peptide is used as negative control. TCR R26P1A9 has an EC50 of 6nM (Figure 36).

Example 2: T-cell receptor R26P2A6

TCR R26P2A6 (SEQ ID NO:13-24) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO:133) (see Figure 12). R26P2A6 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 2 and 23). TCR R26P2A6 does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 12). NYESO1-001 peptide is used as negative control. TCR R26P2A9 has an EC50 of 100nM (Figure 37).

Example 3: T-cell receptor R26P3H1

TCR R26P3H1 (SEQ ID NO:25-36) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO:133) (see Figure 13). R26P3H1 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 3 and 24). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 13). NYESO1-001 peptide is used as negative control. The TCR has an EC50 of 16nM.

Example 4: T-cell receptor R35P3A4

TCR R35P3A4 (SEQ ID NO:37-48) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO:133) (see Figure 14 above). R35P3A4 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells and bind

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HLA-A*02 tetramers, respectively, loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 4 and 25). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 14). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 16nM (Figure 38) and an affinity of 29 μ M.

For CD8⁺ T cells expressing TCR R35P3A4, no activation was observed upon co-culture with HLA-A*02 positive cell types from healthy tissues (see Figure 33), while there was an activity towards the tumor cell lines UACC-257 and U266B1 expressing HLA-A*02 and MAGEA1 as source gene for MAGEA1-003 peptide (Figures 32 and 33). A corresponding pattern of reactivity was observed with CD8⁺ T cells expressing the NYESO1-specific control TCR 1G4, with reactivity towards NYESO1 expressing HLA-A*02 positive tumor cell lines but not towards the indicated panel of healthy tissue cells.

T-cell activation upon co-culture with cell lines expressing HLA-A*02 and MAGEA1 reflects the recognition of endogenously expressed and presented target pHLA (peptide presented on human leukocyte antigen) by TCRs R35P3A4.

Example 5: T-cell receptor R37P1C9

TCR R37P1C9 (SEQ ID NO:49-60) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO:133) (see Figure 15). R37P1C9 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 5 and 26). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 15). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 13nM (Figures 34B and 39) and an affinity of 8.7 μ M.

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Re-expression of R37P1C9 in human primary CD8⁺ T-cells leads to selective binding of HLA-A*02/MAGEA1-003 tetramers but not HLA-A*02/NYESO1-001 tetramers (Figure 21). Re-expression of the NYESO1-001-specific TCR 1G4 and mock expression are used as control.

For CD8⁺ T cells expressing TCR R37P1C9, no activation was observed upon co-culture with HLA-A*02 positive cell types from healthy tissues (see Figure 33), while there was an activity towards the tumor cell lines UACC-257 and U266B1 expressing HLA-A*02 and MAGEA1 as source gene for MAGEA1-003 peptide (Figures 32 and 33). A corresponding pattern of reactivity was observed with CD8⁺ T cells expressing the NYESO1-specific control TCR 1G4, with reactivity towards NYESO1 expressing HLA-A*02 positive tumor cell lines but not towards the indicated panel of healthy tissue cells.

T-cell activation upon co-culture with cell lines expressing HLA-A*02 and MAGEA1 reflects the recognition of endogenously expressed and presented target pHLA by TCRs R37P1C9, independently from the gene delivery method e.g. mRNA electroporation, lentiviral transduction, etc. (Figures 32 and 34).

Example 6: T-cell receptor R37P1H1

TCR R37P1H1 (SEQ ID NO: 61-72) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO: 133) (see Figure 16). R37P1H1 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 6 and 27). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 16). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 26nM (Figure 40).

Re-expression of R37P1H1 in human primary CD8⁺ T-cells leads to selective binding of HLA-A*02/MAGEA1-003 tetramers but not HLA-A*02/NYESO1-001

tetramers (Figure 21). Re-expression of the NYESO1-001-specific TCR 1G4 and mock expression are used as control.

Example 7: T-cell receptor R42P3A9

TCR R42P3A9 (SEQ ID NO: 73-84) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO: 133) (see Figure 17). R42P3A9 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 7 and 28). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 17). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 823nM (Figure 41).

Example 8: T-cell receptor R43P3F2

TCR R43P3F2 (SEQ ID NO: 85-96) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO: 133) (see Figure 18). R43P3F2 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 8 and 29). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 18). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 1,7nM (Figure 42).

Example 9: T-cell receptor R43P3G5

TCR R43P3G5 (SEQ ID NO: 97-108) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO: 133) (see Figure 19). R43P3G5 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFN γ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 9 and 30). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence

similarity to MAGEA1-003 (Figure 19). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 6,6nM (Figure 43) and an affinity of 38μM.

Re-expression of R43P3G5 in human primary CD8⁺ T-cells leads to selective binding of HLA-A*02/MAGEA1-003 tetramers but not HLA-A*02/NYESO1-001 tetramers (Figure 21). Re-expression of the NYESO1-001-specific TCR 1G4 and mock expression are used as control.

For CD8⁺ T cells expressing TCR R43P3G5, no activation was observed upon co-culture with HLA-A*02 positive cell types from healthy tissues (see Figure 33), while there was an activity towards the tumor cell lines UACC-257 and U266B1 expressing HLA-A*02 and MAGEA1 as source gene for MAGEA1-003 peptide (Figures 32 and 33). A corresponding pattern of reactivity was observed with CD8⁺ T cells expressing the NYESO1-specific control TCR 1G4, with reactivity towards NYESO1 expressing HLA-A*02 positive tumor cell lines but not towards the indicated panel of healthy tissue cells. T-cell activation upon co-culture with cell lines expressing HLA-A*02 and MAGEA1 reflects the recognition of endogenously expressed and presented target pHLA by TCRs R43P3G5.

Example 10: T-cell receptor R59P2E7

TCR R59P2E7 (SEQ ID NO: 109-120) is restricted towards HLA-A*02-presented MAGEA1-003 (SEQ ID NO: 133) (see Figure 20). R59P2E7 specifically recognizes MAGEA1-003 as human primary CD8⁺ T-cells re-expressing this TCR release IFNγ upon co-incubation with HLA-A*02⁺ target cells loaded either with MAGEA1-003 peptide or alanine and threonine substitution variants of MAGEA1-003 (Figures 10 and 31). This TCR does specifically recognize MAGEA1-003, but not different peptides showing high degree of sequence similarity to MAGEA1-003 (Figure 20). NYESO1-001 peptide is used as negative control. The TCR has an EC₅₀ of 386nM (Figure 44).

Re-expression of R59P2E7 in human primary CD8⁺ T-cells leads to selective binding of HLA-A*02/MAGEA1-003 tetramers but not HLA-A*02/NYESO1-001 tetramers (Figure 21). Re-expression of the NYESO1-001-specific TCR 1G4 and mock expression are used as control.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A TCR comprising a first TCR chain having at least 80% identity to SEQ ID NO: 54 and comprising the complementary determining regions (CDRs) CDR1, CDR2 and CDR3 having the amino acid sequences of SEQ ID NO: 49, SEQ ID NO: 50 and SEQ ID NO: 51, respectively and a second TCR chain having at least 80% identity to SEQ ID NO: 60 and comprising the complementary determining regions (CDRs) CDR1, CDR2 and CDR3 having the amino acid sequences of SEQ ID NO: 55, SEQ ID NO: 56 and SEQ ID NO: 57, respectively, wherein the CDR sequences comprise not more than two modified amino acids, wherein the modified amino acids are selected from an amino acid insertion, deletion or substitution.
2. The antigen recognizing construct according to claim 1, wherein said modified amino acids are the first or the last amino acid residue of the respective CDR sequence.
3. A nucleic acid or nucleic acids encoding for the TCR according to claim 1 or 2.
4. A vector or vectors comprising the nucleic acid or nucleic acids according to claim 3.
5. A host cell comprising the TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, or the vector(s) according to claim 4.
6. The host cell according to claim 5, wherein the host cell is a T lymphocyte or T lymphocyte progenitor.
7. The host cell according to claim 5, wherein the host cell is a CD4 or CD8 positive T-cell.
8. A pharmaceutical composition comprising the TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, or the vector(s) according to claim 4, or the host cell according to any one of claims 5 to 7, and a pharmaceutical acceptable carrier, stabilizer and/or excipient.

9. The TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, the vector(s) according to claim 4, the host cell according to any one of claims 5 to 7, or the pharmaceutical composition according to claim 8, for use in medicine.
10. The TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, the vector(s) according to claim 4, the host cell according to any one of claims 5 to 7, or the pharmaceutical composition according to claim 8, for use in the diagnosis, prevention, and/or treatment of a proliferative disease.
11. Use of the TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, the vector(s) according to claim 4, or the host cell according to any one of claims 5 to 7 in the preparation of a medicament for the treatment of a proliferative disease.
12. A method of treating a proliferative disease, comprising administration of the TCR according to claim 1 or 2, the nucleic acid(s) according to claim 3, the vector(s) according to claim 4, or the host cell according to any one of claims 5 to 7 to a patient in need thereof.
13. The TCR, the nucleic acid(s), the vector(s), the host cell, the pharmaceutical composition for use according to claim 10, the use according to claim 11 or the method of treatment according to claim 12, wherein the proliferative disease is cancer, such as non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, head and neck cancer, pancreatic cancer, prostate cancer, leukemia, breast cancer, Merkel cell carcinoma, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer, esophageal cancer, or a combination thereof.
14. The TCR, the nucleic acid(s), the vector(s), the host cell, or the pharmaceutical composition for use according to claim 9 or 10, wherein said use comprises an adoptive immune cell transfer to the patient in need of the treatment, such as a heterologous or autologous T cell transfer.
15. A method of manufacturing a MAGEA1 specific antigen recognizing construct, comprising

- a. providing a suitable host cell,
- b. providing a genetic construct comprising a coding sequence encoding the TCR according to claim 1 or 2,
- c. introducing into said suitable host cell said genetic construct,
- d. expressing said genetic construct by said suitable host cell.

16. An *in-vitro* method of detecting cancer in a biological sample comprising:

- a) contacting the biological sample with the TCR according to claim 1 or 2,
- and
- b) detecting binding of the TCR to the biological sample.

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Figure 1:

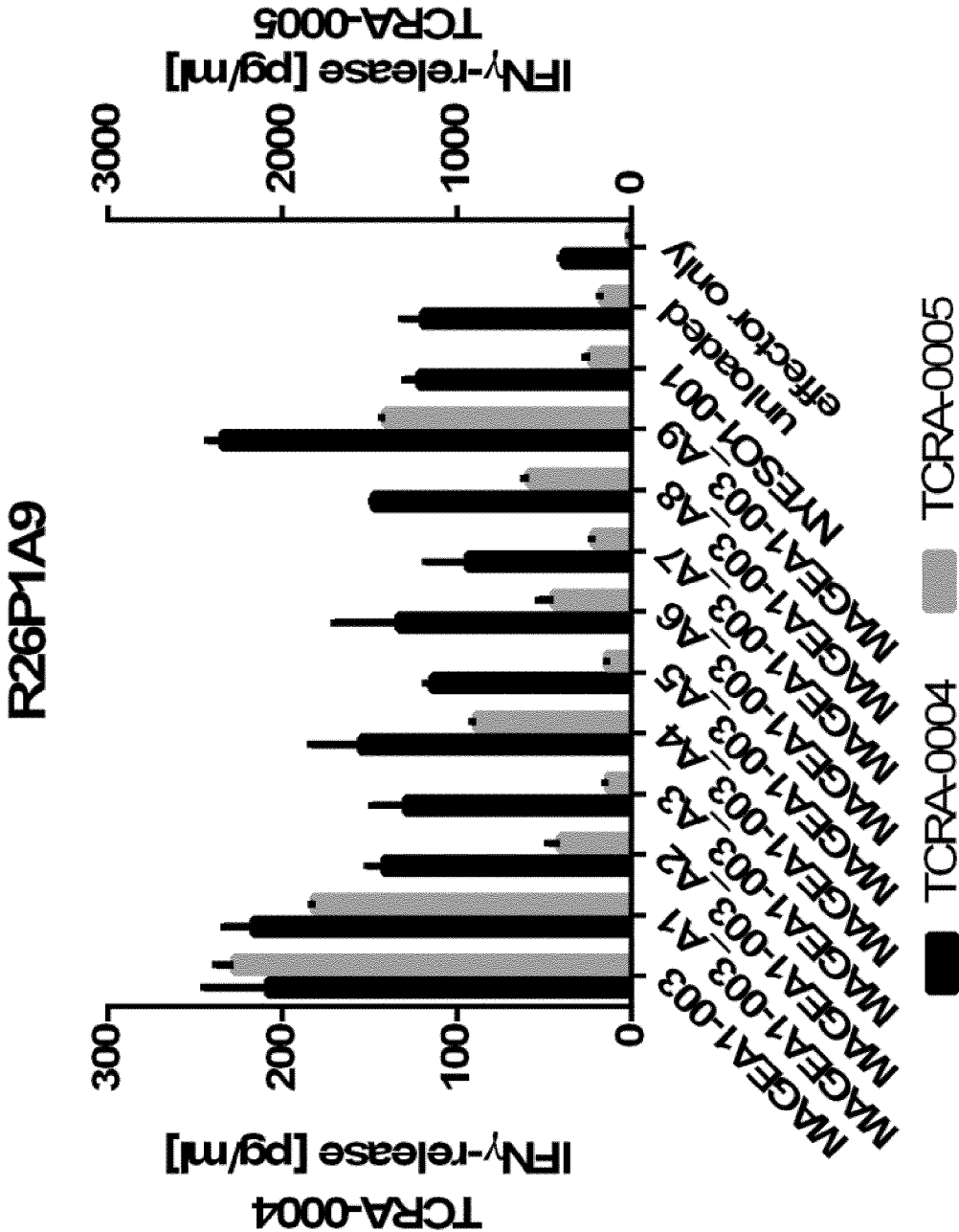


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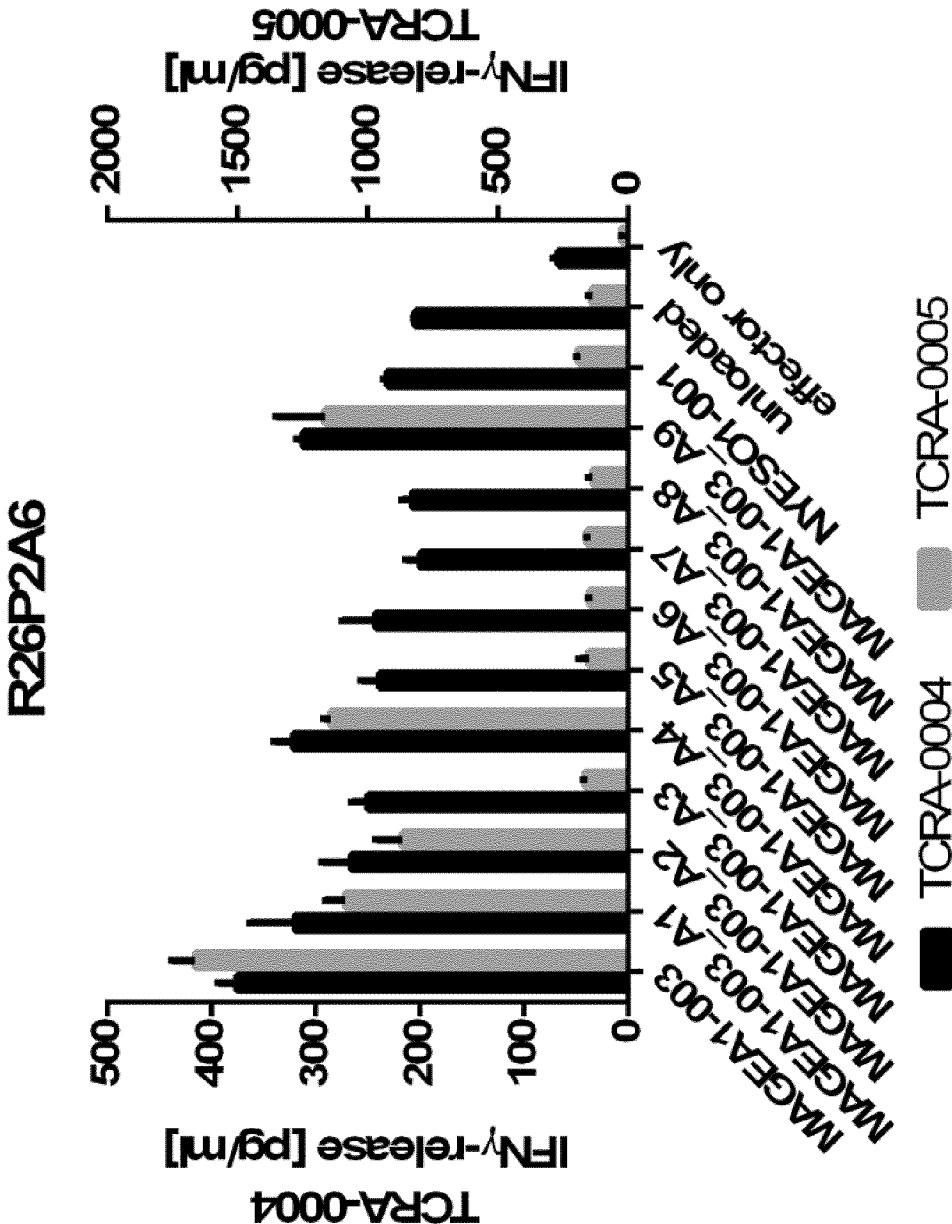


Figure 3:

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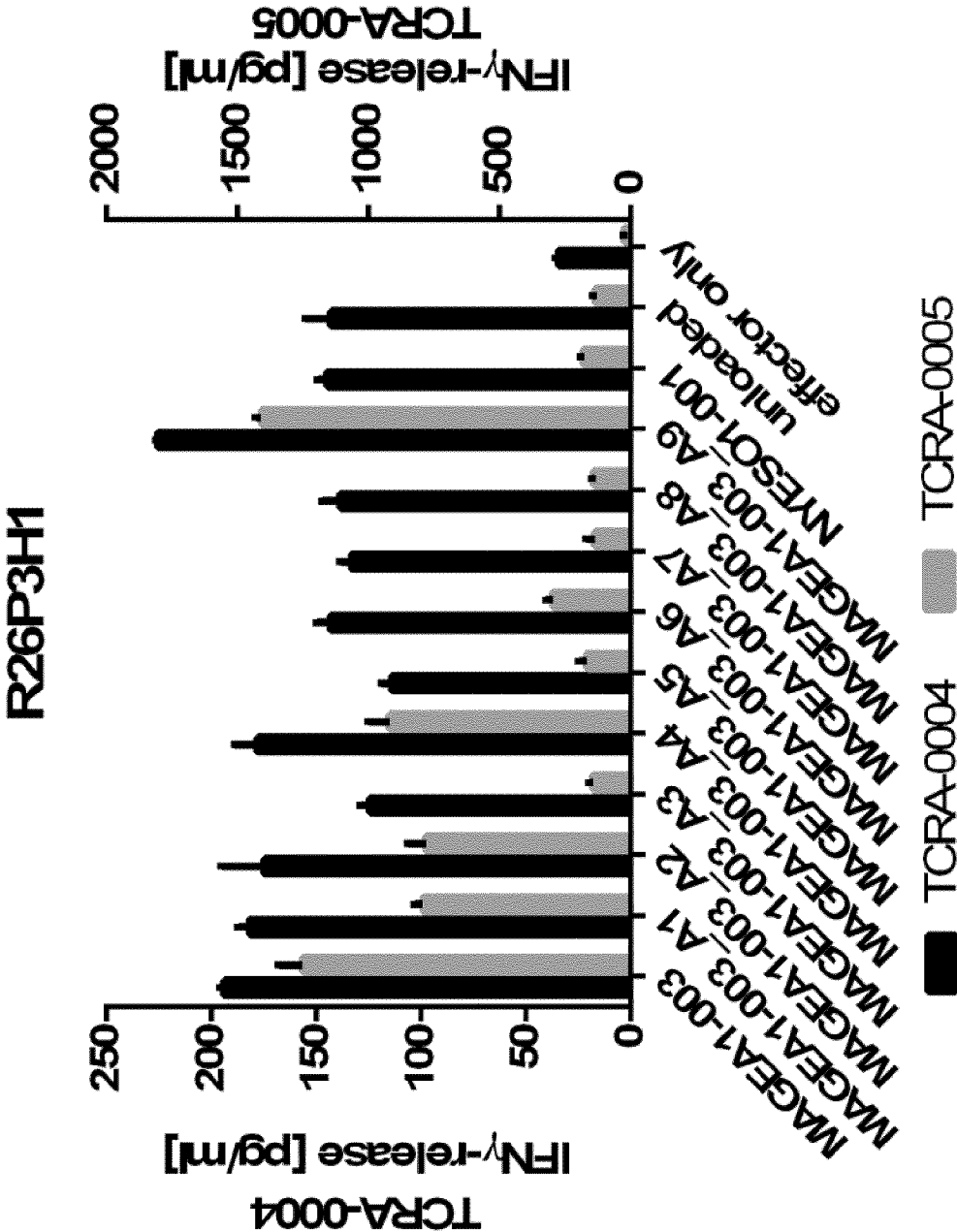
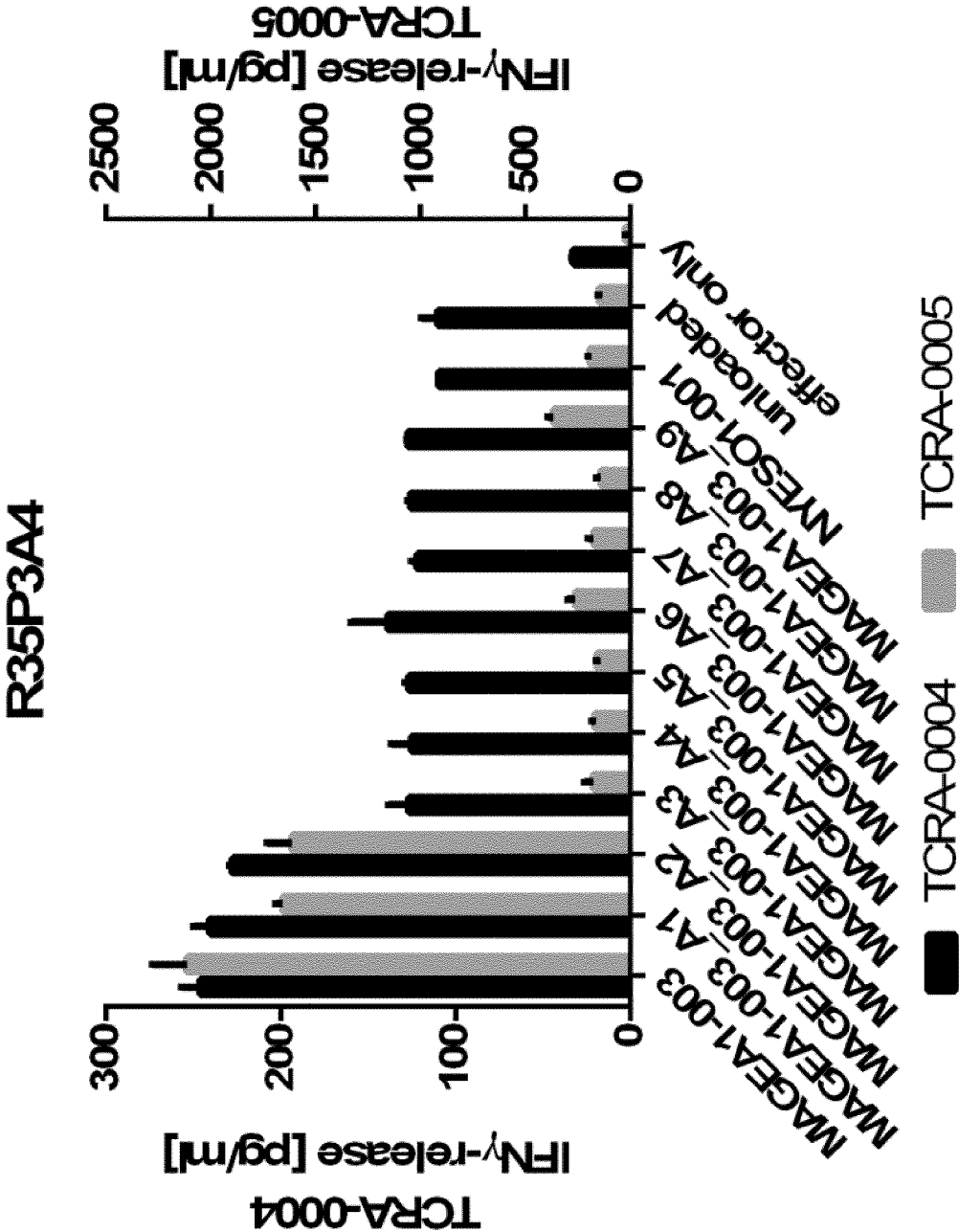


Figure 3

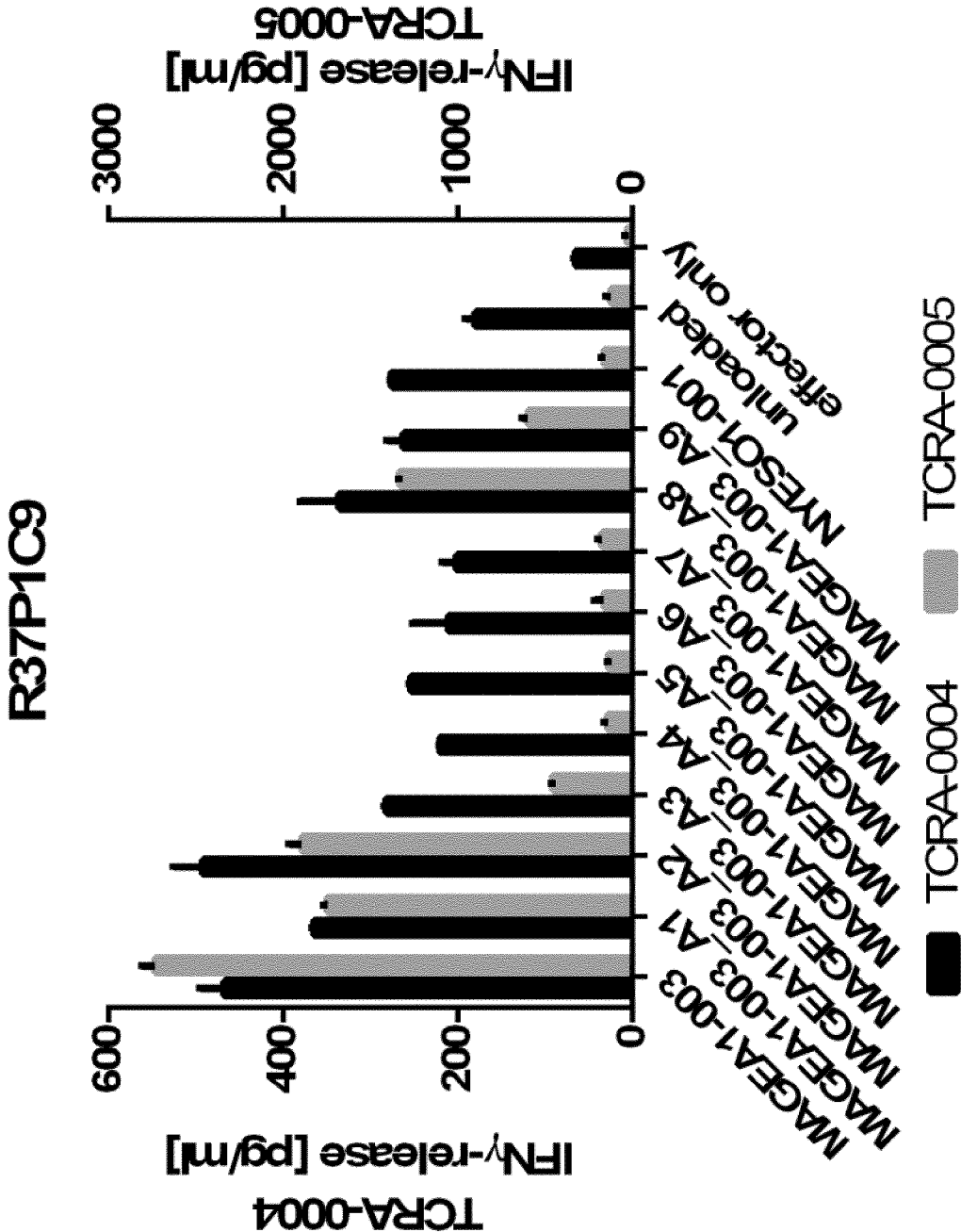
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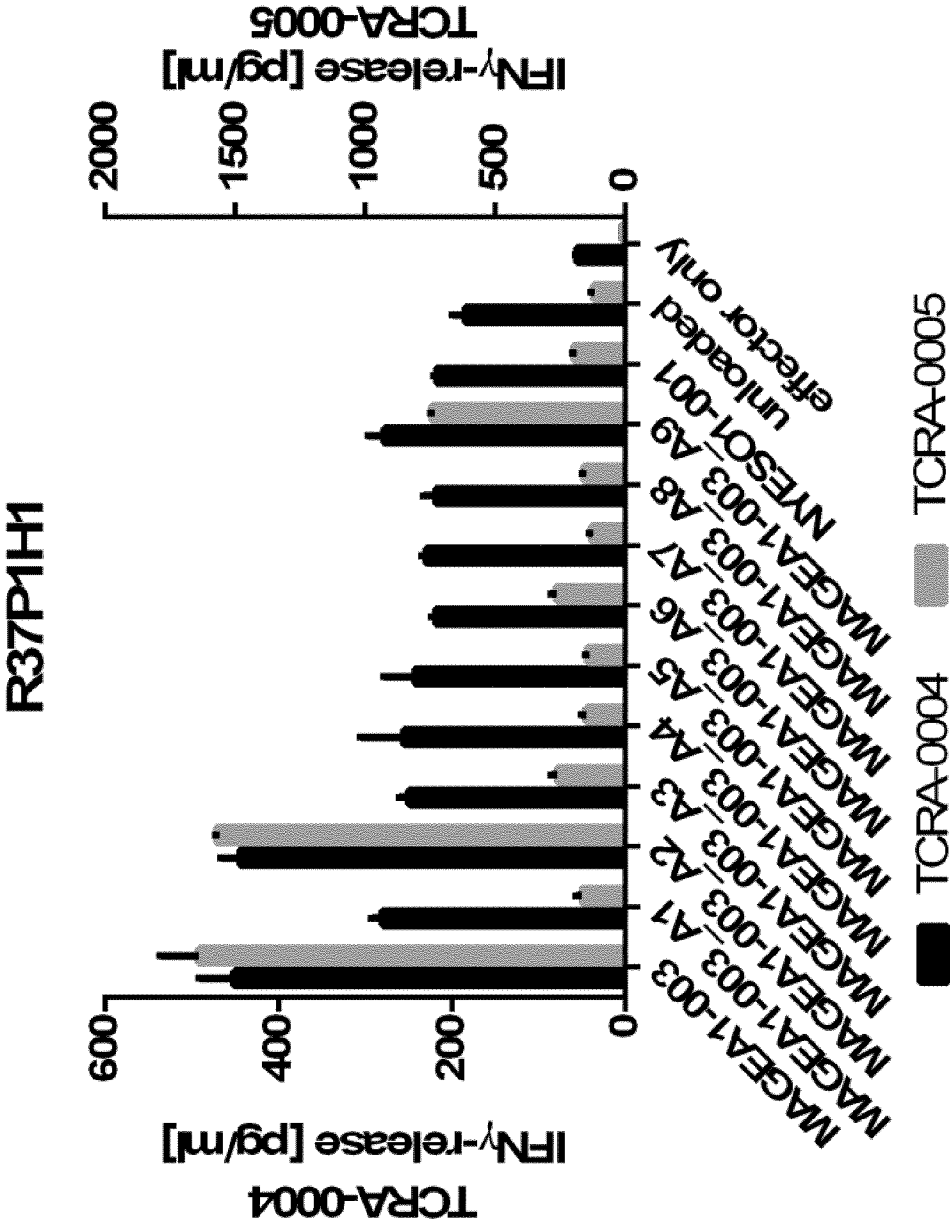
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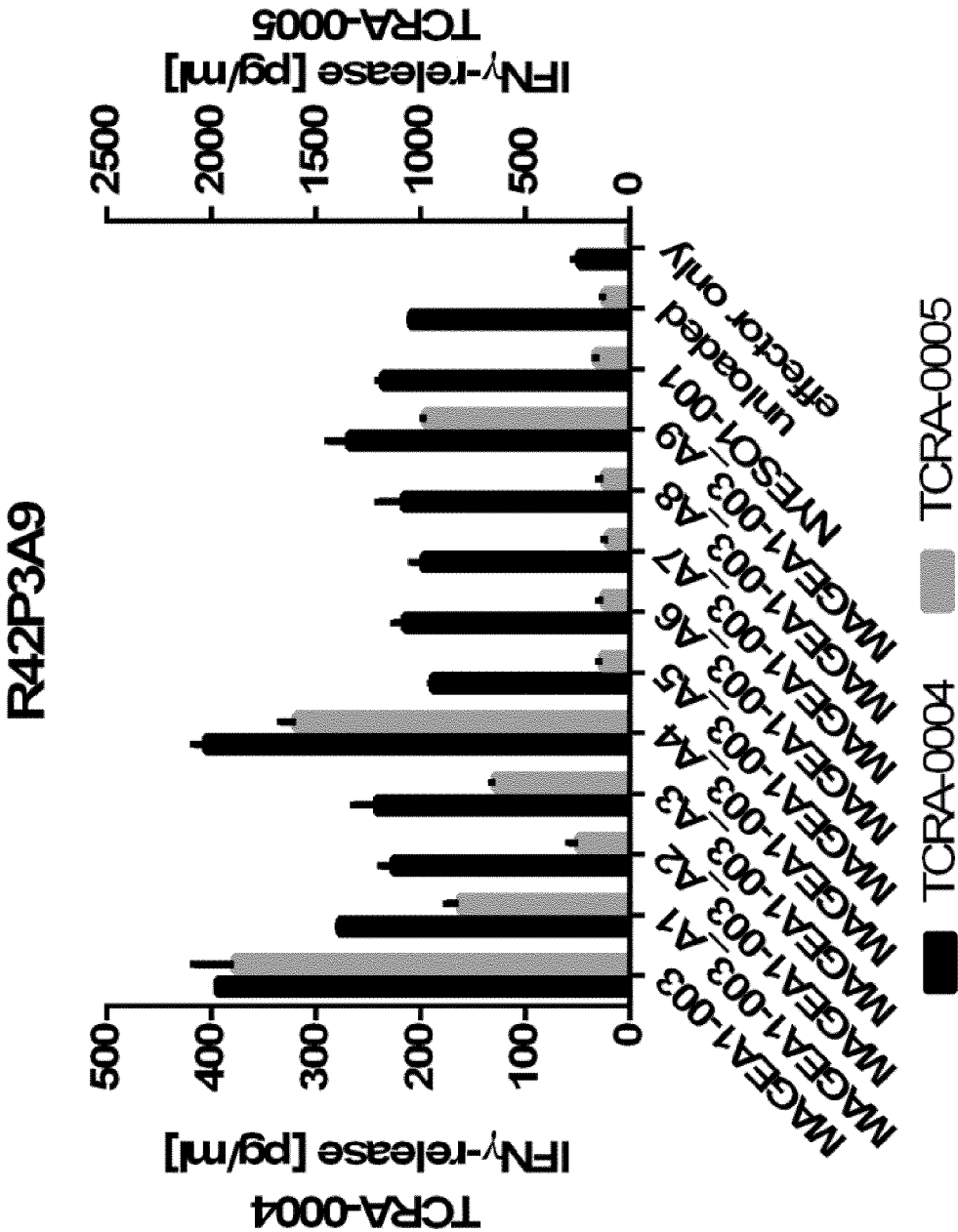
2024227729 29 Oct 2024

Figure 6:



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Figure 7:



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Figure 8:

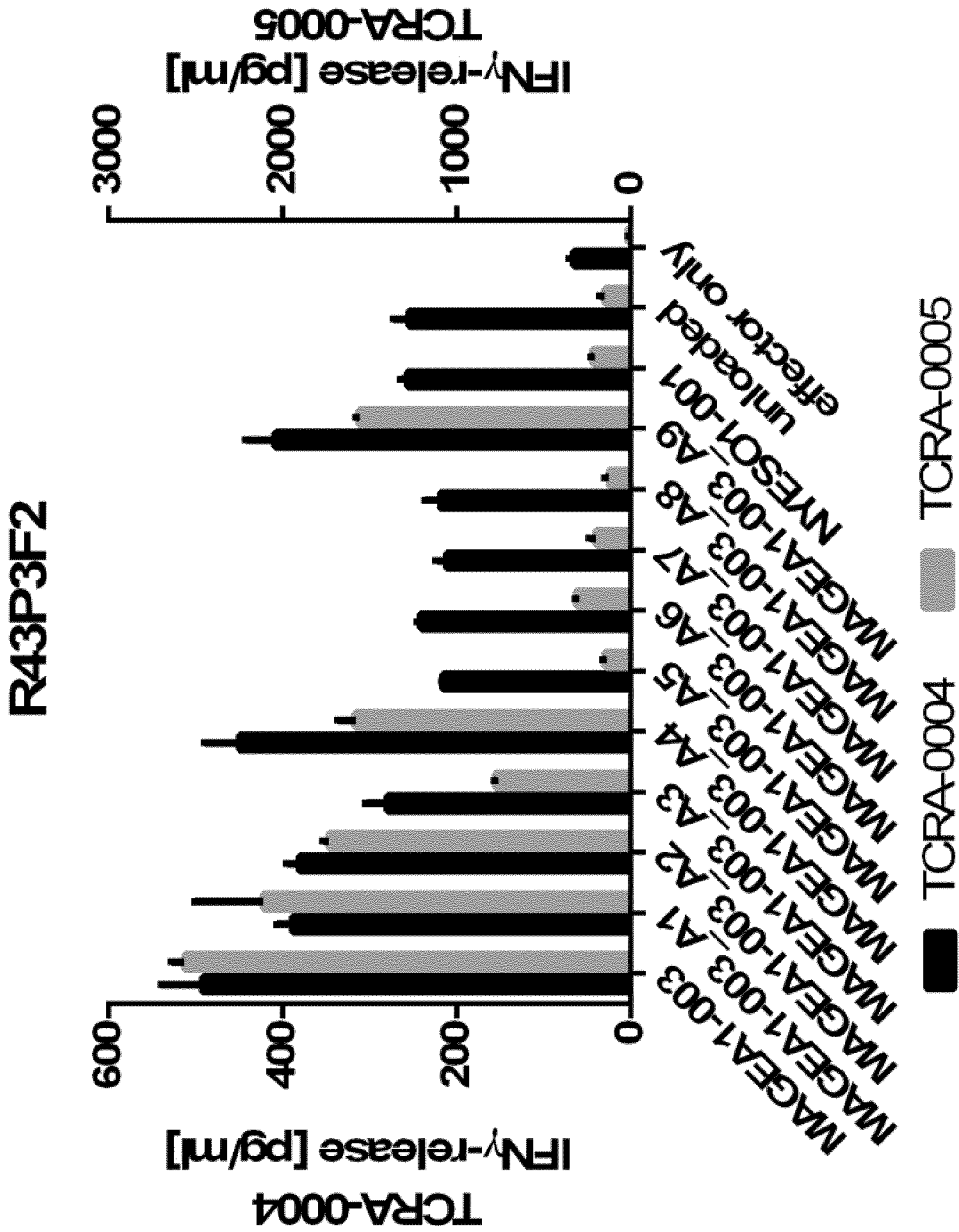


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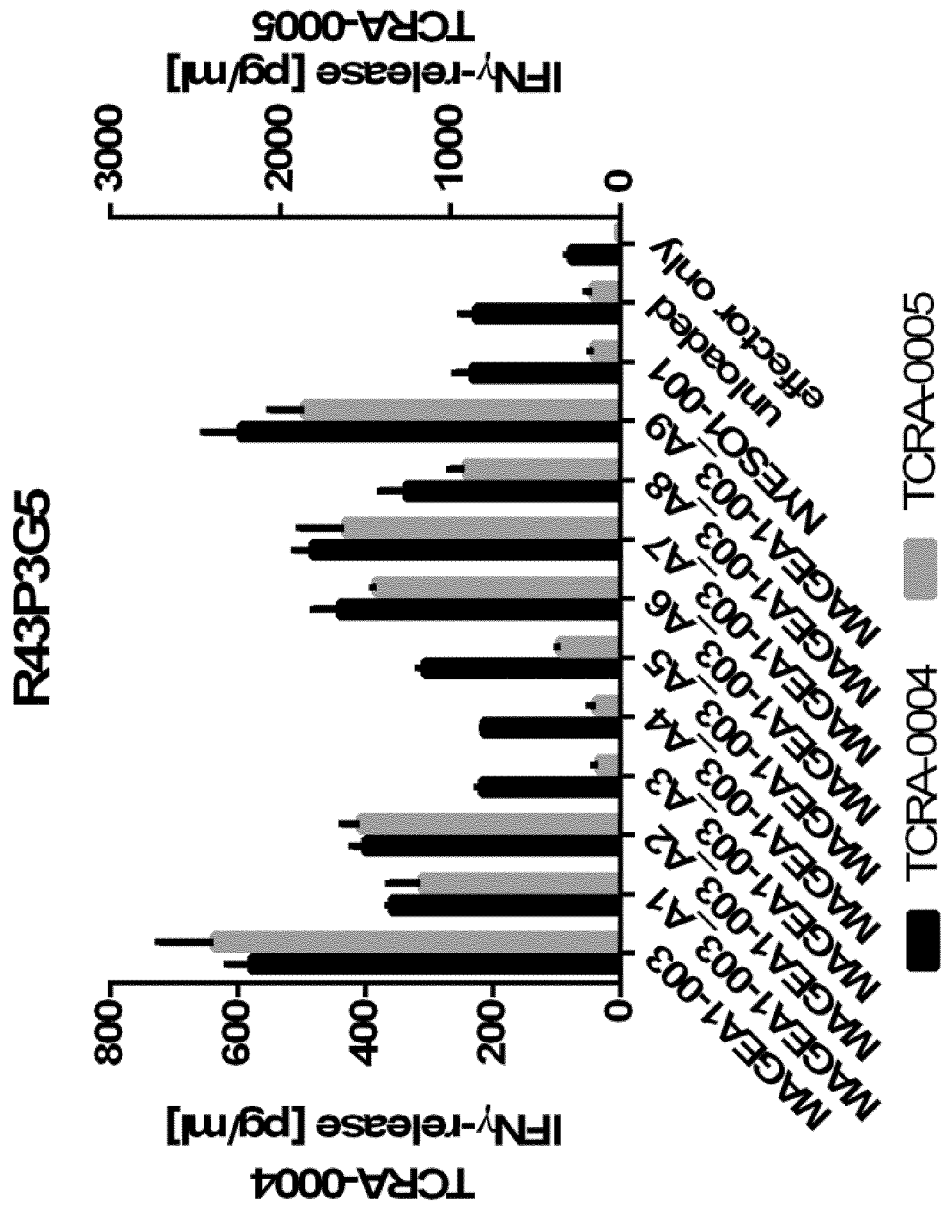
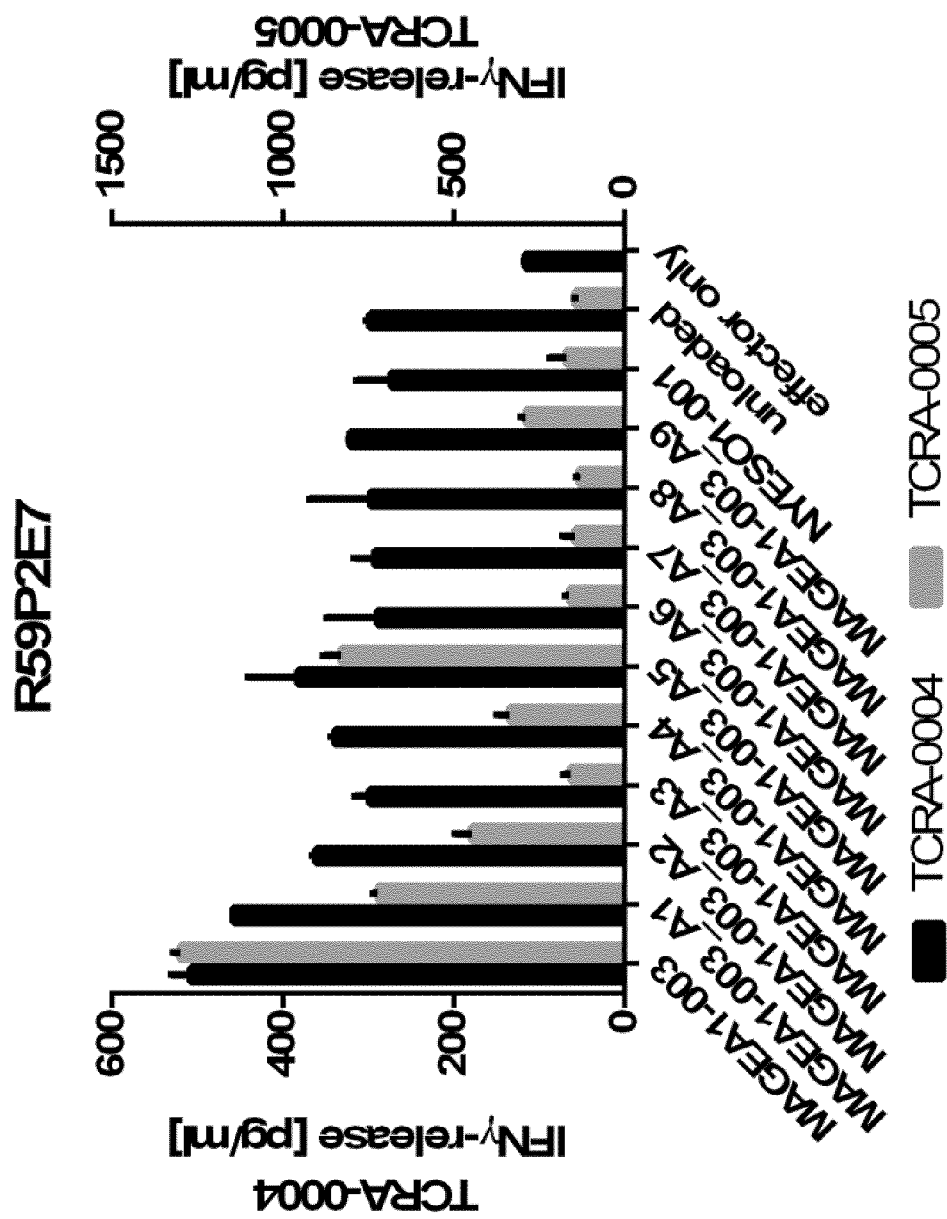
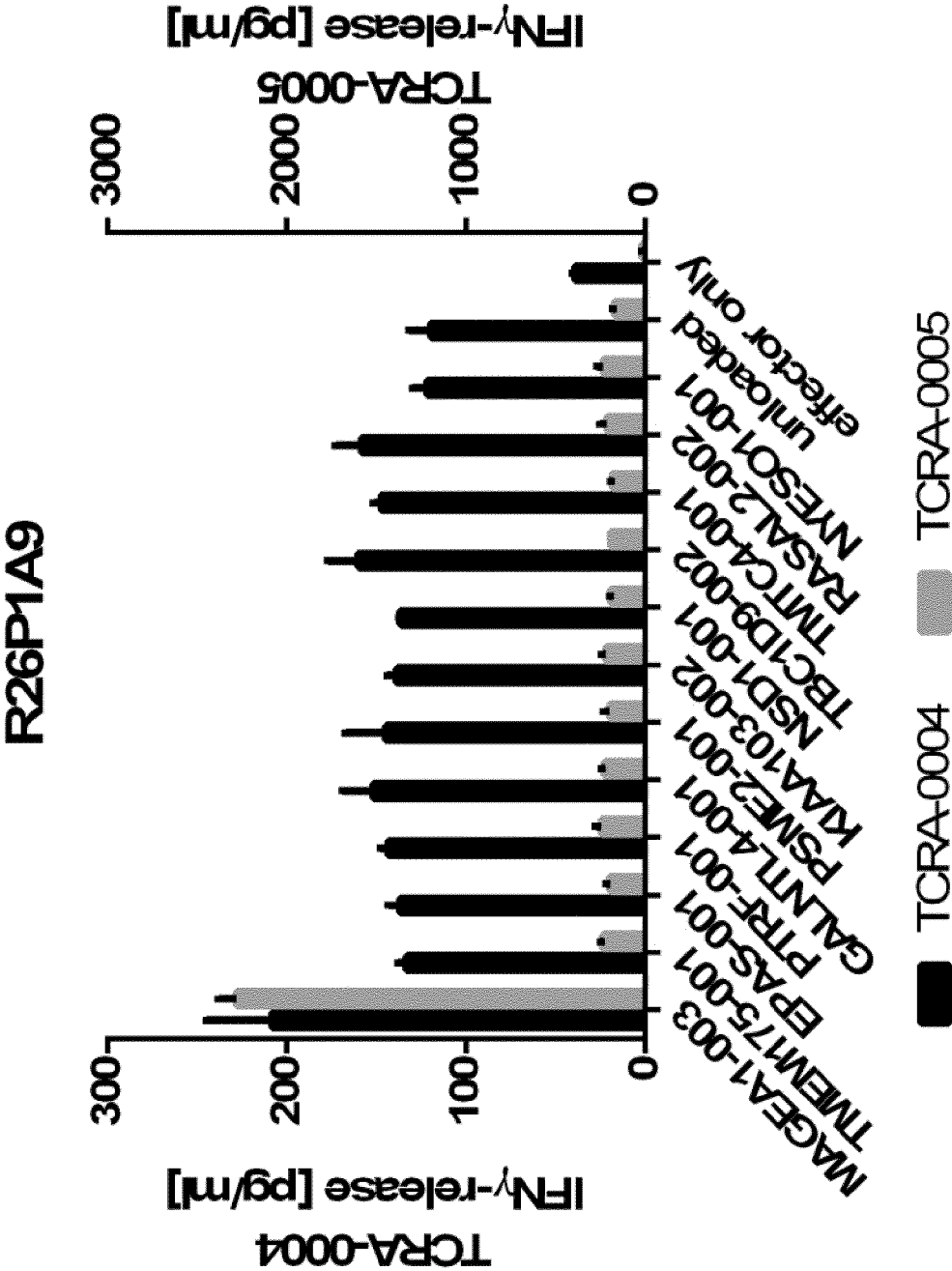


Figure 10:



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Figure 11:



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R26P2A6

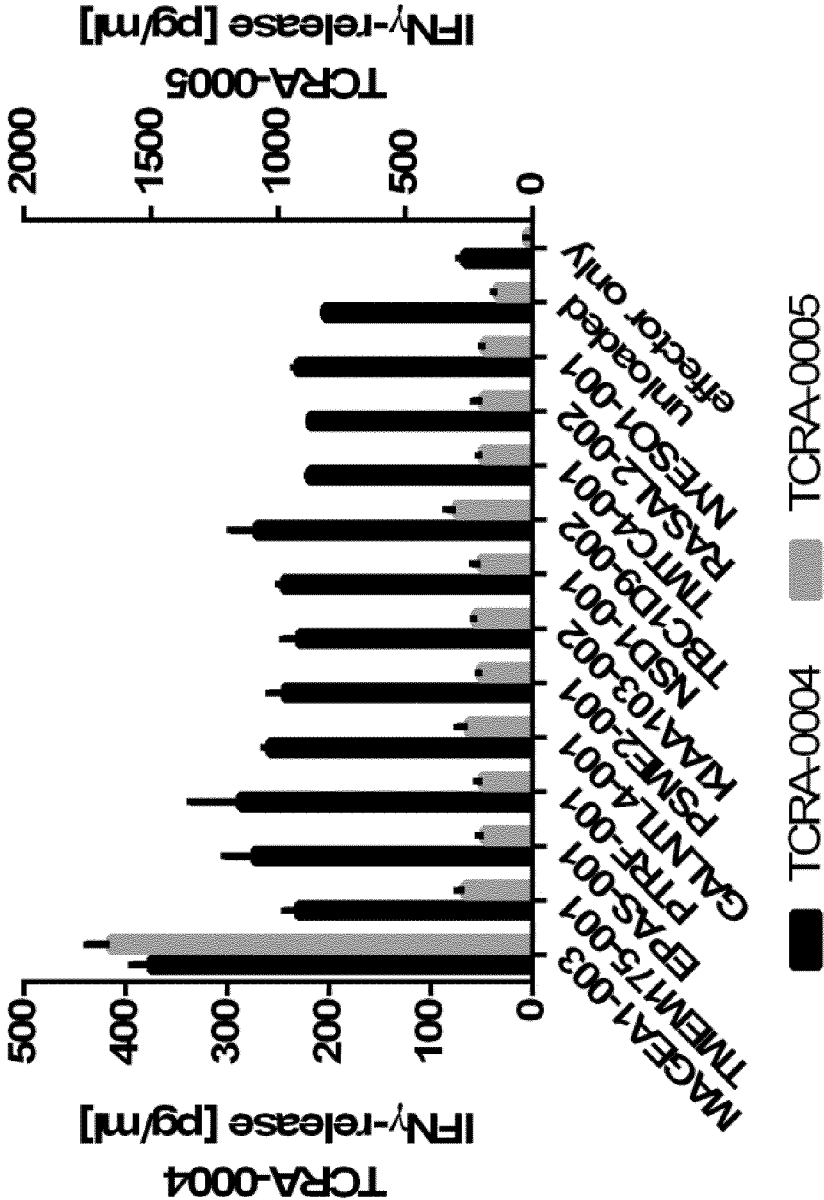
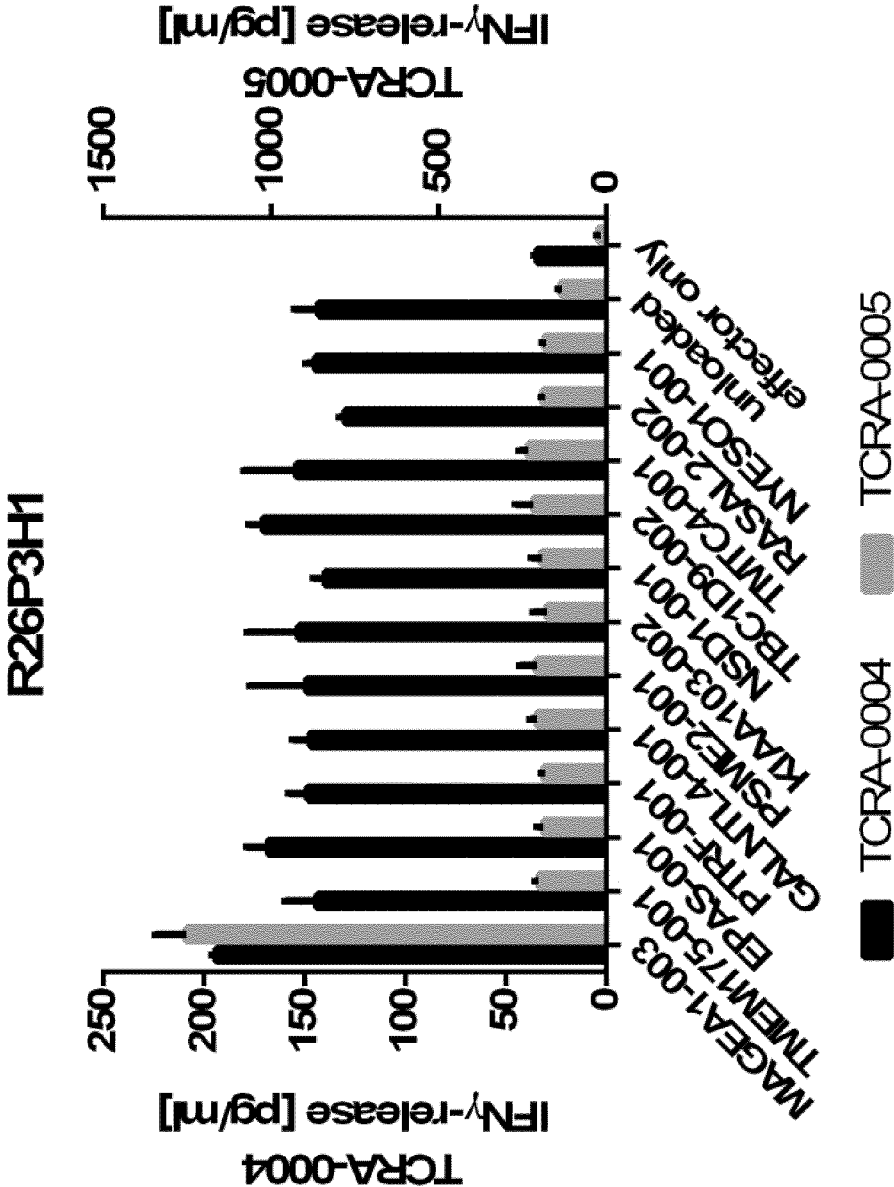


Figure 12:

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Figure 13:



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Figure 14:

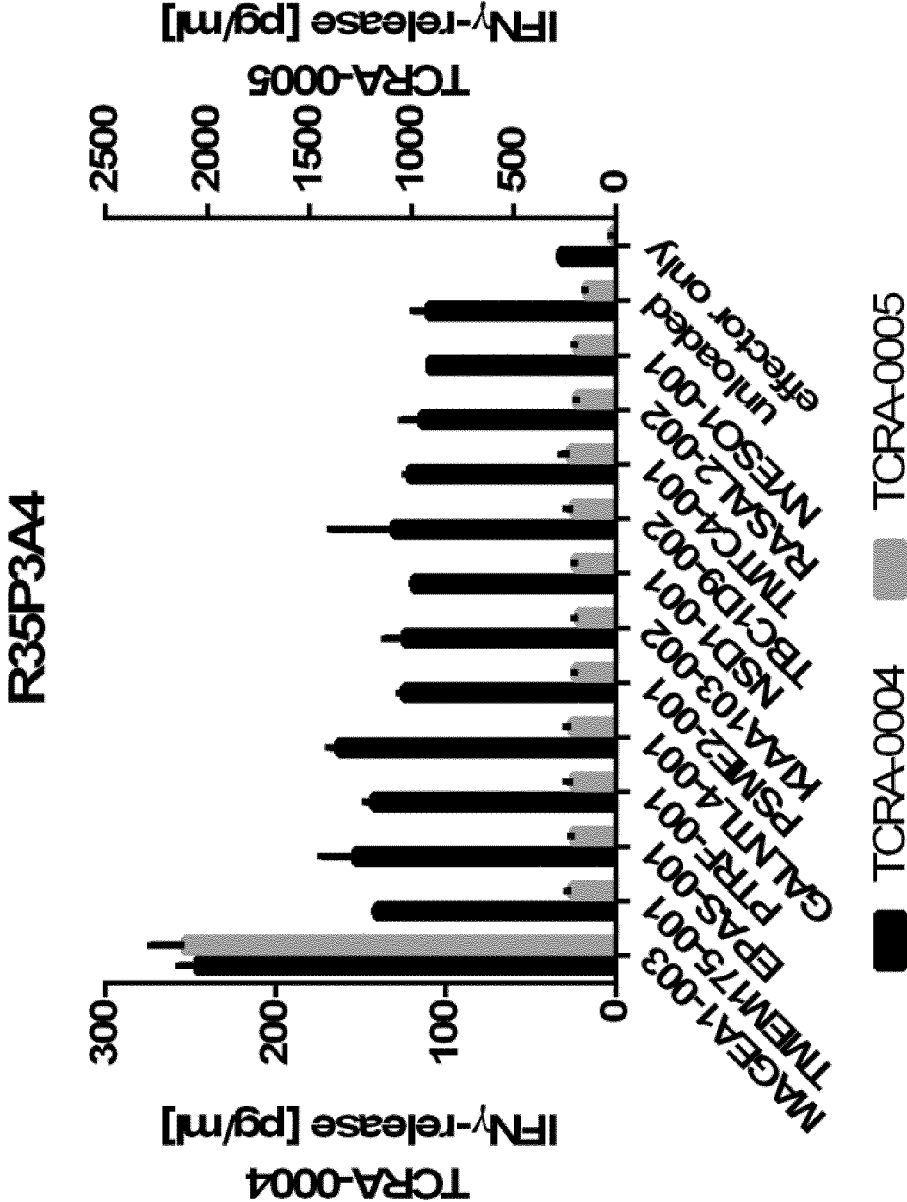
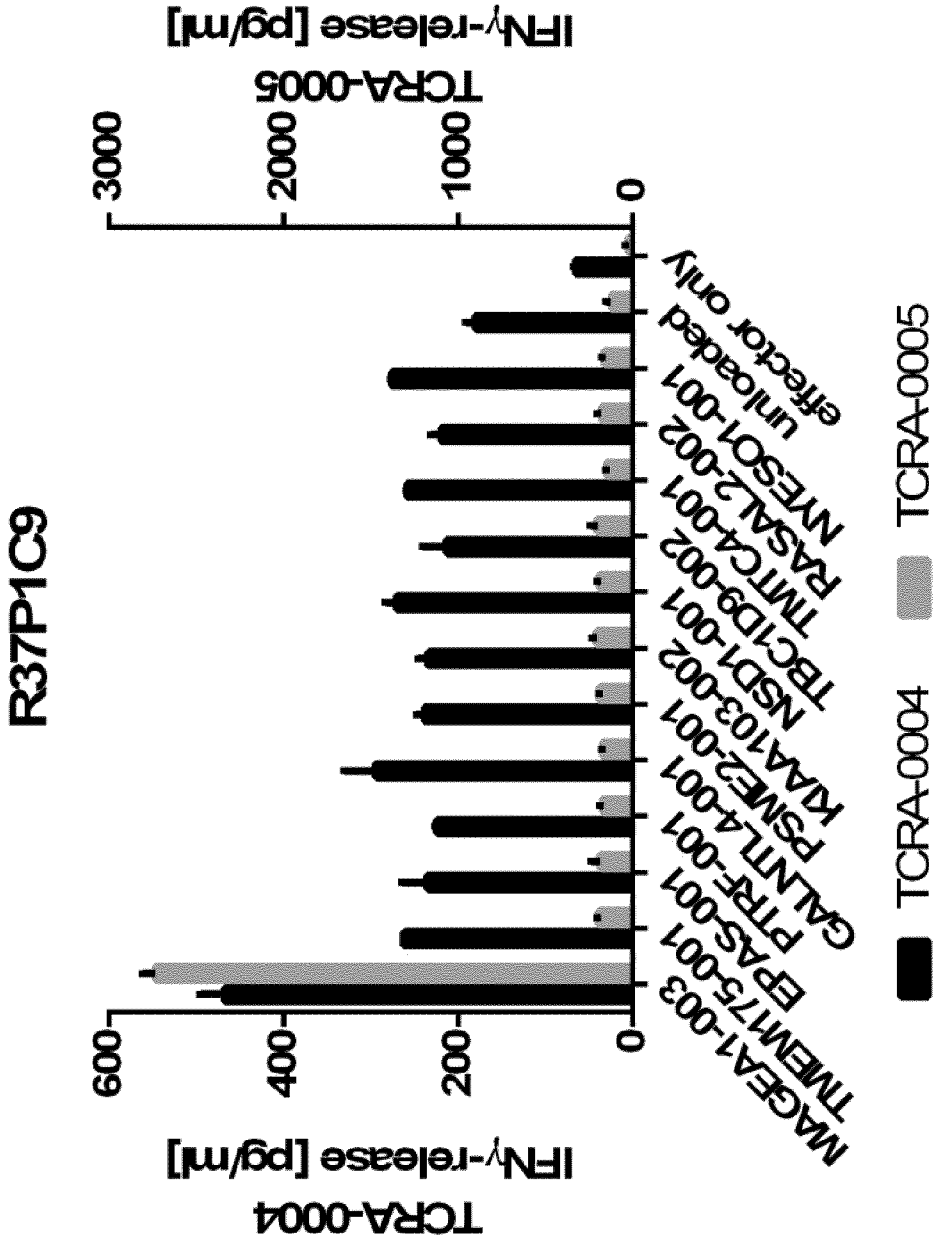
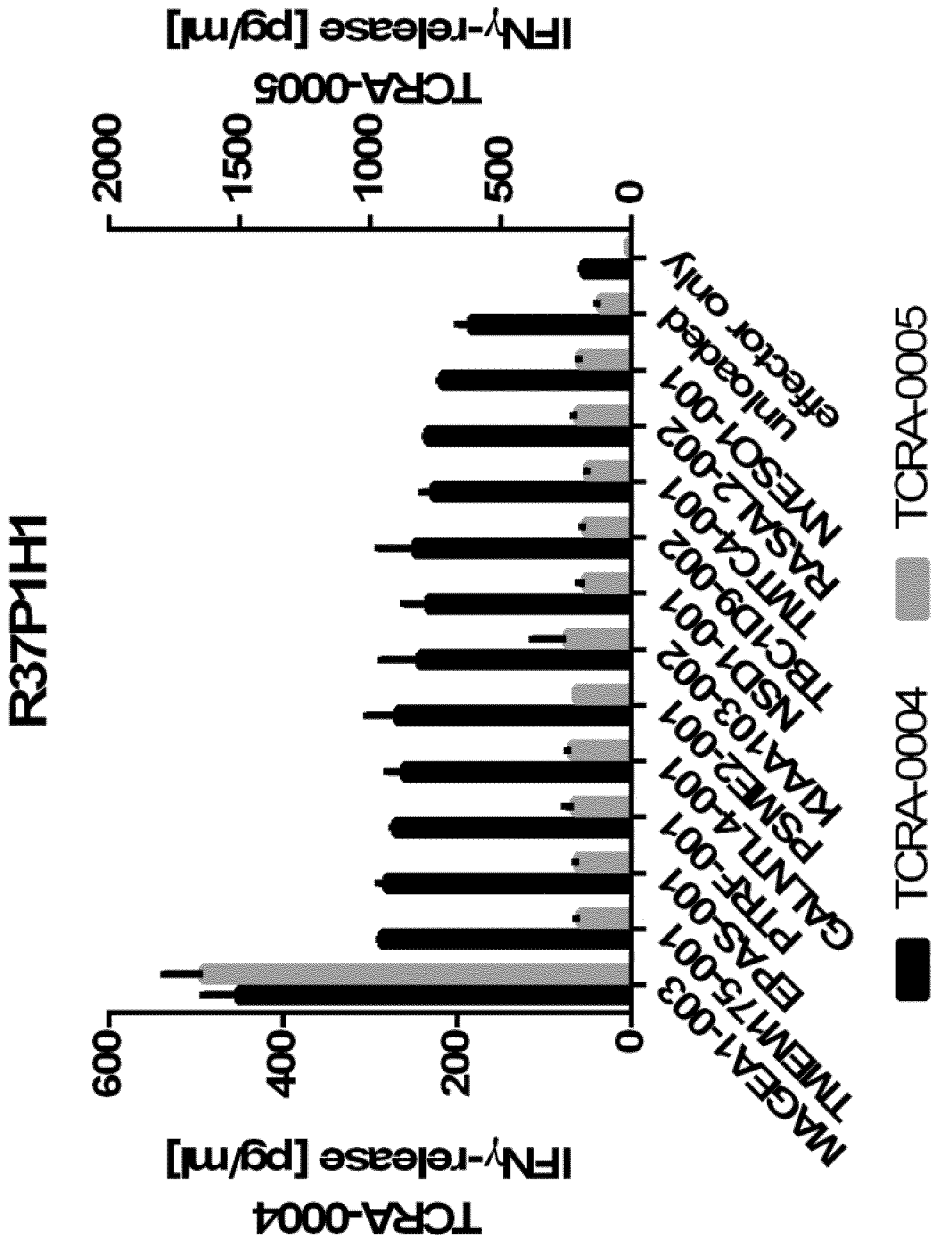


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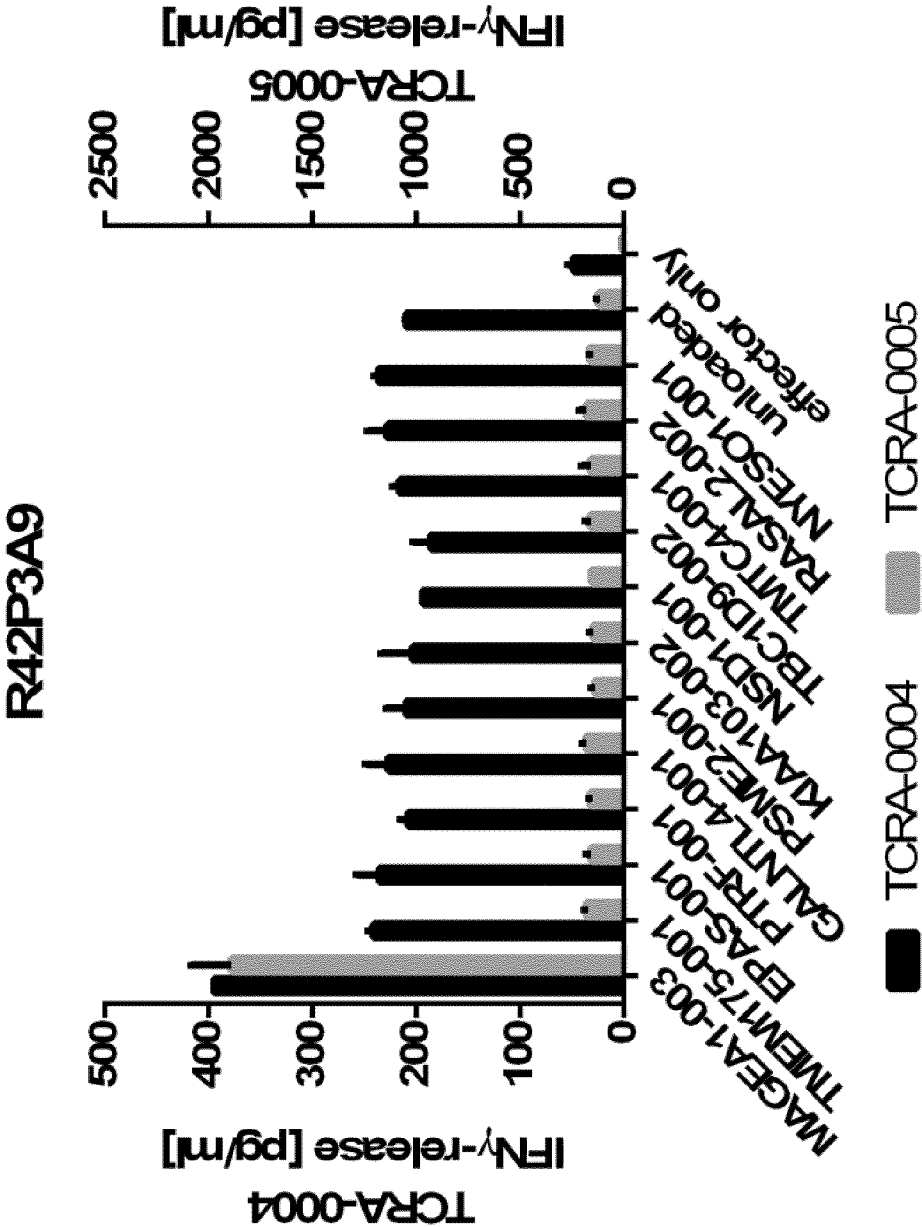
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Figure 16:



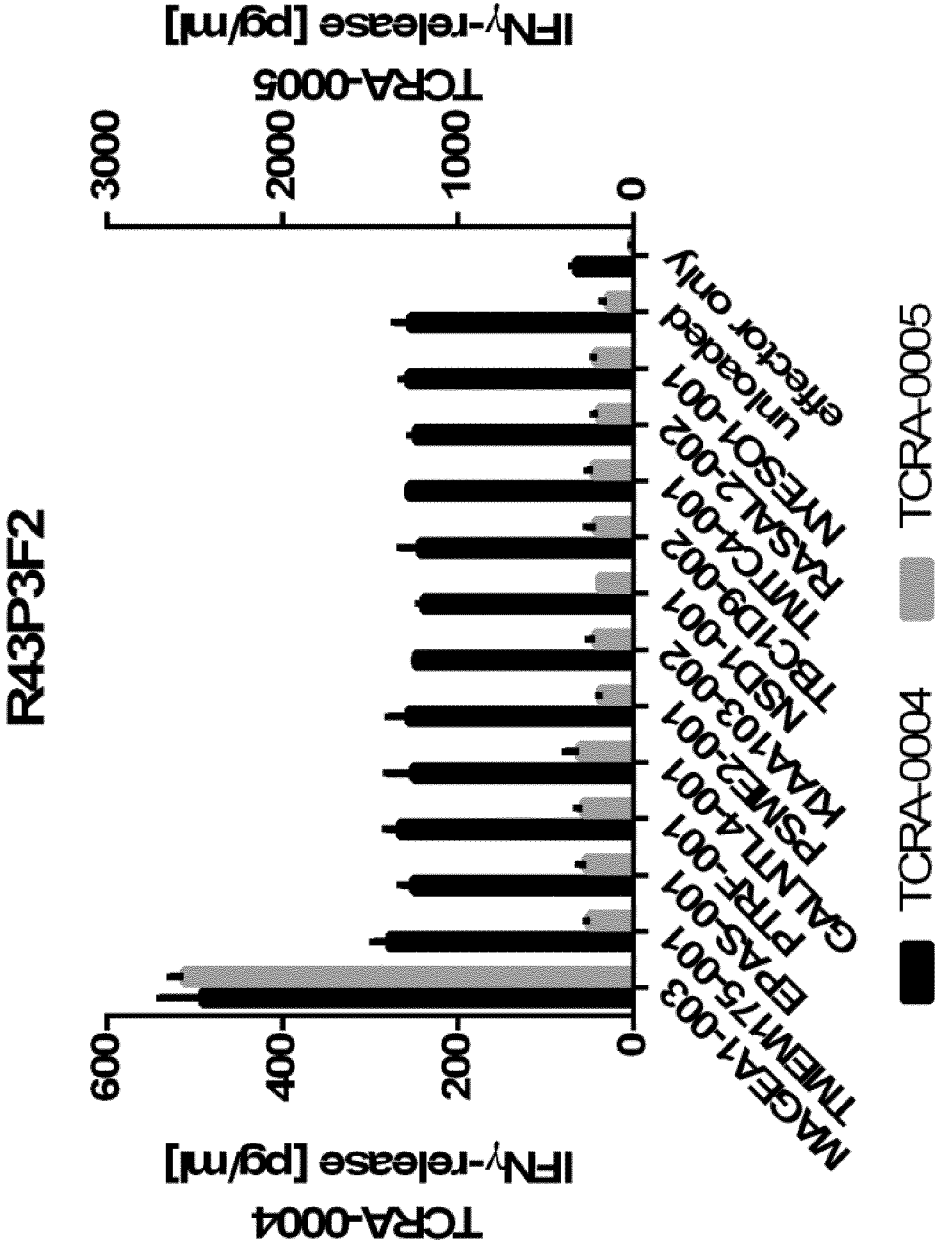
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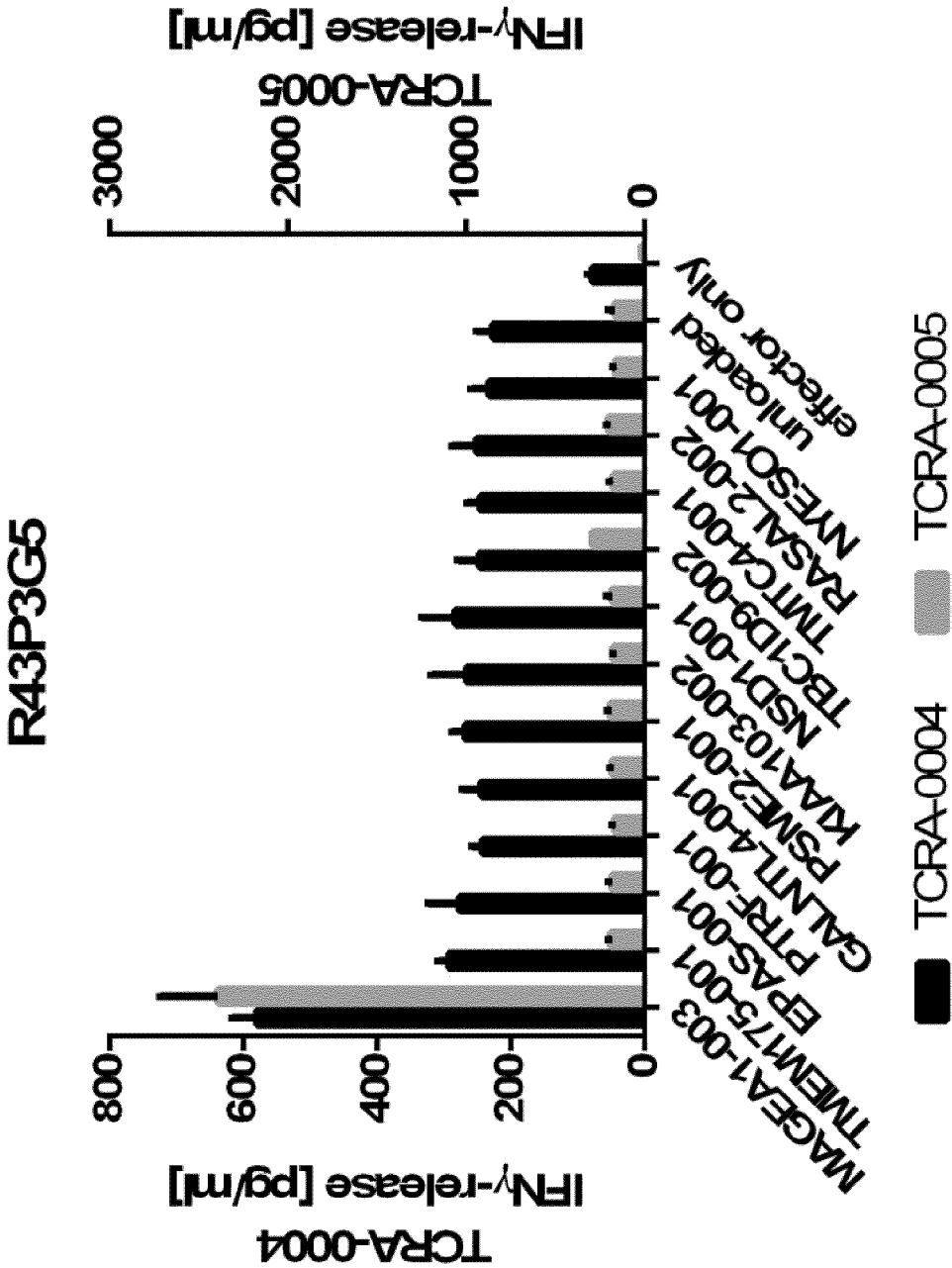
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Figure 18:



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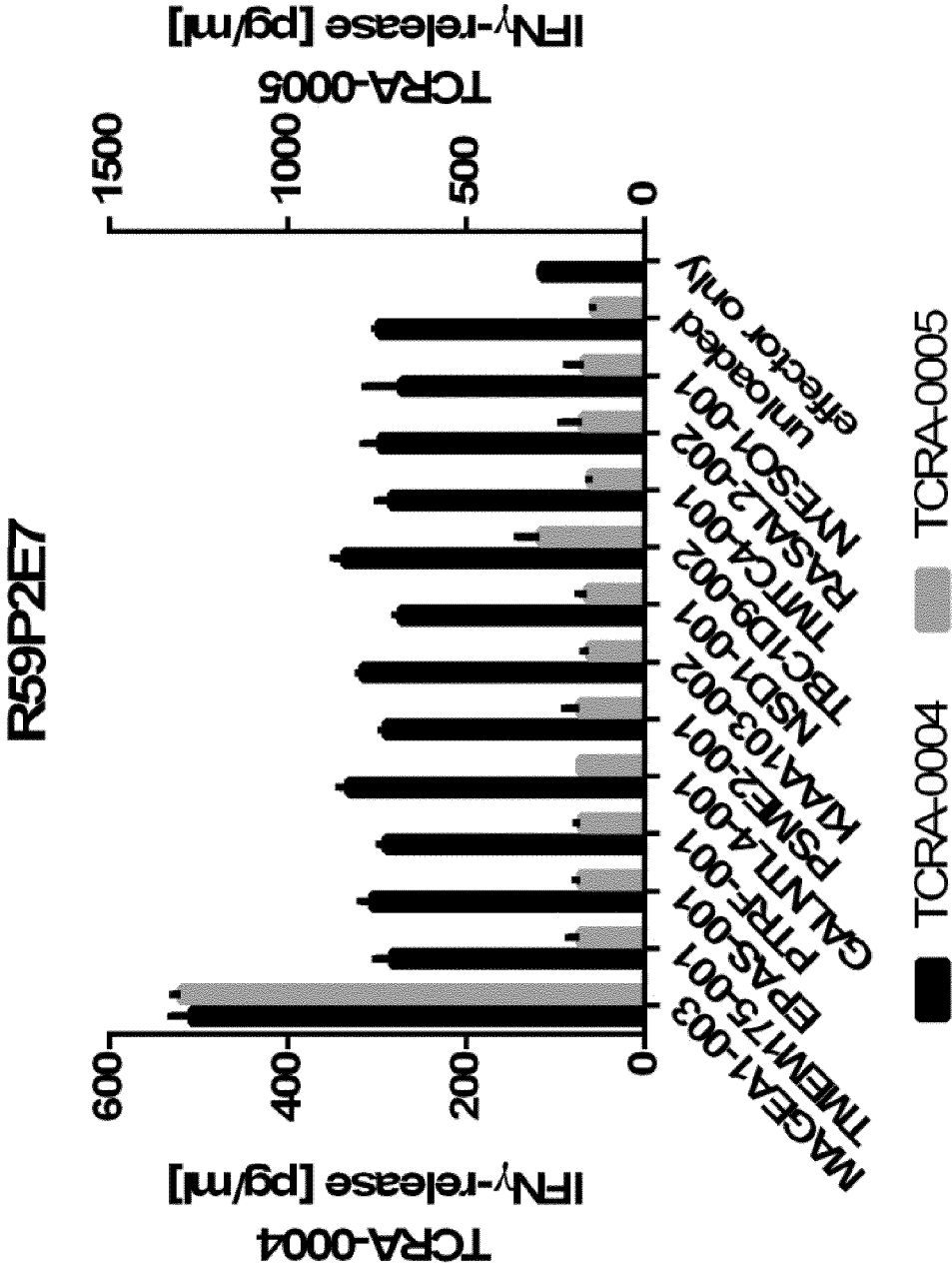
Figure 19:



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Figure 20:



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Figure 21:

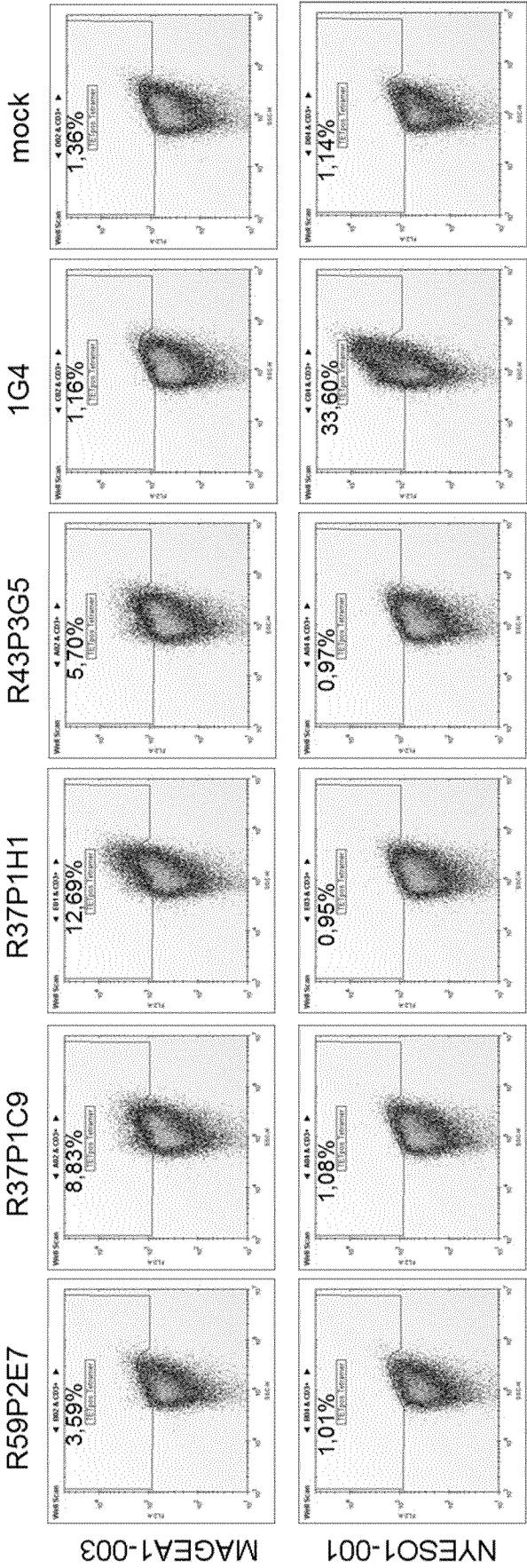
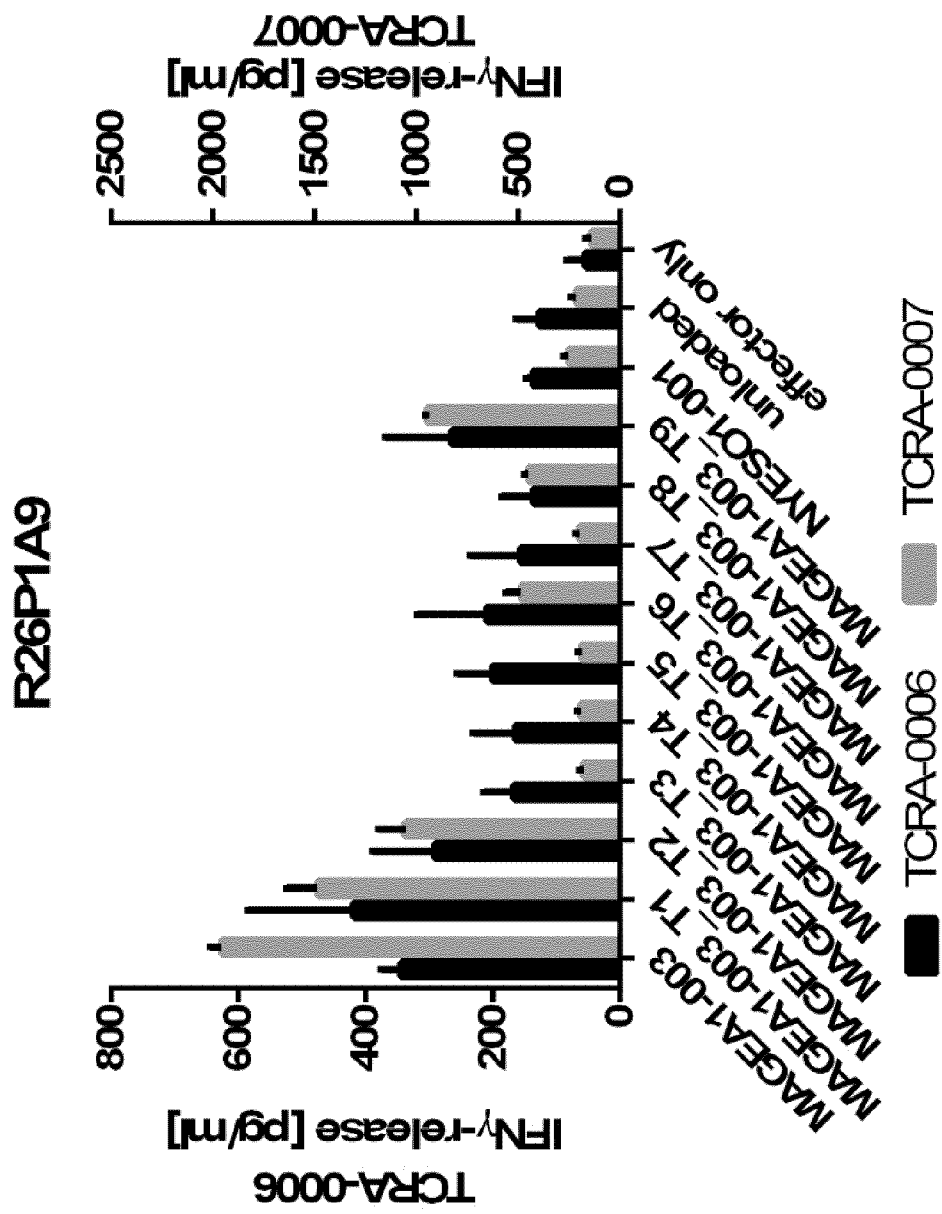


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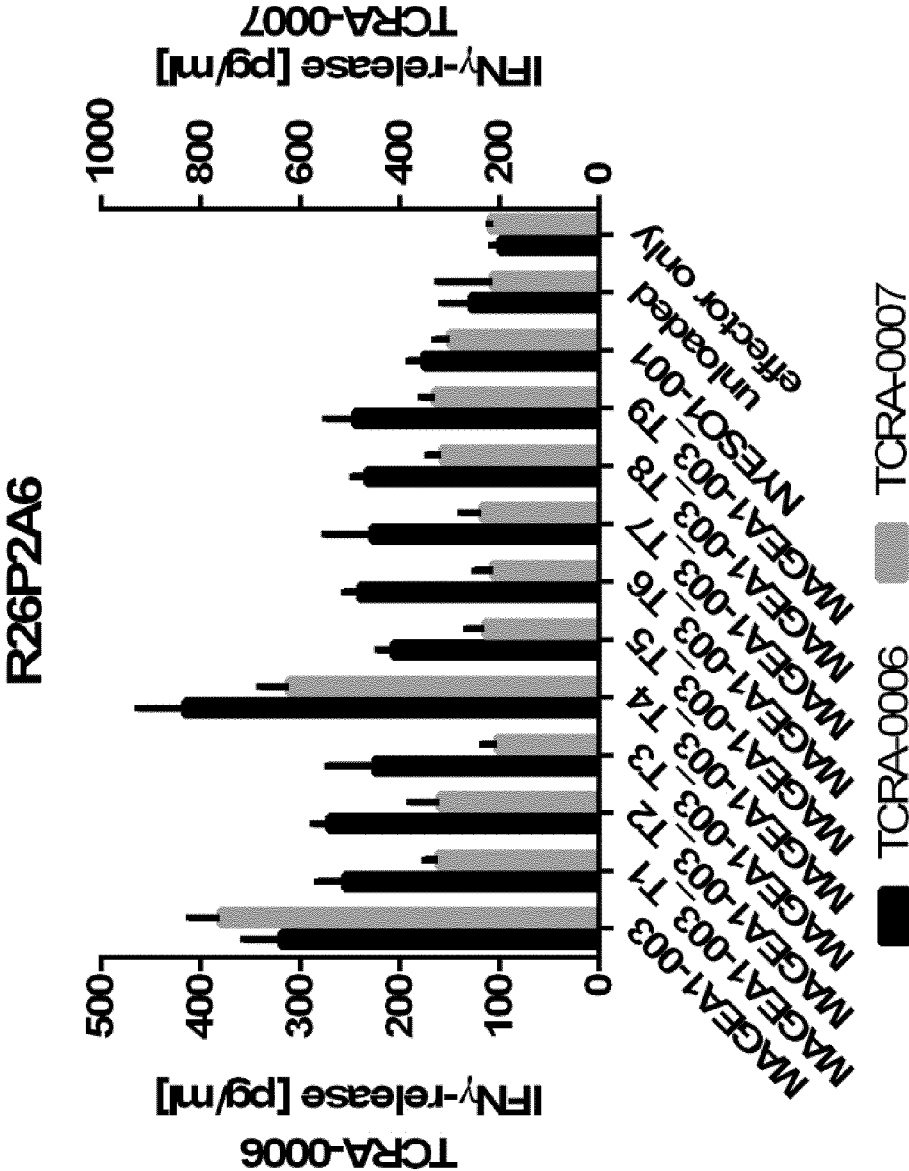
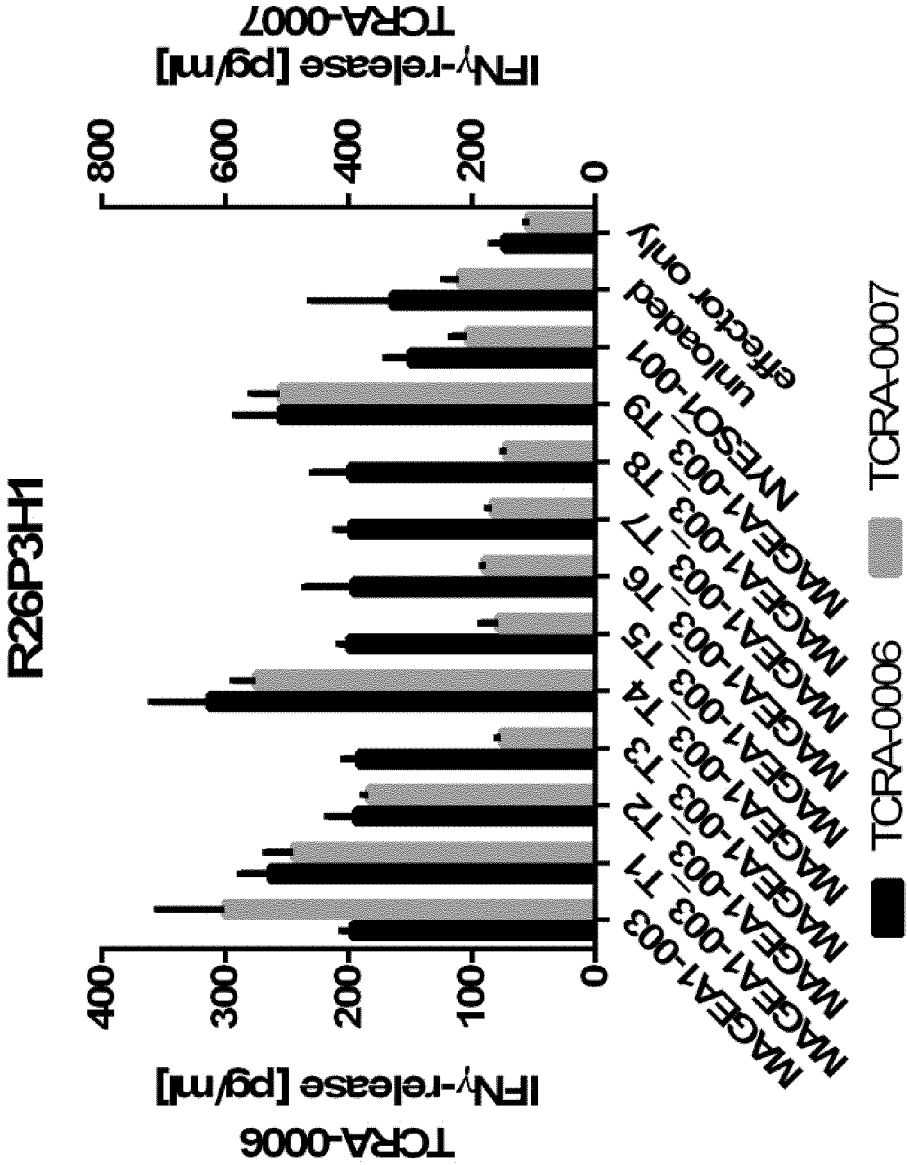


Figure 23:

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Figure 24:



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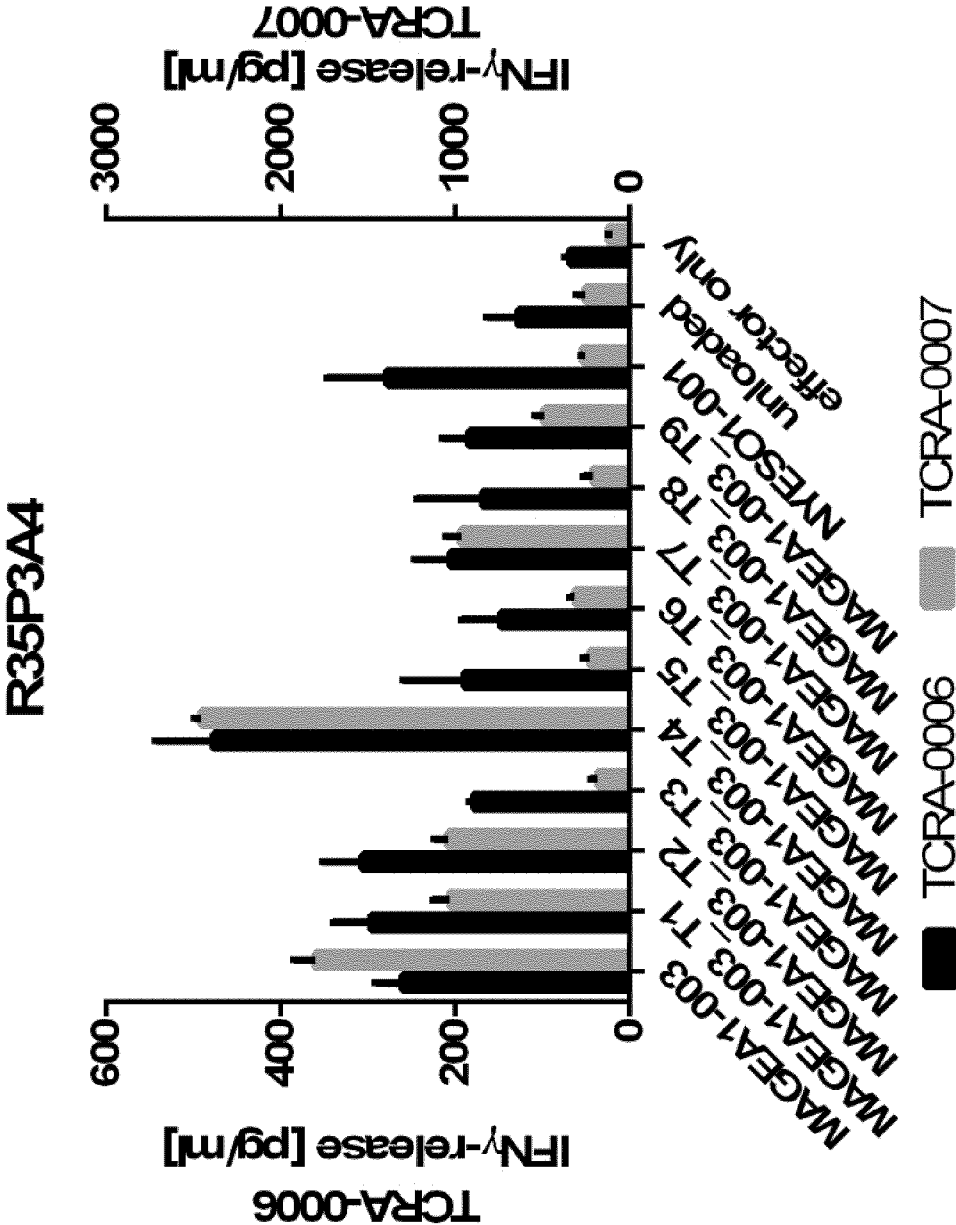


Figure 25:

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R37P1C9

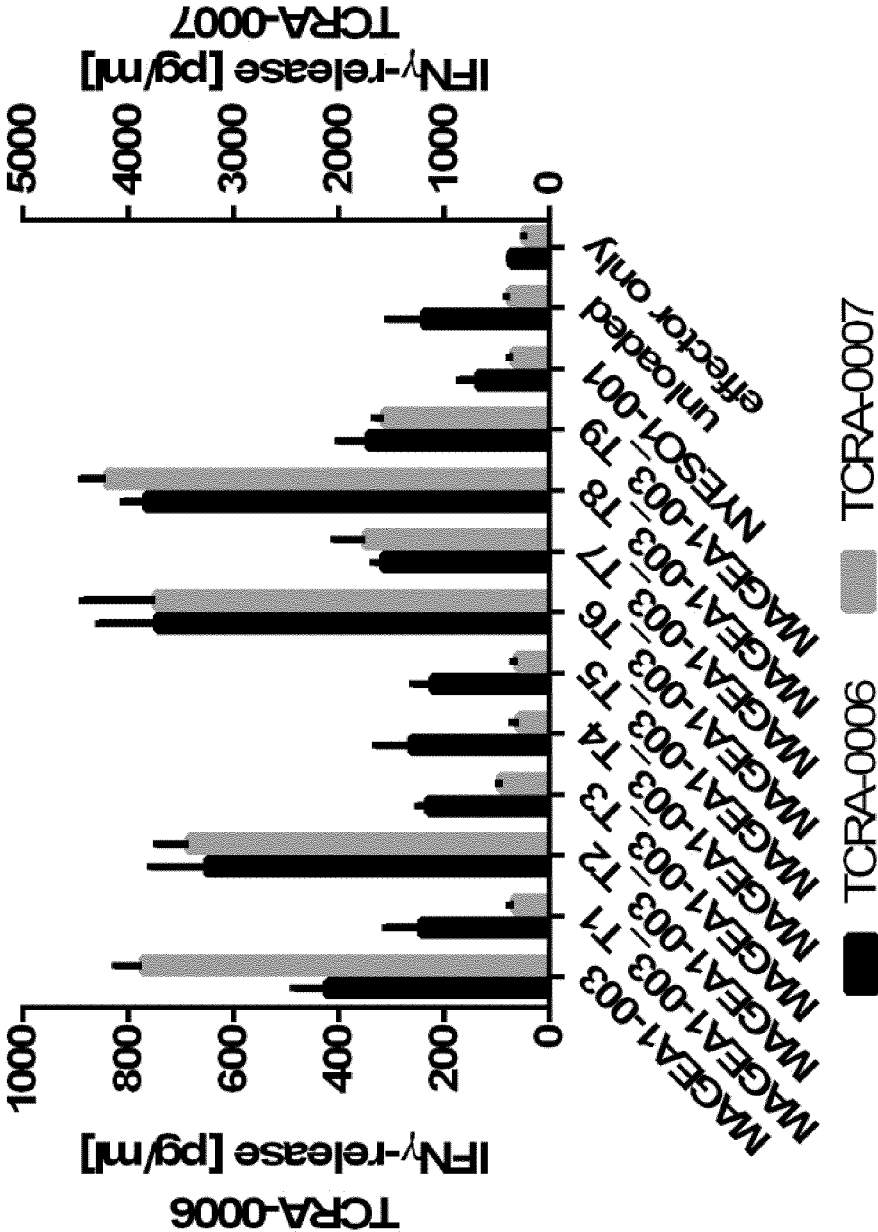
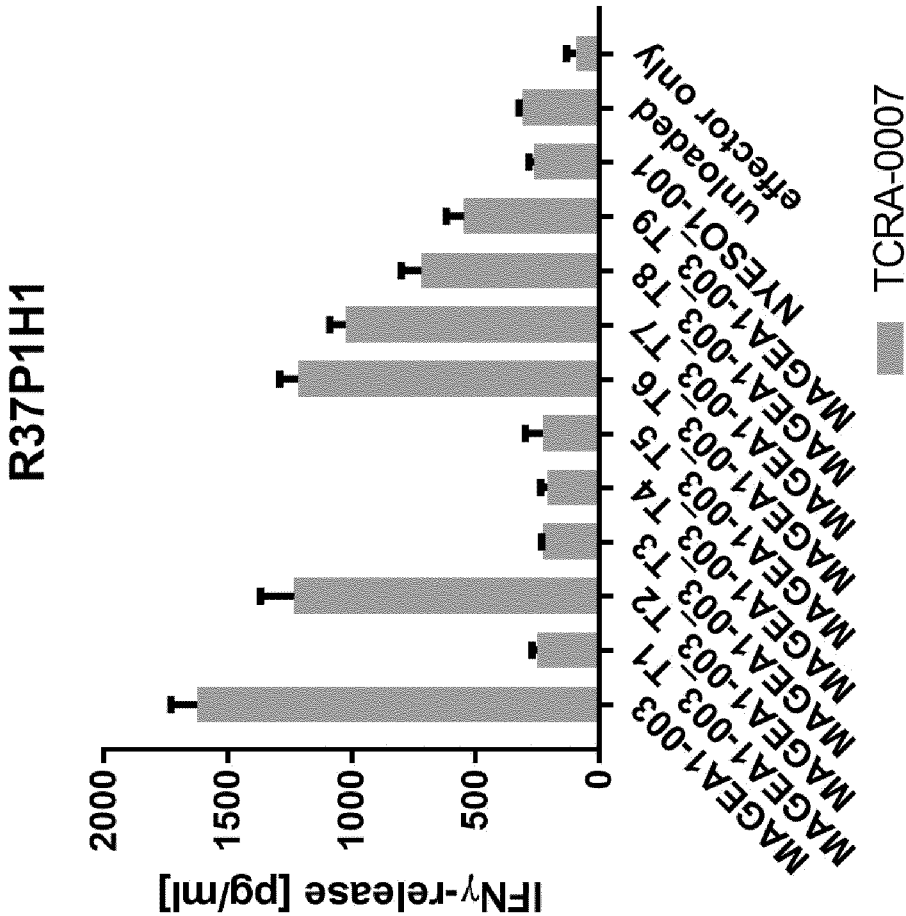


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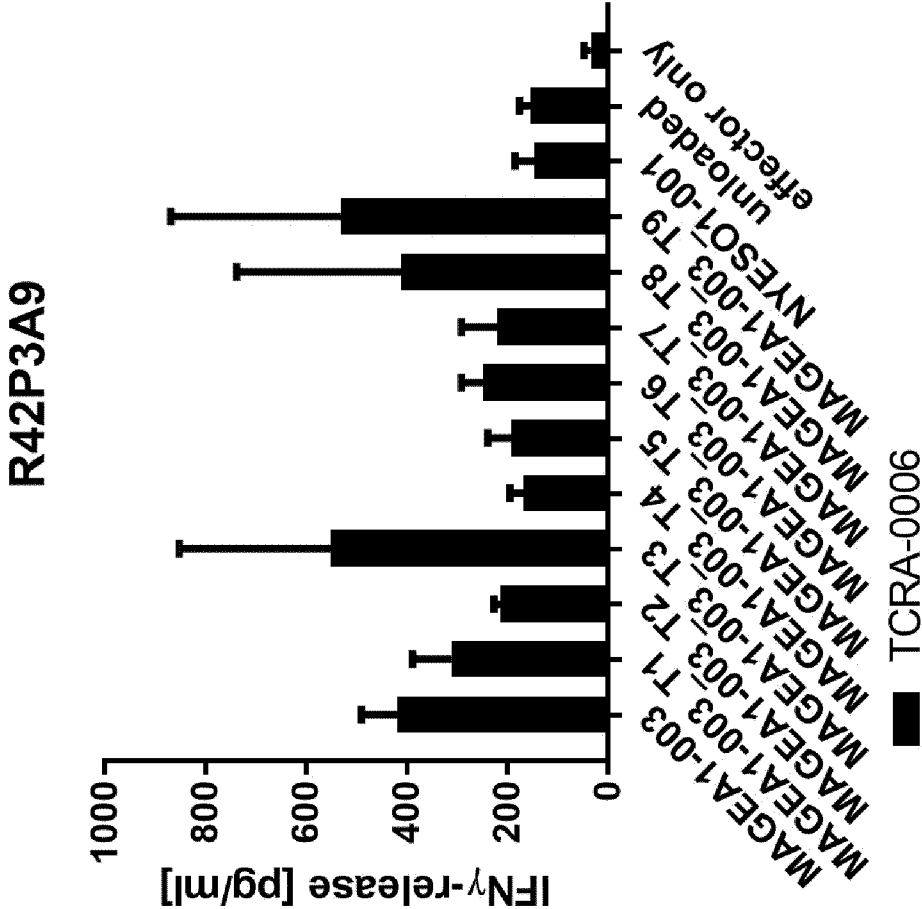
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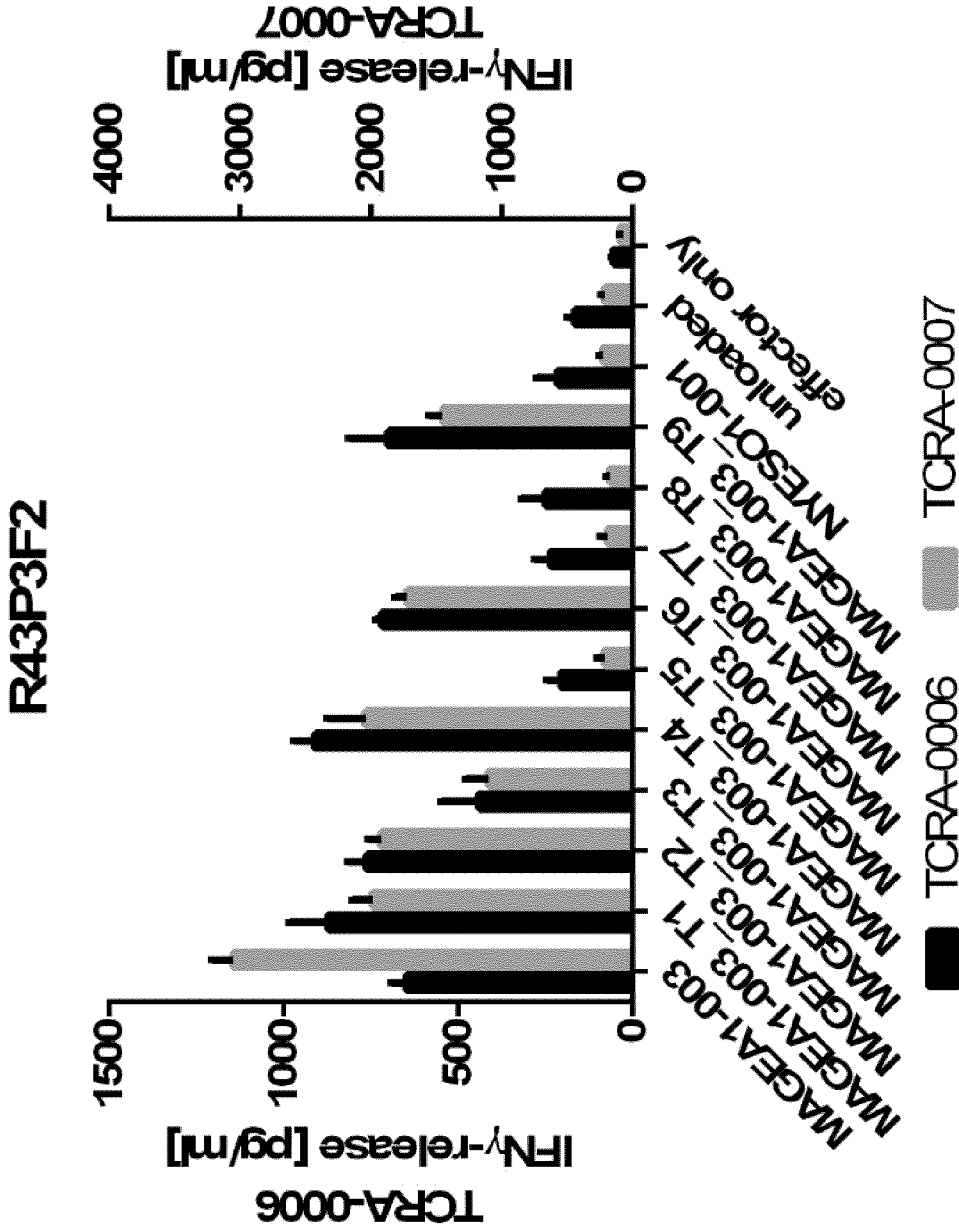
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Figure 28:



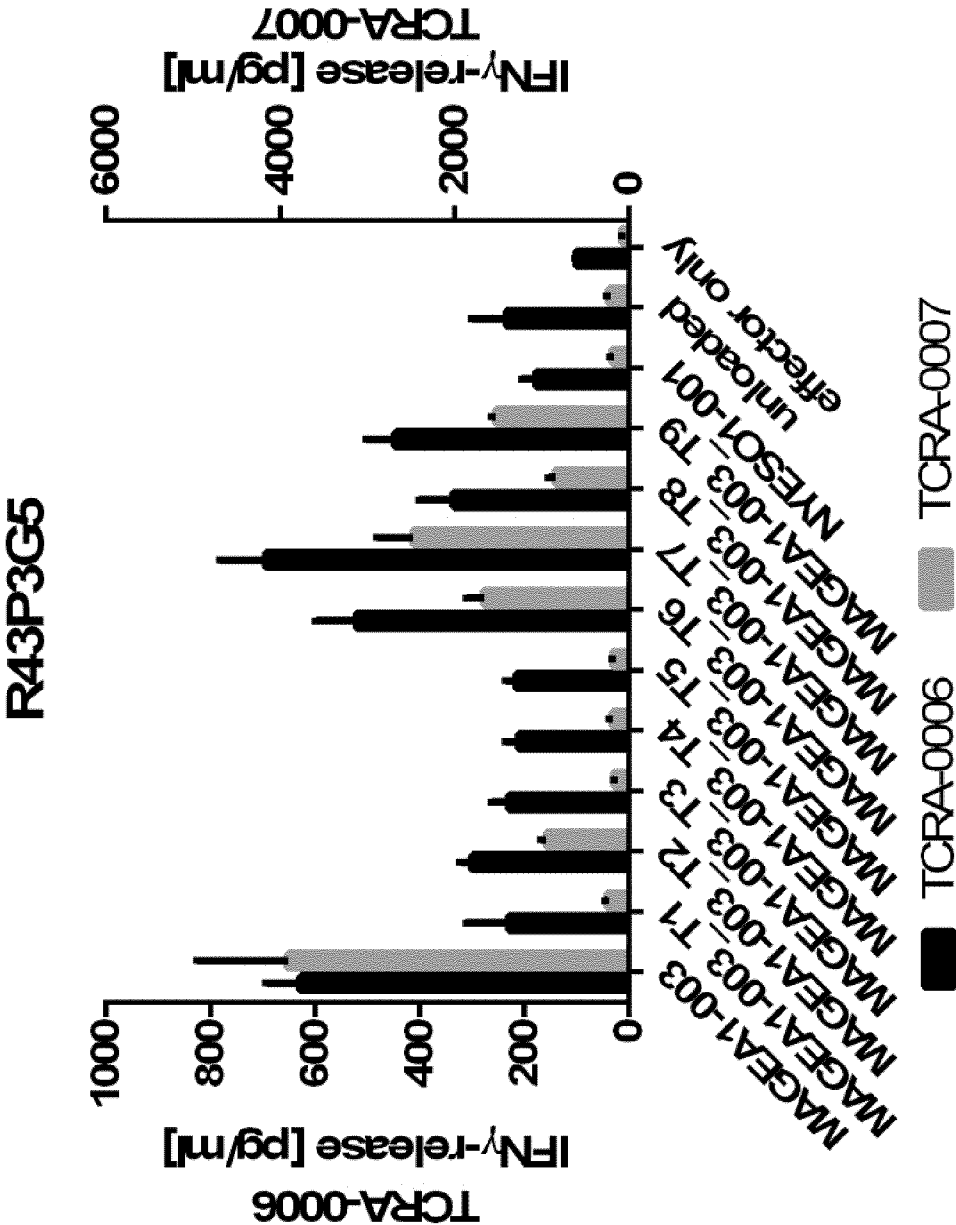
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Figure 29:



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Figure 30:



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Figure 31:

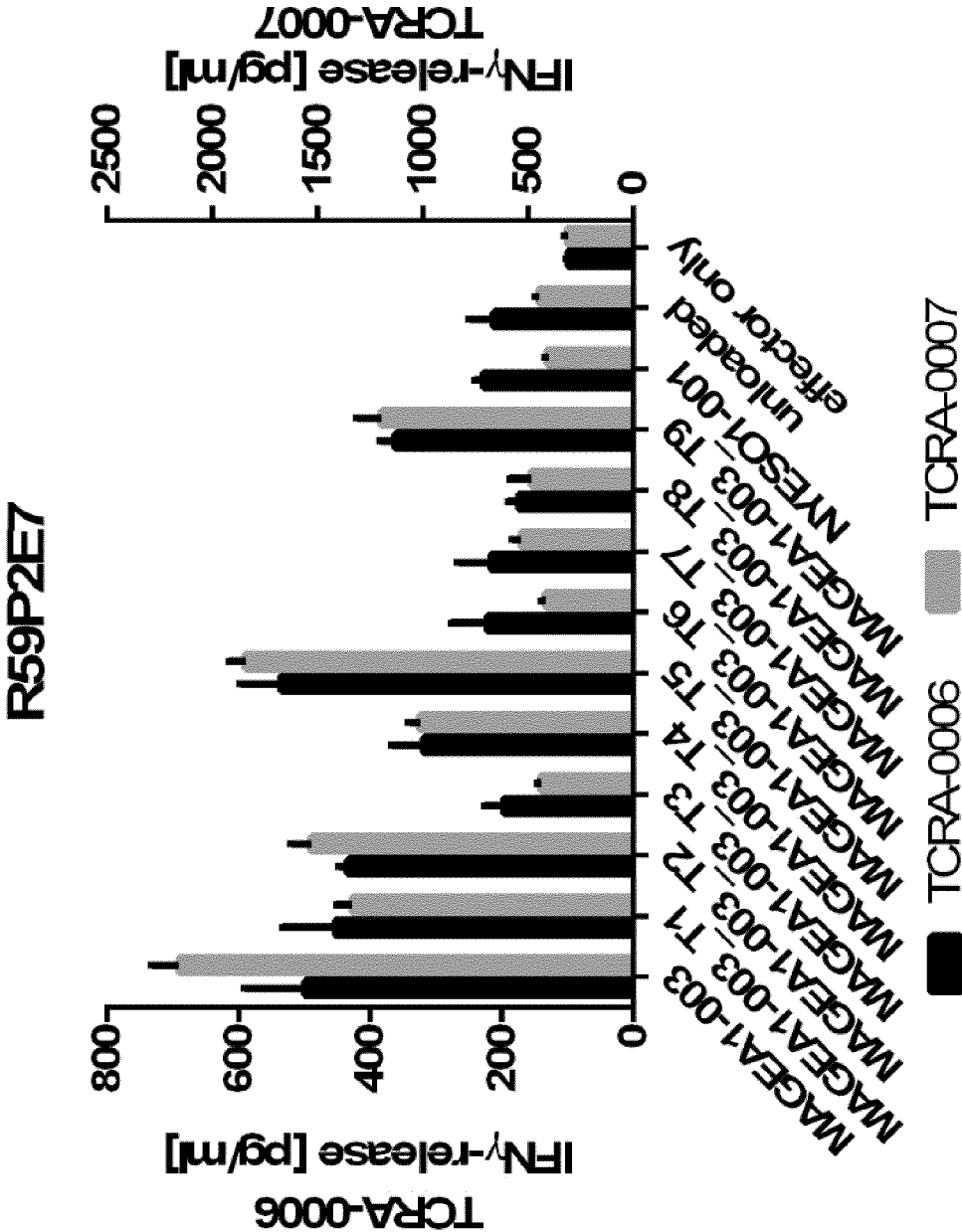
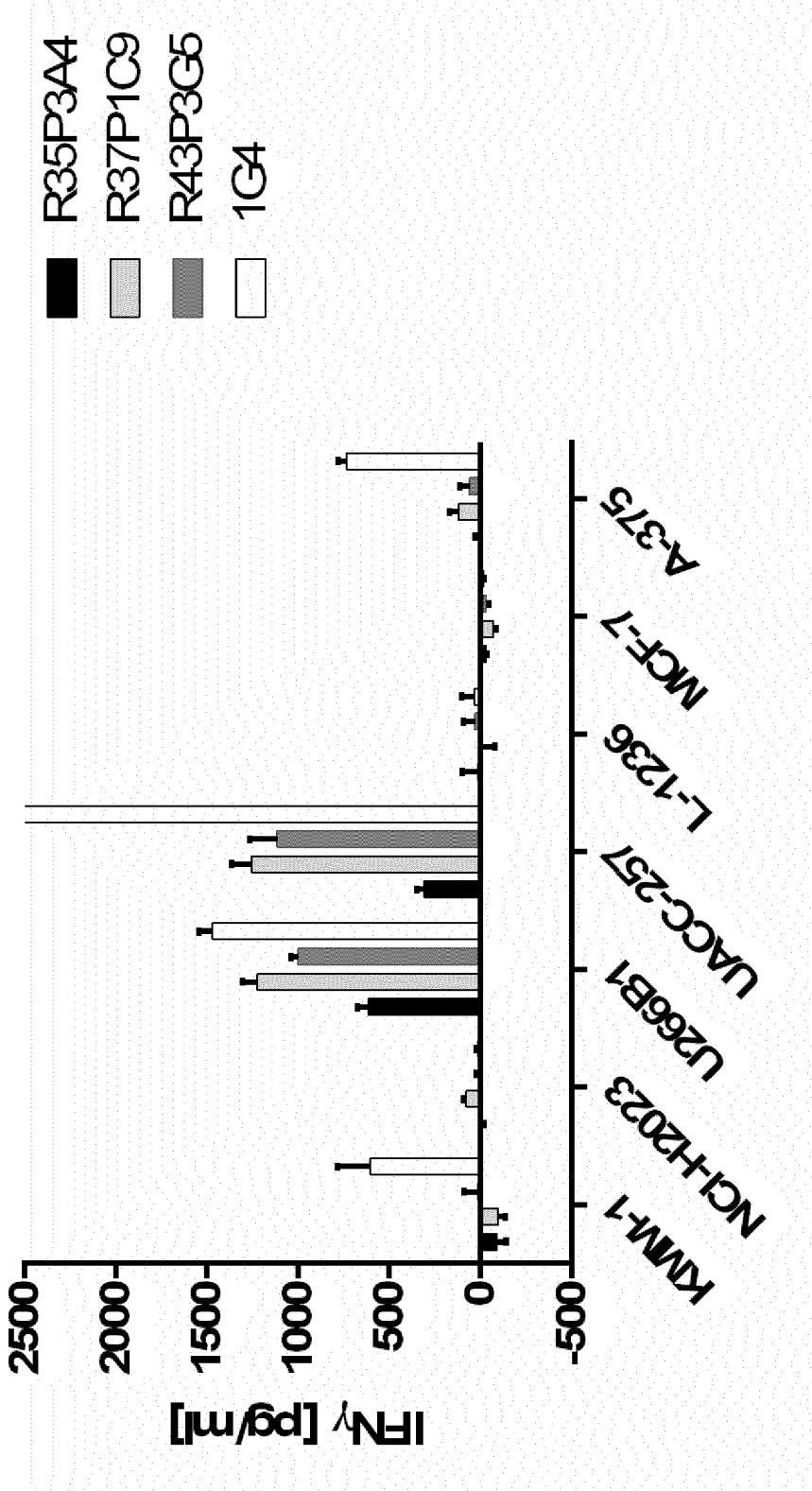
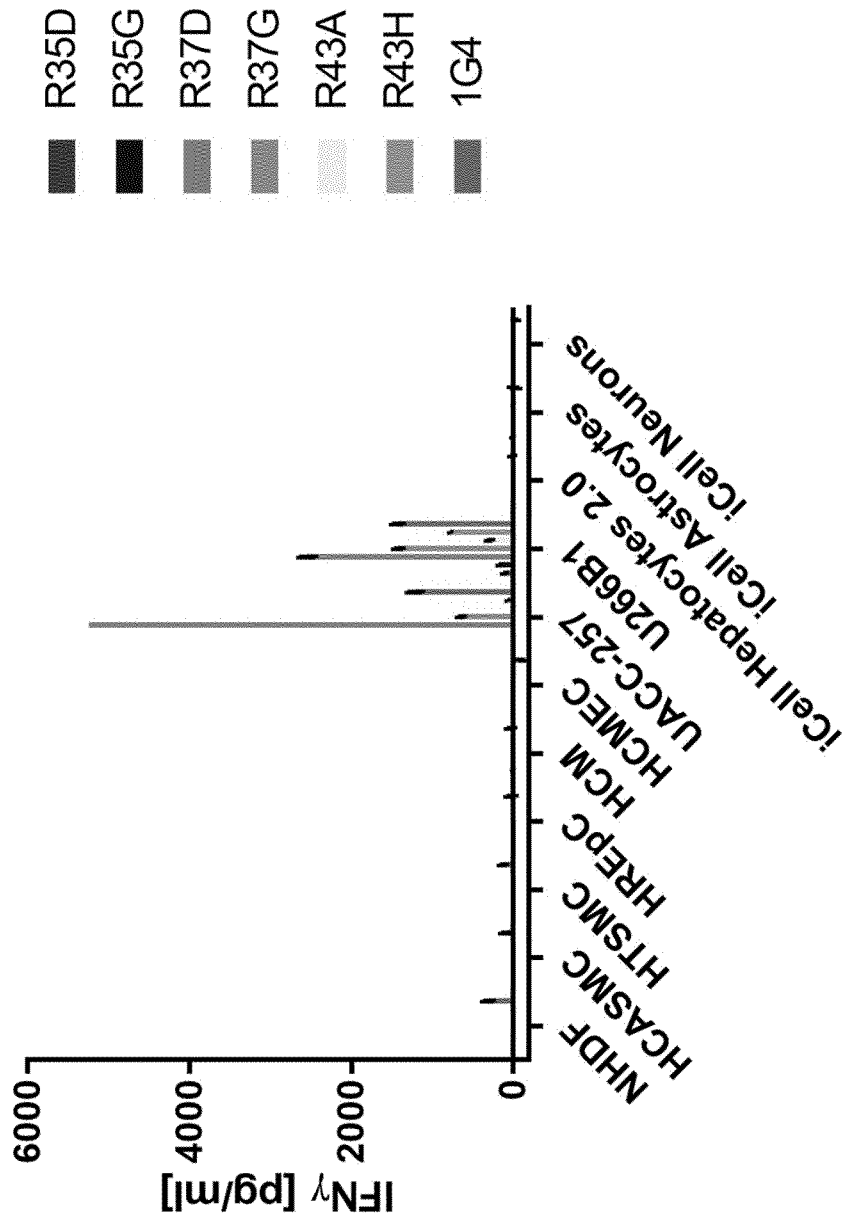


Figure 32:



TCRA-0058



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Figure 34:

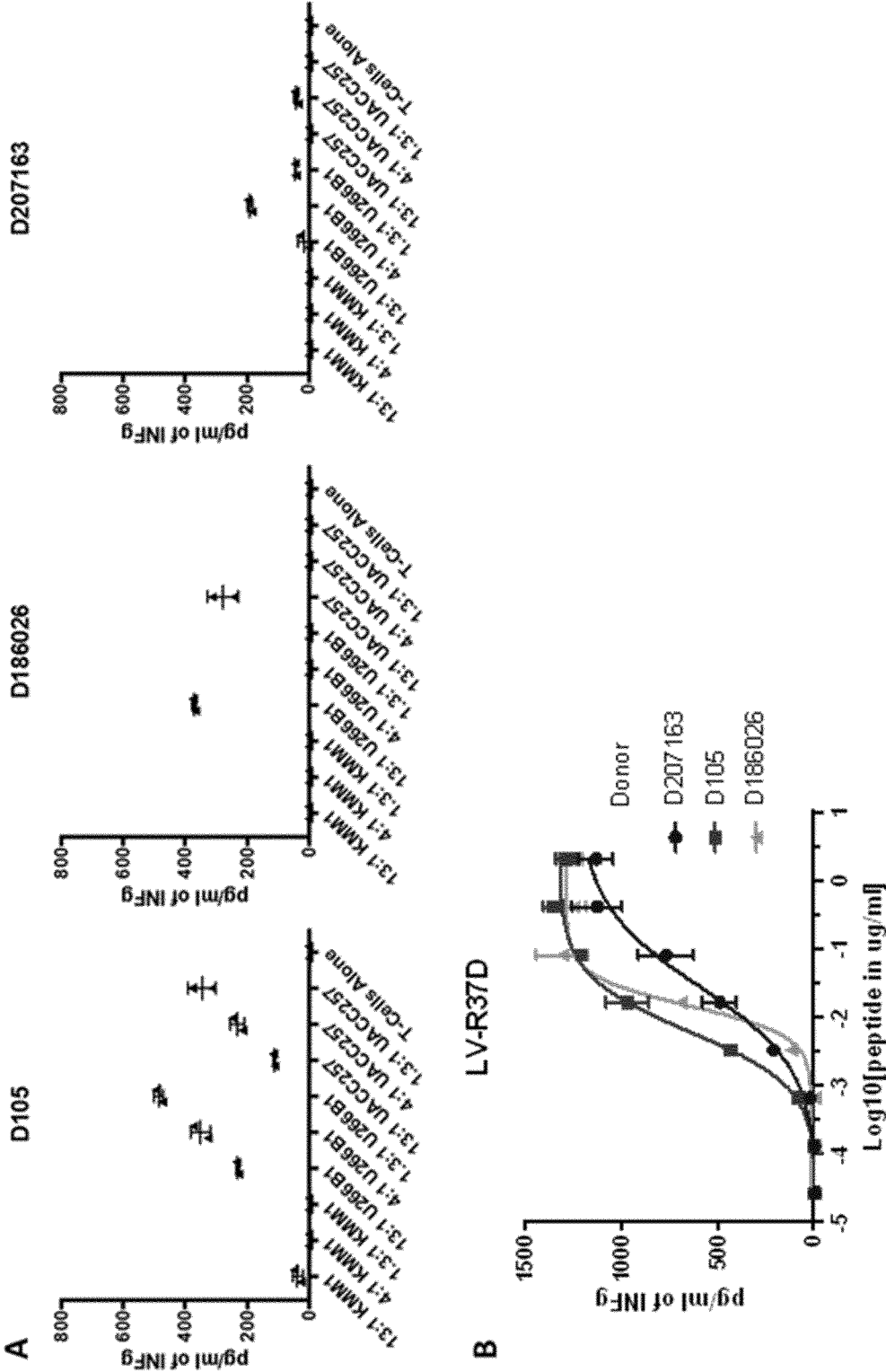
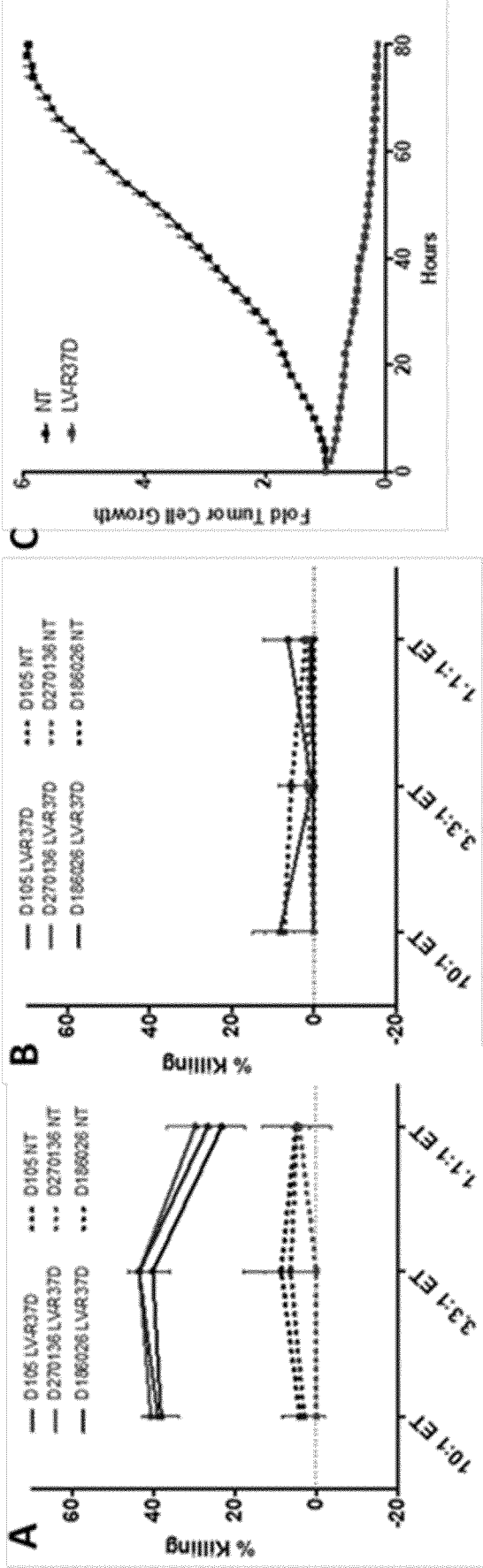
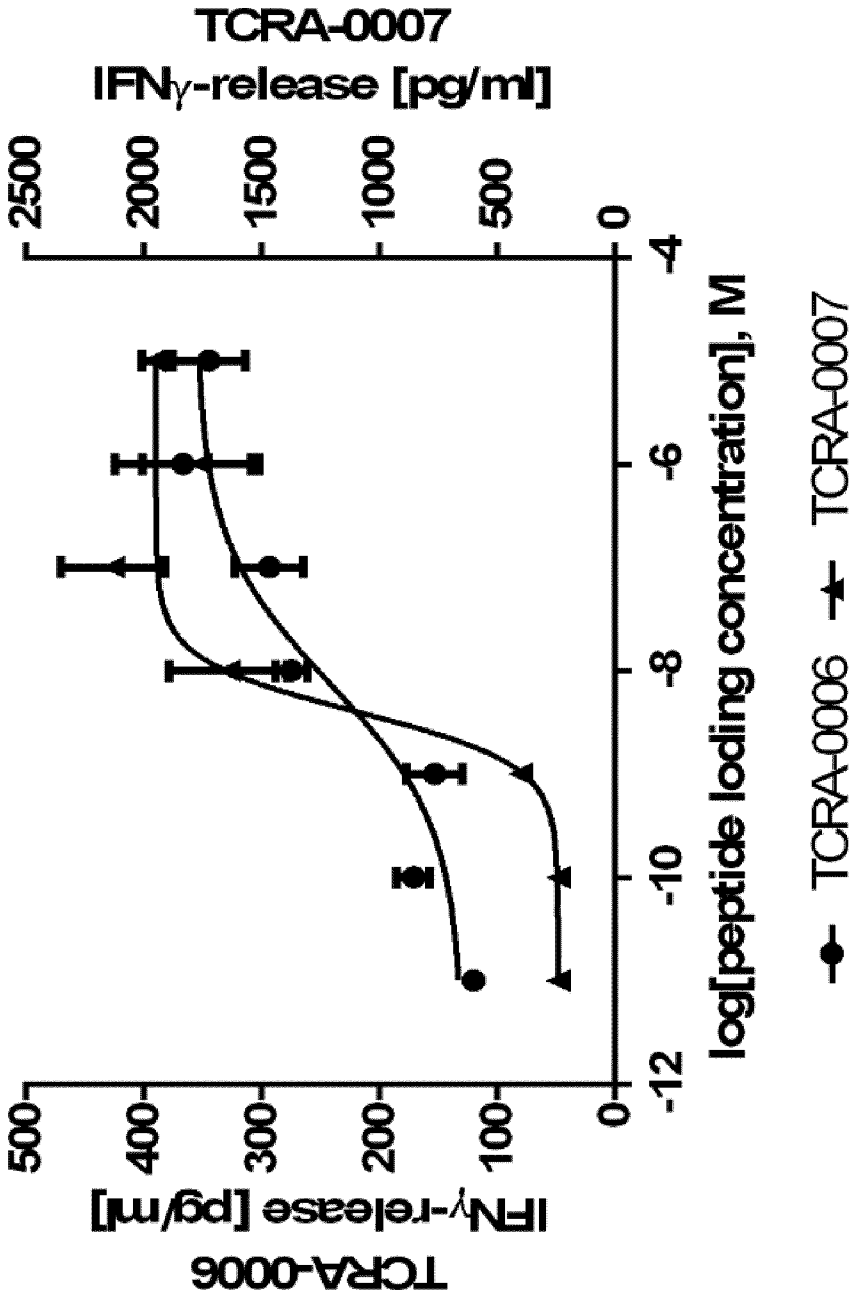


Figure 35:



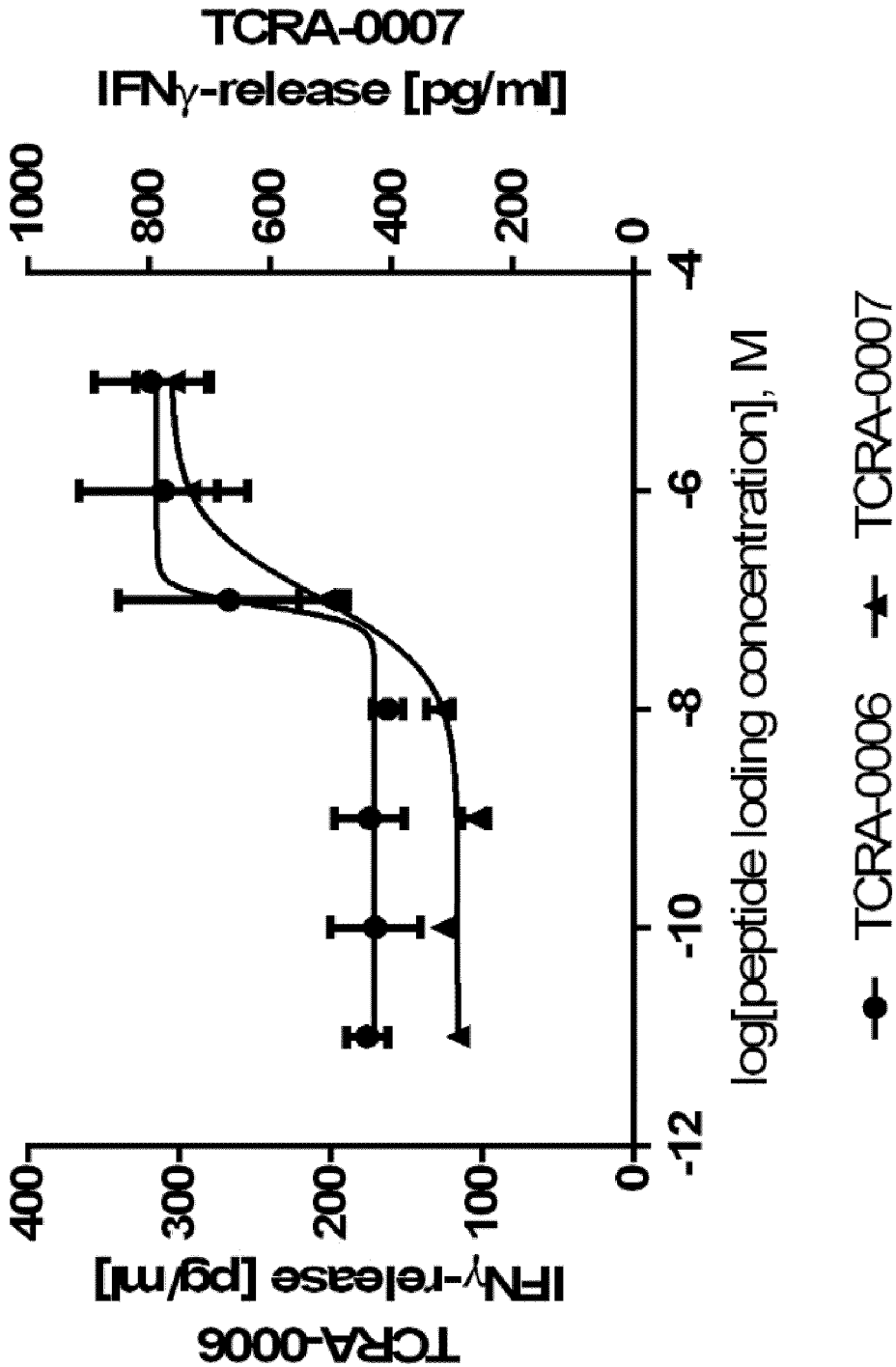
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Figure 36:



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Figure 37:



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Figure 38:

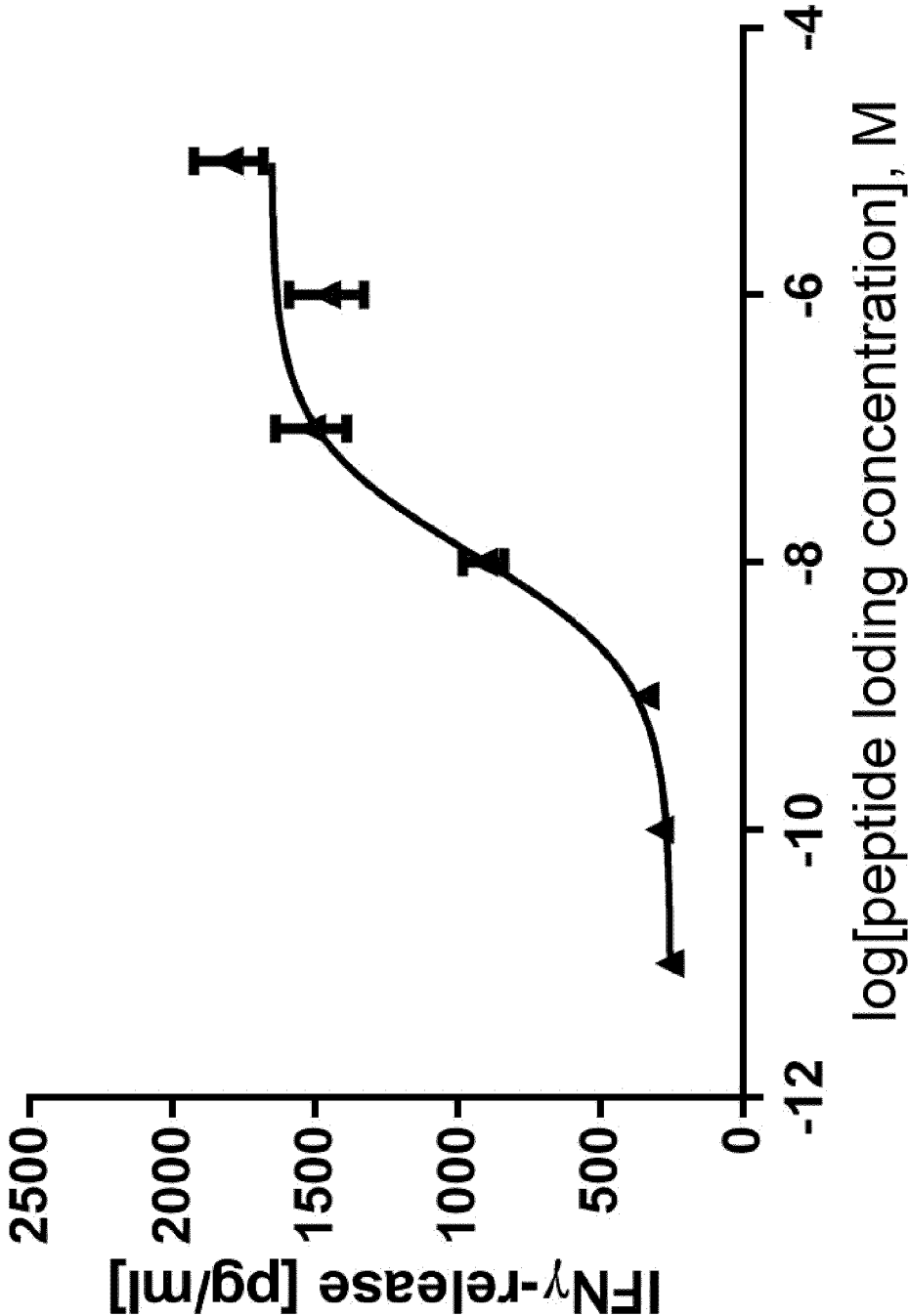
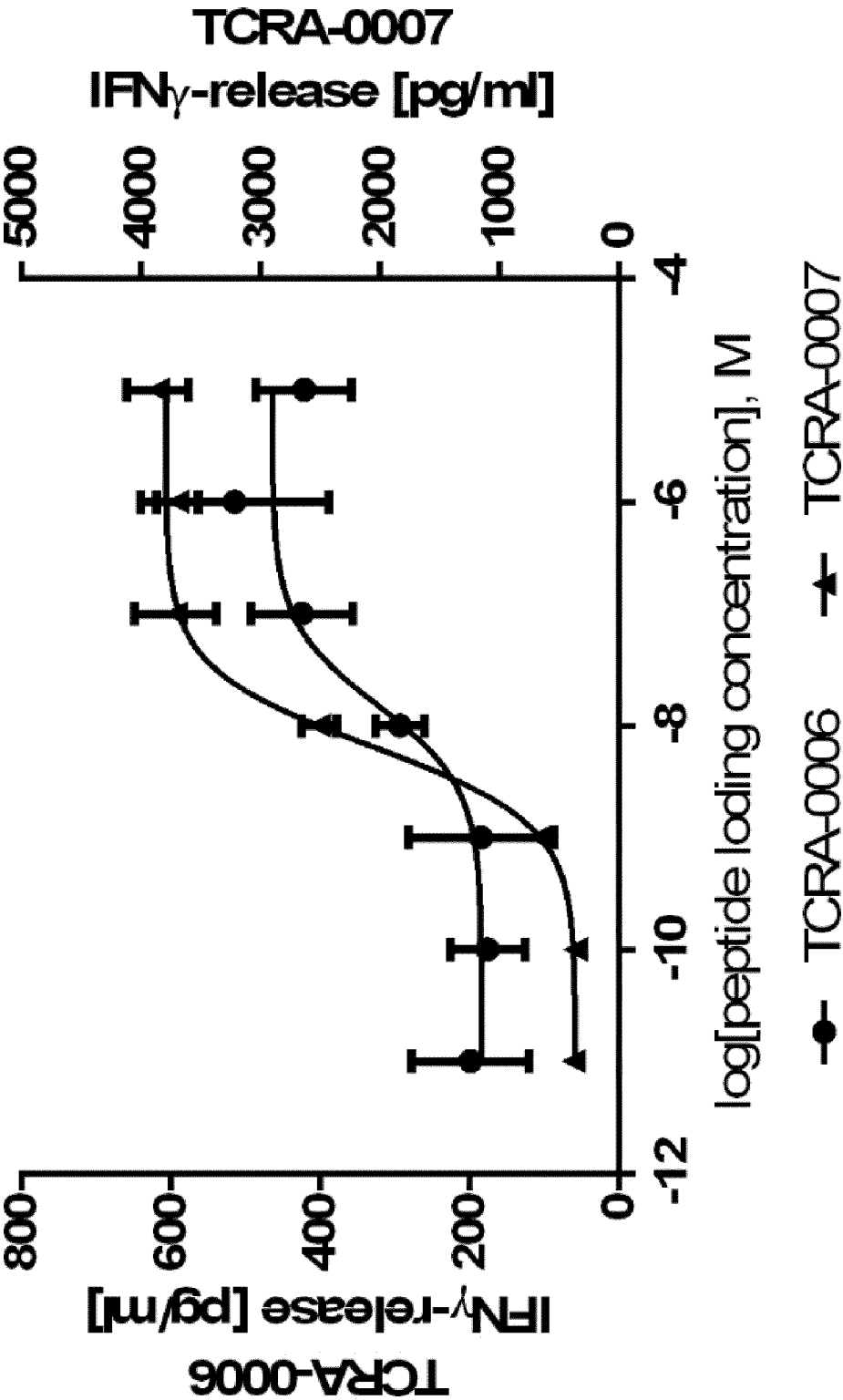
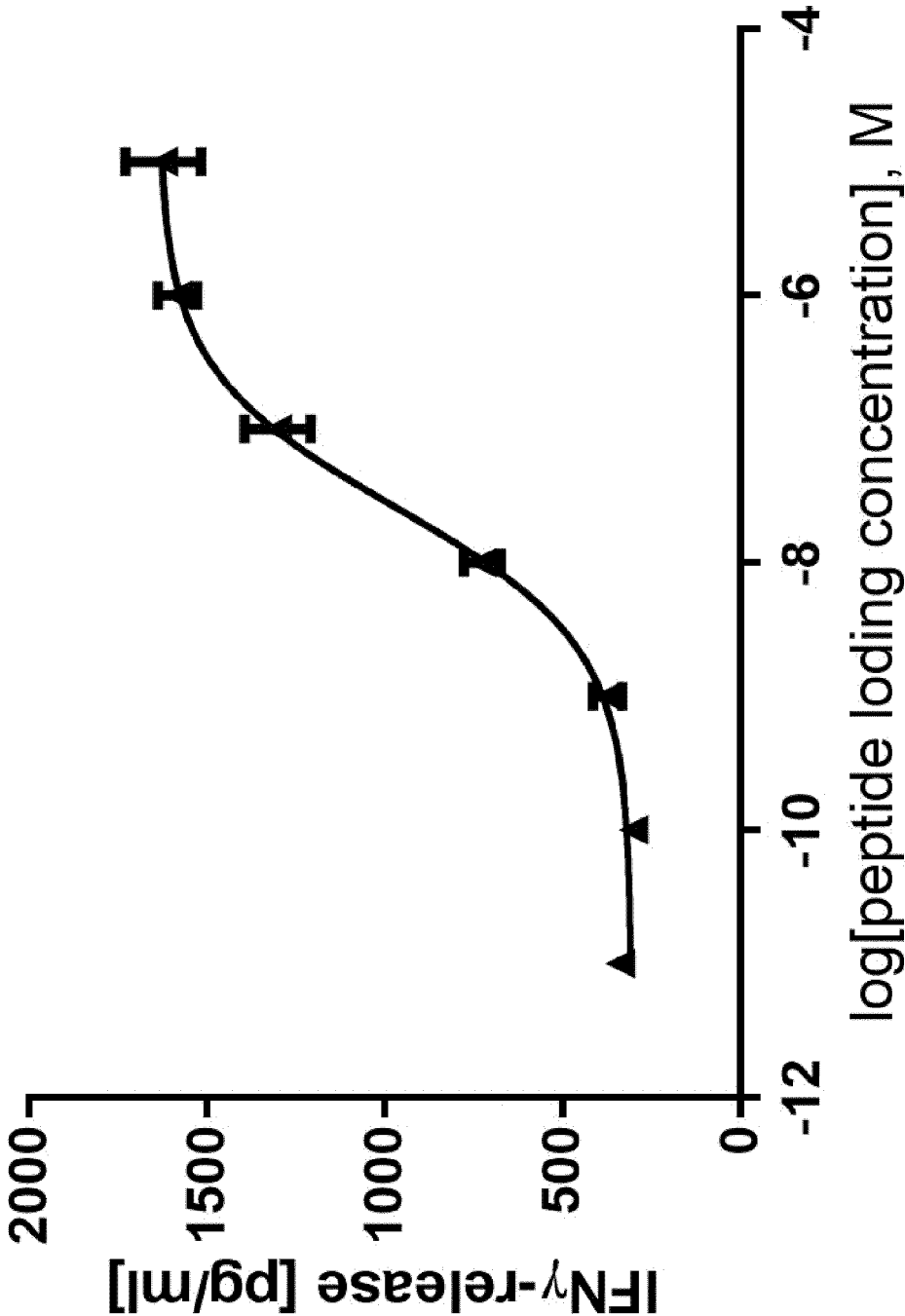


Figure 39:



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Figure 40:



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Figure 41:

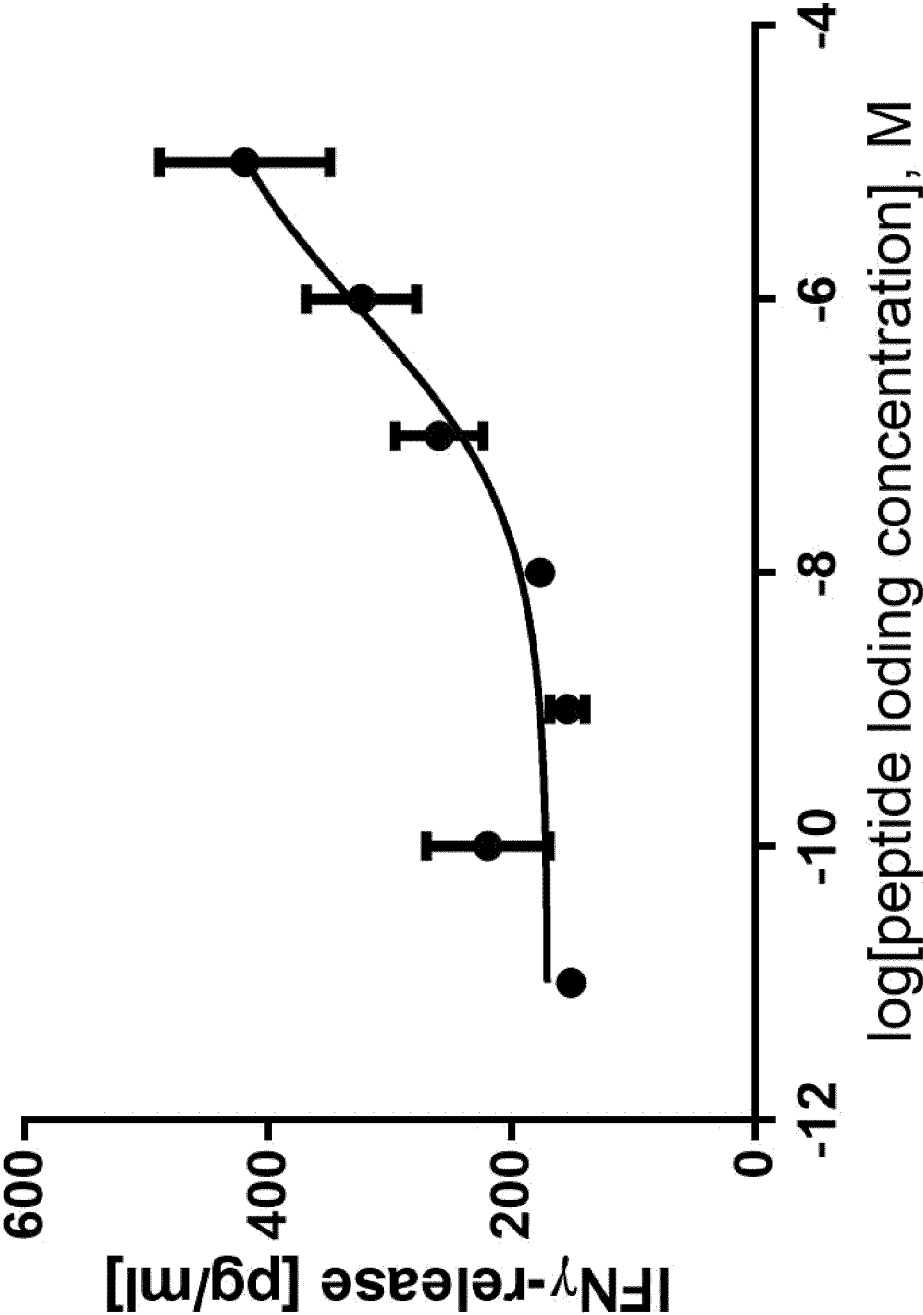
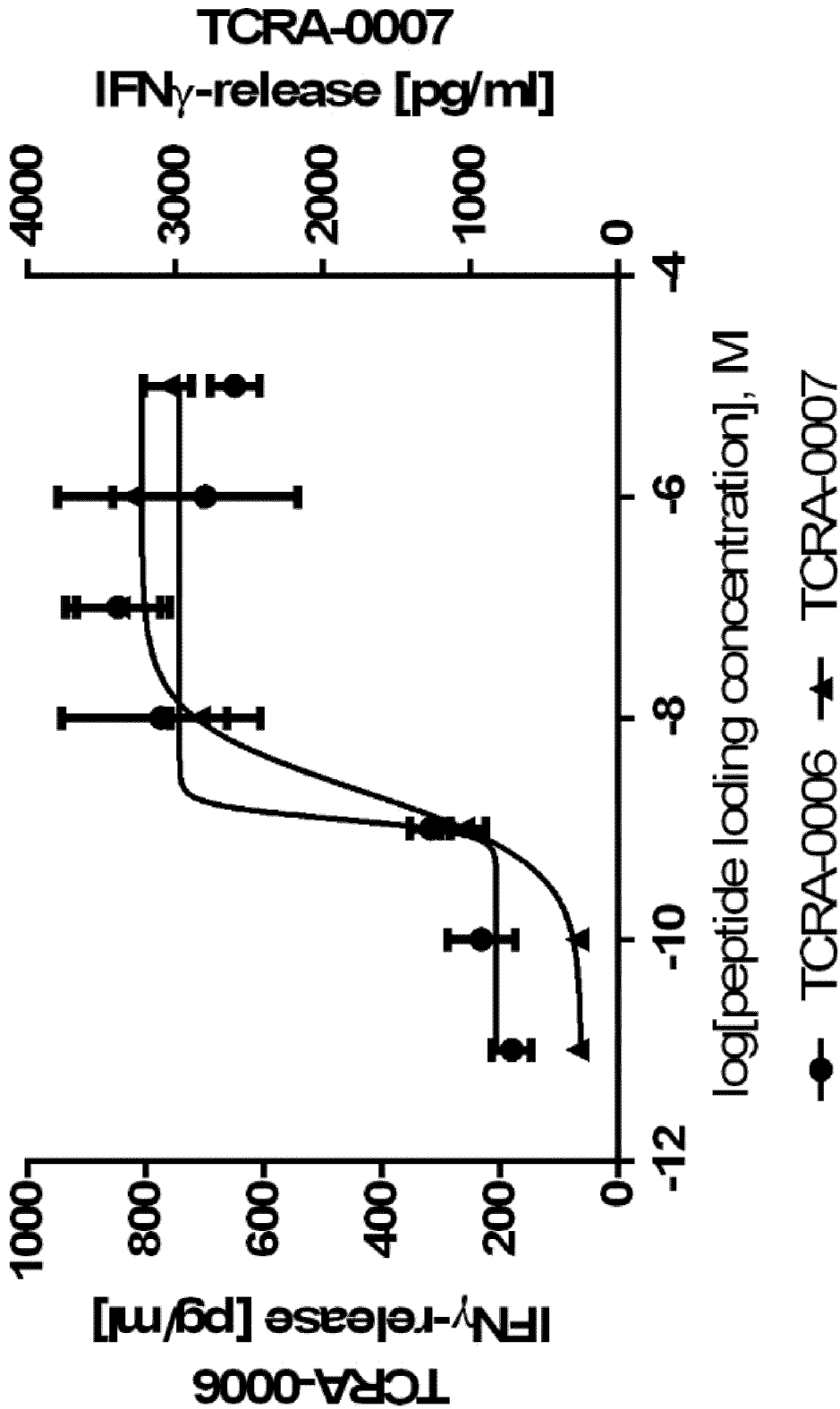


Figure 42:



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Figure 43:

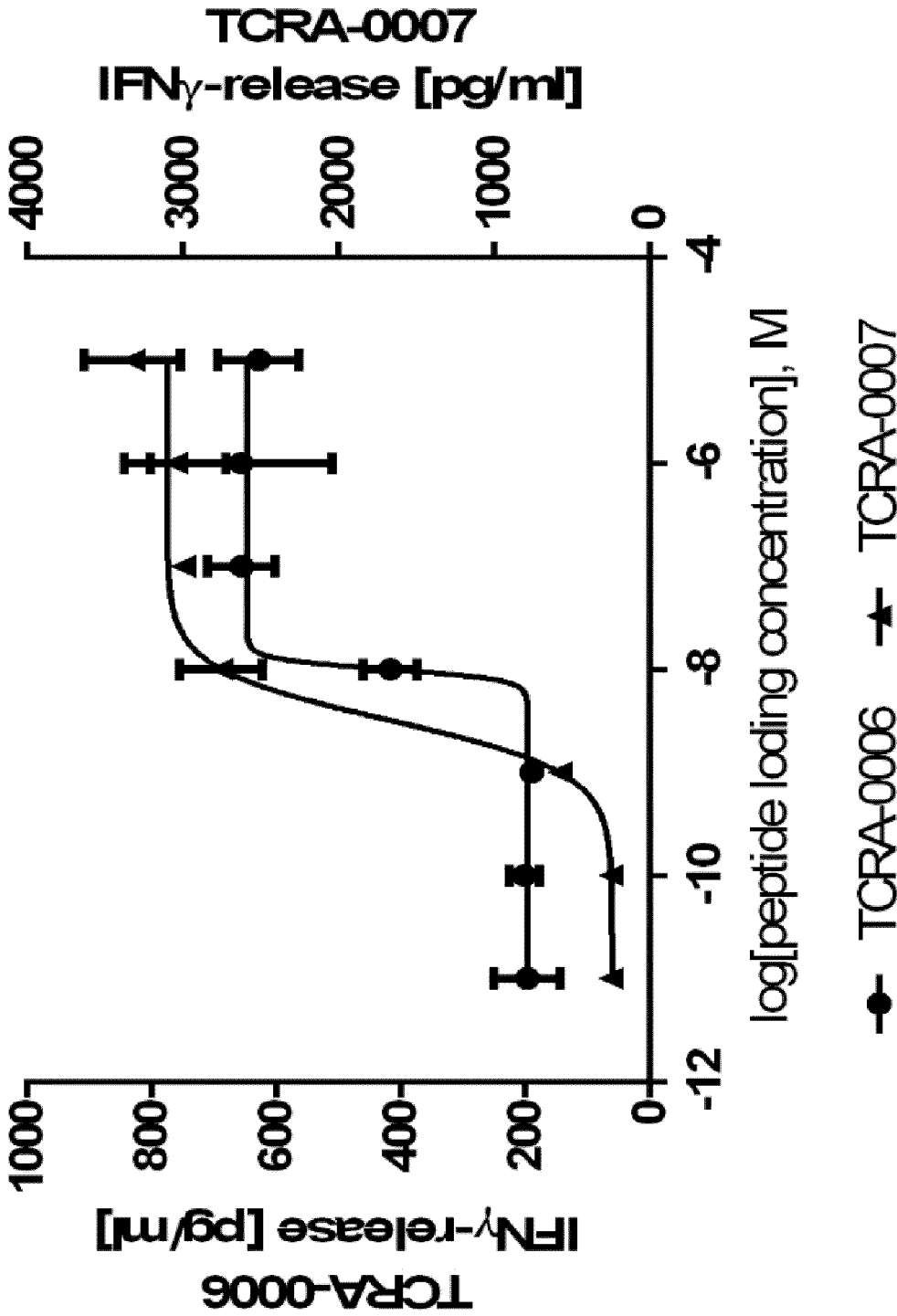
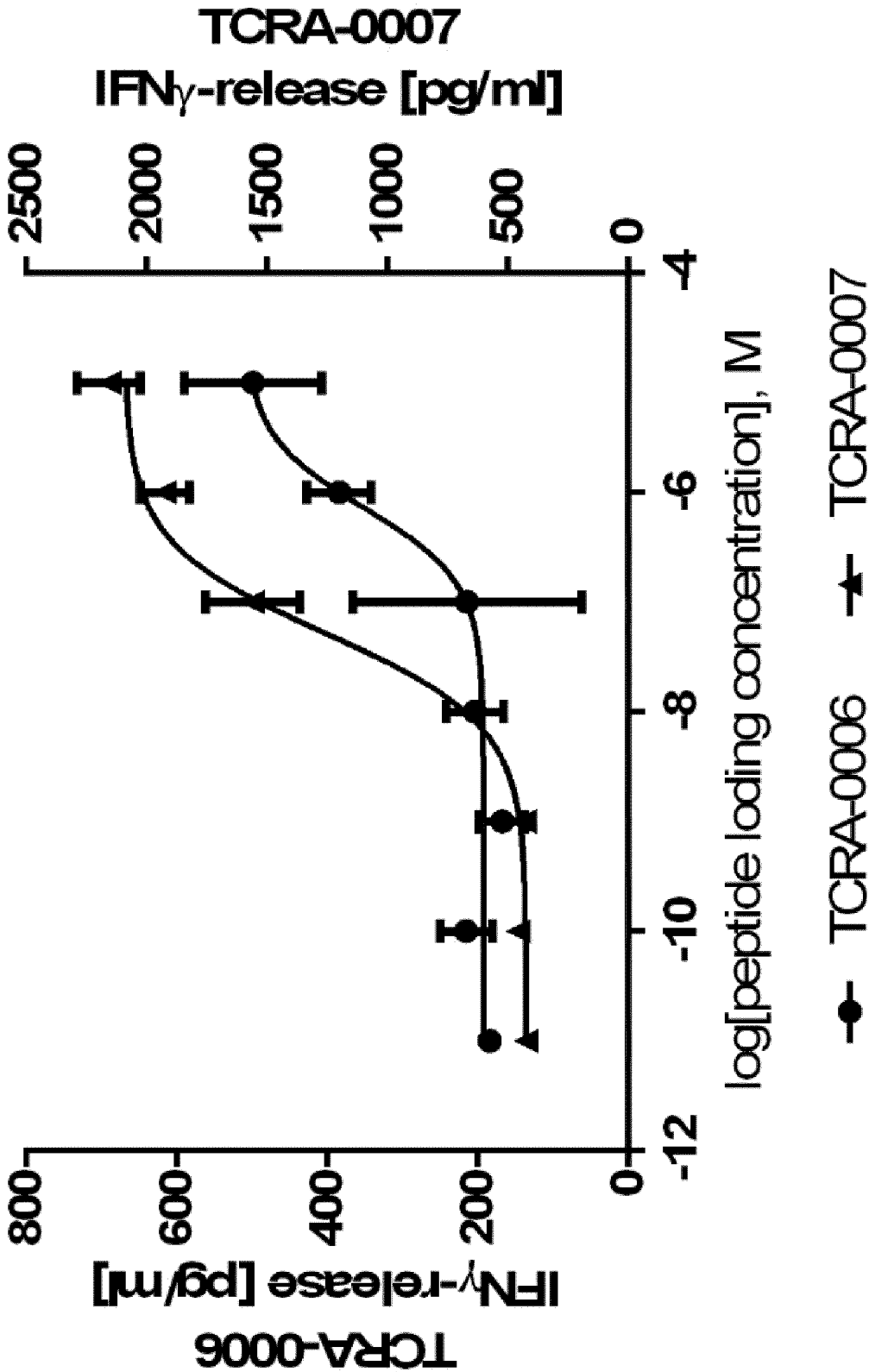


Figure 44:



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1-6	Original free text language code	
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2	General Information	
2-1	Current application: IP Office	
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	1310691
2-5	Earliest priority application: IP Office	DE
2-6	Earliest priority application: Application number	DE 102016123847.3
2-7	Earliest priority application: Filing date	2016-12-08
2-8en	Applicant name	Immatrics Biotechnologies GmbH
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
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	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-11-5	Residues	EDLNKVFPE VAVFEPSEAE ISHTQKATLV CLATGFFPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCVQF YGLSENDEWT QDRAKPTQI 120 VSAEAWGRAD CGFTSVSYQQ GVLSATILYE ILLGKATLYA VLVSALVLMMA MVKRKDF 177	
3-12	Sequences		
3-12-1	Sequence Number [ID]	12	
3-12-2	Molecule Type	AA	
3-12-3	Length	310	
3-12-4	Features	source 1..310	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-12-5	Residues	MGSWTLCCVS LCILVAKHTD AGVIQSPRHE VTEMGQEVTL RCKPISGHDY LFWYRQTMMR 60 GLELLIYFNN NVPIDDSGMP EDRFSAKMPN ASFSTLKIQP SEPRDSAVYF CASSYFGWNE 120 KLFFGSGTQL SVLEDLNKVF PPEVAVFEPS EAEISHTQKA TLVCLATGFF PDHVELSWWV 180 NGKEVHSGVS TDPQPLKEQP ALNDSRYCLS SRLRVSATFW QNPRNHFCRQ VQFYGLSEND 240 EWTQDRAKPV TQIVSAEAWG RADCGFTSVS YQQGVLSATI LYEILLGKAT LYAVLVSALV 300 LMAMVKRKDF 310	
3-13	Sequences		
3-13-1	Sequence Number [ID]	13	
3-13-2	Molecule Type	AA	
3-13-3	Length	6	
3-13-4	Features	source 1..6	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-13-5	Residues	NSAFQY	6
3-14	Sequences		
3-14-1	Sequence Number [ID]	14	
3-14-2	Molecule Type		
3-14-3	Length		
3-14-4	Features		

3-14-5	Location/Qualifiers NonEnglishQualifier Value Residues	000	3
3-15	Sequences		
3-15-1	Sequence Number [ID]	15	
3-15-2	Molecule Type	AA	
3-15-3	Length	15	
3-15-4	Features Location/Qualifiers	source 1..15 mol_type=protein organism=Homo sapiens	
3-15-5	NonEnglishQualifier Value Residues	CAMSDVSGGY NKLIF	15
3-16	Sequences		
3-16-1	Sequence Number [ID]	16	
3-16-2	Molecule Type	AA	
3-16-3	Length	135	
3-16-4	Features Location/Qualifiers	source 1..135 mol_type=protein organism=Homo sapiens	
3-16-5	NonEnglishQualifier Value Residues	MMKSLRVLLV ILWLQLSWW SQQKEVEQDP GPLSVPEGAI VSLNCTYSNS AFQYFMWYRQ 60 YSRKGPELLM YTYSSGNKD GRFTAQVDKS SKYISLFIRD SQPSDSATYL CAMSDVSGGY 120 NKLIFGAGTR LAVHP 135	
3-17	Sequences		
3-17-1	Sequence Number [ID]	17	
3-17-2	Molecule Type	AA	
3-17-3	Length	141	
3-17-4	Features Location/Qualifiers	source 1..141 mol_type=protein organism=Homo sapiens	
3-17-5	NonEnglishQualifier Value Residues	YIQNPDAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLVIGF 120 RILLKLVAGF NLLMTLRLWS S 141	
3-18	Sequences		
3-18-1	Sequence Number [ID]	18	
3-18-2	Molecule Type	AA	
3-18-3	Length	276	
3-18-4	Features Location/Qualifiers	source 1..276 mol_type=protein organism=Homo sapiens	
3-18-5	NonEnglishQualifier Value Residues	MMKSLRVLLV ILWLQLSWW SQQKEVEQDP GPLSVPEGAI VSLNCTYSNS AFQYFMWYRQ 60 YSRKGPELLM YTYSSGNKD GRFTAQVDKS SKYISLFIRD SQPSDSATYL CAMSDVSGGY 120 NKLIFGAGTR LAVHPYIQNP DPAVYQLRDS KSSDKSVCLF TDFDSQTNVS QSKSDVYIT 180 DKTVLDMRSM DFKSNSAVAW SNKSDFACAN AFNNSIIPED TFFPSPESSC DVKLVEKSFE 240 TDTNLFQNL SVIGFRILL KVAGFNLLMT LRLWSS 276	
3-19	Sequences		
3-19-1	Sequence Number [ID]	19	
3-19-2	Molecule Type	AA	
3-19-3	Length	5	
3-19-4	Features Location/Qualifiers	source 1..5 mol_type=protein organism=Homo sapiens	
3-19-5	NonEnglishQualifier Value Residues	MNHEY	5
3-20	Sequences		
3-20-1	Sequence Number [ID]	20	
3-20-2	Molecule Type	AA	
3-20-3	Length	6	
3-20-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens	
3-20-5	NonEnglishQualifier Value Residues	SMNVEV	6
3-21	Sequences		
3-21-1	Sequence Number [ID]	21	
3-21-2	Molecule Type	AA	
3-21-3	Length	14	

3-21-4	Features Location/Qualifiers	source 1..14 mol_type=protein organism=Homo sapiens	
3-21-5	NonEnglishQualifier Value Residues	CASTTPDGTG EQFF	14
3-22	Sequences		
3-22-1	Sequence Number [ID]	22	
3-22-2	Molecule Type	AA	
3-22-3	Length	132	
3-22-4	Features Location/Qualifiers	source 1..132 mol_type=protein organism=Homo sapiens	
3-22-5	NonEnglishQualifier Value Residues	MGPQLLGYYV LCLLGAGPLE AQVTQNPRYL ITVTGKKLTV TCSQNMNHEY MSWYRQDPGL 60 GLRQIYYSMN VEVTDKGDVP EGYKVSRRKEK RNFPILILESP SPNQTSLYFC ASTTPDGTDE 120 QFFGPGTRLT VL 132	
3-23	Sequences		
3-23-1	Sequence Number [ID]	23	
3-23-2	Molecule Type	AA	
3-23-3	Length	179	
3-23-4	Features Location/Qualifiers	source 1..179 mol_type=protein organism=Homo sapiens	
3-23-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTDI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMMA MVKRKDSRG 179	
3-24	Sequences		
3-24-1	Sequence Number [ID]	24	
3-24-2	Molecule Type	AA	
3-24-3	Length	311	
3-24-4	Features Location/Qualifiers	source 1..311 mol_type=protein organism=Homo sapiens	
3-24-5	NonEnglishQualifier Value Residues	MGPQLLGYYV LCLLGAGPLE AQVTQNPRYL ITVTGKKLTV TCSQNMNHEY MSWYRQDPGL 60 GLRQIYYSMN VEVTDKGDVP EGYKVSRRKEK RNFPILILESP SPNQTSLYFC ASTTPDGTDE 120 QFFGPGTRLT VLEDLKNVFP PEVAVFEPSE AEISHTQKAT LVCLATGFYP DHVELSWWVN 180 GKEVHSGVST DPQPLKEQPA LNDSTRYCLSS RLRVSATFWQ NPRNHFRQV QFYGLSENDE 240 WTQDRAKPVTD QIVSAEAWGR ADCGFTSESY QQGVLSATIL YEILLGKATL YAVLVSALVL 300 MAMVKRKDSR G 311	
3-25	Sequences		
3-25-1	Sequence Number [ID]	25	
3-25-2	Molecule Type	AA	
3-25-3	Length	6	
3-25-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens	
3-25-5	NonEnglishQualifier Value Residues	VSGNPY	6
3-26	Sequences		
3-26-1	Sequence Number [ID]	26	
3-26-2	Molecule Type	AA	
3-26-3	Length	4	
3-26-4	Features Location/Qualifiers	source 1..4 mol_type=protein organism=Homo sapiens	
3-26-5	NonEnglishQualifier Value Residues	YITG	4
3-27	Sequences		
3-27-1	Sequence Number [ID]	27	
3-27-2	Molecule Type	AA	
3-27-3	Length	14	
3-27-4	Features Location/Qualifiers	source 1..14 mol_type=protein organism=Homo sapiens	
3-27-5	NonEnglishQualifier Value Residues	CAVRDMNRDD KIIF	14
3-28	Sequences		

3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	AA
3-28-3	Length	133
3-28-4	Features	source 1..133
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-28-5	NonEnglishQualifier Value Residues	MASAPISMLA MLFTLSGLRA QSVAQPEDQV NVAEGNPLTV KCTYSVSGNP YLFWYVQYPN 60 RGLQFLLKYI TGDNLVKGSY GFEEAFNKSQ TSFHLKKPSA LVSDSALYFC AVRDMNRDDK 120 IIFGKGTRLH ILP 133
3-29	Sequences	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	AA
3-29-3	Length	141
3-29-4	Features	source 1..141
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-29-5	NonEnglishQualifier Value Residues	NIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RILLKLVAGF NLLMTLRLWS S 141
3-30	Sequences	
3-30-1	Sequence Number [ID]	30
3-30-2	Molecule Type	AA
3-30-3	Length	274
3-30-4	Features	source 1..274
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-30-5	NonEnglishQualifier Value Residues	MASAPISMLA MLFTLSGLRA QSVAQPEDQV NVAEGNPLTV KCTYSVSGNP YLFWYVQYPN 60 RGLQFLLKYI TGDNLVKGSY GFEEAFNKSQ TSFHLKKPSA LVSDSALYFC AVRDMNRDDK 120 IIFGKGTRLH ILPNIQNPD AVYQLRDSKS SDKSVCLFTD FDSQTNVSQS KSDSVYITDK 180 TVLDMRSMDF KNSAVAWSN KSDFACANAF NNSIIPEDTF FPSPESSCDV KLVEKSFETD 240 TNLNFQNLSV IGFRILLKLV AGFNLLMTLR LWSS 274
3-31	Sequences	
3-31-1	Sequence Number [ID]	31
3-31-2	Molecule Type	AA
3-31-3	Length	5
3-31-4	Features	source 1..5
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-31-5	NonEnglishQualifier Value Residues	LNHDA 5
3-32	Sequences	
3-32-1	Sequence Number [ID]	32
3-32-2	Molecule Type	AA
3-32-3	Length	6
3-32-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-32-5	NonEnglishQualifier Value Residues	SQIVND 6
3-33	Sequences	
3-33-1	Sequence Number [ID]	33
3-33-2	Molecule Type	AA
3-33-3	Length	13
3-33-4	Features	source 1..13
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-33-5	NonEnglishQualifier Value Residues	CASSRAEGGE QYF 13
3-34	Sequences	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	AA
3-34-3	Length	131
3-34-4	Features	source 1..131
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	

3-34-5	Residues	MSNQVLCCVV LCFLGANTVD GGITQSPKYL FRKEGQNVTL SCEQNLNHDA MYWYRQDPGQ 60 GLRLIYYSQI VNDFQKGDIA EGYSVSREKK ESFPLTVTSA QKNPTAFYLC ASSRAEGGEQ 120 YFGPGTRLTV T 131
3-35	Sequences	
3-35-1	Sequence Number [ID]	35
3-35-2	Molecule Type	AA
3-35-3	Length	179
3-35-4	Features	source 1..179
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-35-5	NonEnglishQualifier Value	
	Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLM MA MVKRKDSRG 179
3-36	Sequences	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	AA
3-36-3	Length	310
3-36-4	Features	source 1..310
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-36-5	NonEnglishQualifier Value	
	Residues	MSNQVLCCVV LCFLGANTVD GGITQSPKYL FRKEGQNVTL SCEQNLNHDA MYWYRQDPGQ 60 GLRLIYYSQI VNDFQKGDIA EGYSVSREKK ESFPLTVTSA QKNPTAFYLC ASSRAEGGEQ 120 YFGPGTRLTV TEDLKNVFPP EVAVFEPSEA EISHTQKATL VCLATGFYPD HVELSWWVNG 180 KEVHSGVSTD PQPLKEQPAL NDSRYCLSSR LRVSATFWQN PRNHFRCQVQ FYGLSENDEW 240 TQDRAKPVTQ IVSAEAWGRA DCGFTSESYQ QGVLSATILY EILLGKATLY AVLVSALVLM 300 AMVKRKDSRG 310
3-37	Sequences	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	AA
3-37-3	Length	6
3-37-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-37-5	NonEnglishQualifier Value	
	Residues	DSASNY 6
3-38	Sequences	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	
3-38-3	Length	
3-38-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-38-5	Residues	000 3
3-39	Sequences	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	AA
3-39-3	Length	14
3-39-4	Features	source 1..14
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-39-5	Residues	CAASPTGGYN KLIF 14
3-40	Sequences	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	AA
3-40-3	Length	132
3-40-4	Features	source 1..132
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-40-5	Residues	MTSIRAVFIF LWLQLDLVNG ENVEQHPSTL SVQEGDSAVI KCTYSDSASN YFPWYKQELG 60 KRPQLIIDIR SNVGEKKDQR IAVTLNKTAK HFSLHITETQ PEDSAVYFCA ASPTGGYNKL 120 IFGAGTRLAV HP 132
3-41	Sequences	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	AA
3-41-3	Length	141

3-41-4	Features Location/Qualifiers	source 1..141 mol_type=protein organism=Homo sapiens
3-41-5	NonEnglishQualifier Value Residues	YIQNPDPNAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RILLKLVAGF NLLMTLRLWS S 141
3-42	Sequences	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	AA
3-42-3	Length	273
3-42-4	Features Location/Qualifiers	source 1..273 mol_type=protein organism=Homo sapiens
3-42-5	NonEnglishQualifier Value Residues	MTSIRAVFIF LWLQLDLVNG ENVEQHPSTL SVQEGDSAVI KCTYSDSASN YFPWYKQELG 60 KRPQLIIDIR SNVGEKKDQR IAVTLNKTAK HFSLHITETQ PEDSAVYFCA ASPTGGYNKL 120 IFGAGTRLAV HPYIQNPDA VYQLRDSKSS DKSVCCLFTDF DSQTNVSQSK DSDVYITDKT 180 VLDMRSMDFK SNSAVAWSNK SDFACANAFN NSIIPEDTFF PSESSCDVK LVEKSFETDT 240 NLNFQNLSEVI GFRILLKVA GFNLLMTLRL WSS 273
3-43	Sequences	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	AA
3-43-3	Length	5
3-43-4	Features Location/Qualifiers	source 1..5 mol_type=protein organism=Homo sapiens
3-43-5	NonEnglishQualifier Value Residues	MNHEY 5
3-44	Sequences	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	AA
3-44-3	Length	6
3-44-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens
3-44-5	NonEnglishQualifier Value Residues	SVGAGI 6
3-45	Sequences	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	AA
3-45-3	Length	14
3-45-4	Features Location/Qualifiers	source 1..14 mol_type=protein organism=Homo sapiens
3-45-5	NonEnglishQualifier Value Residues	CASSLGASQ EQYF 14
3-46	Sequences	
3-46-1	Sequence Number [ID]	46
3-46-2	Molecule Type	AA
3-46-3	Length	132
3-46-4	Features Location/Qualifiers	source 1..132 mol_type=protein organism=Homo sapiens
3-46-5	NonEnglishQualifier Value Residues	MSIGLLCCAA LSLLWAGPVN AGVTQTPKFQ VLKTGQSMTL QCAQDMNHEY MSWYRQDPGM 60 GLRLIHYSVG AGITDQGEVP NGYNVSRSTT EDFPLRLLSA APSQTSVYFC ASSLGASQE 120 QYFGPGTRLT VT 132
3-47	Sequences	
3-47-1	Sequence Number [ID]	47
3-47-2	Molecule Type	AA
3-47-3	Length	179
3-47-4	Features Location/Qualifiers	source 1..179 mol_type=protein organism=Homo sapiens
3-47-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWVWNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTDI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMMA MVKRKDSRG 179

3-48	Sequences	
3-48-1	Sequence Number [ID]	48
3-48-2	Molecule Type	AA
3-48-3	Length	311
3-48-4	Features	source 1..311
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-48-5	NonEnglishQualifier Value	
	Residues	MSIGLLCCAA LSLWAGPVN AGVTQTPKFQ VLKTGQSMTL QCAQDMNHEY MSWYRQDPGM 60 GLRLIHYSVG AGITDQGEVP NGYNVSRSTT EDFPLRLLSA APSQTSVYFC ASSLGGSQE 120 QYFGPGTRLT VTEDLKNVFP PEVAVFEPSE AEISHTQKAT LVCLATGFYP DHVELSWWVN 180 GKEVHSGVST DPQPLKEQPA LNSRYCLSS RLRVSATFWQ NPRNHFRQV QFYGLSENDE 240 WTQDRAKPVT QIVSAEAWGR ADCGFTSESY QQGVLSATIL YEILLGKATL YAVLVSALVL 300 MAMVKRKDSR G 311
3-49	Sequences	
3-49-1	Sequence Number [ID]	49
3-49-2	Molecule Type	AA
3-49-3	Length	7
3-49-4	Features	source 1..7
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-49-5	Residues	TISGTDY 7
3-50	Sequences	
3-50-1	Sequence Number [ID]	50
3-50-2	Molecule Type	
3-50-3	Length	
3-50-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-50-5	Residues	000 3
3-51	Sequences	
3-51-1	Sequence Number [ID]	51
3-51-2	Molecule Type	AA
3-51-3	Length	11
3-51-4	Features	source 1..11
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-51-5	Residues	CILFNFNKFY F 11
3-52	Sequences	
3-52-1	Sequence Number [ID]	52
3-52-2	Molecule Type	AA
3-52-3	Length	125
3-52-4	Features	source 1..125
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-52-5	Residues	MKLVTSTITVL LSLGIMGDAK TTQPNMESN EEEPVHLPCN HSTISGTDYI HWYRQLPSQG 60 PEYVIHGLTS NVNNRMASLA IAEDRKSTL ILHRATLRDA AVYYCILFNF NKFYFGSGTK 120 LNVKP 125
3-53	Sequences	
3-53-1	Sequence Number [ID]	53
3-53-2	Molecule Type	AA
3-53-3	Length	141
3-53-4	Features	source 1..141
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-53-5	Residues	NIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLVIGF 120 RIILLKVAGF NLLMTLRLWS S 141
3-54	Sequences	
3-54-1	Sequence Number [ID]	54
3-54-2	Molecule Type	AA
3-54-3	Length	266
3-54-4	Features	source 1..266
	Location/Qualifiers	mol_type=protein organism=Homo sapiens

3-54-5	NonEnglishQualifier Value Residues	MKLVTSITVL LSLGIMGDAK TTQPNMESN EEEPVHLPCN HSTISGTDYI HWYRQLPSQG 60 PEYVIHGLTS NVNNRMASLA IAEDRKSSTL ILHRATLRDA AVYYCILFNF NKFYFGSGTK 120 LNVKPNIQNP DPAVYQLRDS KSSDKSVCLF TDFDSQTNVS QSKDSDVYIT DKTVLDMRSM 180 DFKSNSAVAW SNKSDFACAN AFNNSIIPED TFFPSPESSC DVKLVEKSFE TDTNLFQNL 240 SVIGFRILLL KVAGFNLLMT LRLWSS 266
3-55 3-55-1 3-55-2 3-55-3 3-55-4 3-55-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	55 AA 5 source 1..5 mol_type=protein organism=Homo sapiens LNHNV 5
3-56 3-56-1 3-56-2 3-56-3 3-56-4 3-56-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	56 AA 6 source 1..6 mol_type=protein organism=Homo sapiens YYDKDF 6
3-57 3-57-1 3-57-2 3-57-3 3-57-4 3-57-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	57 AA 14 source 1..14 mol_type=protein organism=Homo sapiens CATSSGETNE KLFF 14
3-58 3-58-1 3-58-2 3-58-3 3-58-4 3-58-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	58 AA 132 source 1..132 mol_type=protein organism=Homo sapiens MGPGLLHWMA LCLLGTGHGD AMVIQNPRYQ VTQFGKPVTL SCSQTLNHNH MYWYQQKSSQ 60 APKLLFHYDD KDFNNEADTP DNFQSRRPNT SFCFLDIRSP GLGDAAMYLC ATSSGETNEK 120 LFFGSGTQLS VL 132
3-59 3-59-1 3-59-2 3-59-3 3-59-4 3-59-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	59 AA 177 source 1..177 mol_type=protein organism=Homo sapiens EDLNKVPPE VAVFEPSEAE ISHTQKATLV CLATGFFPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI 120 VSAEAWGRAD CGFTSVSYQQ GVLSATILYE ILLGKATLYA VLVSALVLMA MVKRKDF 177
3-60 3-60-1 3-60-2 3-60-3 3-60-4 3-60-5	Sequences Sequence Number [ID] Molecule Type Length Features Location/Qualifiers NonEnglishQualifier Value Residues	60 AA 309 source 1..309 mol_type=protein organism=Homo sapiens MGPGLLHWMA LCLLGTGHGD AMVIQNPRYQ VTQFGKPVTL SCSQTLNHNH MYWYQQKSSQ 60 APKLLFHYDD KDFNNEADTP DNFQSRRPNT SFCFLDIRSP GLGDAAMYLC ATSSGETNEK 120 LFFGSGTQLS VLEDLNKVP PEVAVFEPSE AEISHTQKAT LVCLATGFFP DHVELSWWVN 180 GKEVHSGVST DPQPLKEQPA LNSRYCLSS RLRVSATFWQ NPRNHFRQV QFYGLSENDE 240 WTQDRAKPVT QIVSAEAWGR ADCGFTSVSY QQGVLSATIL YEILLGKATL YAVLVSALVL 300 MAMVKRKDF 309
3-61	Sequences	

3-61-1	Sequence Number [ID]	61	
3-61-2	Molecule Type	AA	
3-61-3	Length	7	
3-61-4	Features	source 1..7	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-61-5	Residues	TSESNNY	7
3-62	Sequences		
3-62-1	Sequence Number [ID]	62	
3-62-2	Molecule Type	AA	
3-62-3	Length	4	
3-62-4	Features	source 1..4	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-62-5	Residues	QEAY	4
3-63	Sequences		
3-63-1	Sequence Number [ID]	63	
3-63-2	Molecule Type	AA	
3-63-3	Length	15	
3-63-4	Features	source 1..15	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-63-5	Residues	CAFGYSGGGA DGLTF	15
3-64	Sequences		
3-64-1	Sequence Number [ID]	64	
3-64-2	Molecule Type	AA	
3-64-3	Length	136	
3-64-4	Features	source 1..136	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-64-5	Residues	MTRVSLWAV VVSTCLES GM AQTVTQSQPE MSVQEAETVT LSCTYDTSES NYLFWYKQP 60 PSRQMILVIR QEAYKQQNAT ENRFSVNFQK AAKSFSLKIS DSQLGDTAMY FCAFGYSGGG 120 ADGLTFGKGT HLIIQP 136	
3-65	Sequences		
3-65-1	Sequence Number [ID]	65	
3-65-2	Molecule Type	AA	
3-65-3	Length	141	
3-65-4	Features	source 1..141	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-65-5	Residues	YIQNPDPVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLVIGF 120 RILLKLVAGF NLLMTLRLWS S 141	
3-66	Sequences		
3-66-1	Sequence Number [ID]	66	
3-66-2	Molecule Type	AA	
3-66-3	Length	277	
3-66-4	Features	source 1..277	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-66-5	Residues	MTRVSLWAV VVSTCLES GM AQTVTQSQPE MSVQEAETVT LSCTYDTSES NYLFWYKQP 60 PSRQMILVIR QEAYKQQNAT ENRFSVNFQK AAKSFSLKIS DSQLGDTAMY FCAFGYSGGG 120 ADGLTFGKGT HLIIQPYIQN PDPVYQLRD SKSSDKSVCL FTDFDSQTNV SQSKDSVDYI 180 TDKTVLDMRS MDFKSNSAVA WSNKSDFACA NAFNNSIPE DTFFPSPESS CDVKLVEKSF 240 ETDTNLNFQN LSVIGFRILL LKVAGFNLLM TLRLWSS 277	
3-67	Sequences		
3-67-1	Sequence Number [ID]	67	
3-67-2	Molecule Type	AA	
3-67-3	Length	5	
3-67-4	Features	source 1..5	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		

3-67-5	Residues	SGHDT	5
3-68	Sequences		
3-68-1	Sequence Number [ID]	68	
3-68-2	Molecule Type	AA	
3-68-3	Length	6	
3-68-4	Features	source 1..6	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-68-5	Residues	YYEEEE	6
3-69	Sequences		
3-69-1	Sequence Number [ID]	69	
3-69-2	Molecule Type	AA	
3-69-3	Length	16	
3-69-4	Features	source 1..16	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-69-5	Residues	CASSNEGQGW EAEAFF	16
3-70	Sequences		
3-70-1	Sequence Number [ID]	70	
3-70-2	Molecule Type	AA	
3-70-3	Length	134	
3-70-4	Features	source 1..134	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-70-5	Residues	MGPGLLCWAL LCLLGAGLVD AGVTQSPTHL IKTRGQQVTL RCSPKSGHDT VSWYQQALGQ 60 GPQFIFQYYE EEERQRGNFP DRFSGHQFPN YSSELNVNAL LLGDSALYLC ASSNEGQGWE 120 AEAFFGQGTR LTVV 134	
3-71	Sequences		
3-71-1	Sequence Number [ID]	71	
3-71-2	Molecule Type	AA	
3-71-3	Length	177	
3-71-4	Features	source 1..177	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-71-5	Residues	EDLNKVFPE VAVFEPSEAE ISHTQKATLV CLATGFFPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCVQF YGLSENDEWT QDRAKPVTDI 120 VSAEAWGRAD CGFTSVSYQQ GVLSATILYE ILLGKATLYA VLVSALVMA MVKRKDF 177	
3-72	Sequences		
3-72-1	Sequence Number [ID]	72	
3-72-2	Molecule Type	AA	
3-72-3	Length	311	
3-72-4	Features	source 1..311	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-72-5	Residues	MGPGLLCWAL LCLLGAGLVD AGVTQSPTHL IKTRGQQVTL RCSPKSGHDT VSWYQQALGQ 60 GPQFIFQYYE EEERQRGNFP DRFSGHQFPN YSSELNVNAL LLGDSALYLC ASSNEGQGWE 120 AEAFFGQGTR LTVVEDLNKV FPPEVAVFEP SEAEISHTQK ATLVCLATGF FPDHVELSWW 180 VNGKEVHSGV STDPQPLKEQ PALNDSRYCL SSRLRVSATF WQNPRNHFRQ QVQFYGLSEN 240 DEWTQDRAKP VTQIVSAEAW GRADCGFTSV SYQQGVLSAT ILYEILLGKA TLYAVLVSA 300 VLMAMVKRKD F 311	
3-73	Sequences		
3-73-1	Sequence Number [ID]	73	
3-73-2	Molecule Type	AA	
3-73-3	Length	5	
3-73-4	Features	source 1..5	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-73-5	Residues	DSVNN	5
3-74	Sequences		
3-74-1	Sequence Number [ID]	74	
3-74-2	Molecule Type		
3-74-3	Length		
3-74-4	Features		

3-74-5	Location/Qualifiers NonEnglishQualifier Value Residues	000	3
3-75	Sequences		
3-75-1	Sequence Number [ID]	75	
3-75-2	Molecule Type	AA	
3-75-3	Length	11	
3-75-4	Features Location/Qualifiers	source 1..11 mol_type=protein organism=Homo sapiens	
3-75-5	NonEnglishQualifier Value Residues	CAVHNFNKFY F	11
3-76	Sequences		
3-76-1	Sequence Number [ID]	76	
3-76-2	Molecule Type	AA	
3-76-3	Length	127	
3-76-4	Features Location/Qualifiers	source 1..127 mol_type=protein organism=Homo sapiens	
3-76-5	NonEnglishQualifier Value Residues	MKRILGALLG LLSAQVCCVR GIQVEQSPPD LILQEGANST LRCNFSDSVN NLQWFHQNPW 60 GQLINLFYIP SGTKQNGRLS ATTVATERYS LLYISSSQTT DSGVYFCAVH NFNKFYFGSG 120 TKLNVKP 127	
3-77	Sequences		
3-77-1	Sequence Number [ID]	77	
3-77-2	Molecule Type	AA	
3-77-3	Length	141	
3-77-4	Features Location/Qualifiers	source 1..141 mol_type=protein organism=Homo sapiens	
3-77-5	NonEnglishQualifier Value Residues	NIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFNQLSVIGF 120 RILLKLVAGF NLLMTLRLWS S 141	
3-78	Sequences		
3-78-1	Sequence Number [ID]	78	
3-78-2	Molecule Type	AA	
3-78-3	Length	268	
3-78-4	Features Location/Qualifiers	source 1..268 mol_type=protein organism=Homo sapiens	
3-78-5	NonEnglishQualifier Value Residues	MKRILGALLG LLSAQVCCVR GIQVEQSPPD LILQEGANST LRCNFSDSVN NLQWFHQNPW 60 GQLINLFYIP SGTKQNGRLS ATTVATERYS LLYISSSQTT DSGVYFCAVH NFNKFYFGSG 120 TKLNVKPNIQ NPDPAVYQLR DSKSSDKSVC LFTDFDSQTN VSQSKSDSVY ITDKTVLDMR 180 SMDFKSNSAV AWSNKSDFAC ANAFNNSIIP EDTFFPSPES SCDVKLVEKS FETDTNLNFQ 240 NLSVIGFRIL LLKVAGFNLL MTLRLWSS 268	
3-79	Sequences		
3-79-1	Sequence Number [ID]	79	
3-79-2	Molecule Type	AA	
3-79-3	Length	5	
3-79-4	Features Location/Qualifiers	source 1..5 mol_type=protein organism=Homo sapiens	
3-79-5	NonEnglishQualifier Value Residues	PRHDT	5
3-80	Sequences		
3-80-1	Sequence Number [ID]	80	
3-80-2	Molecule Type	AA	
3-80-3	Length	6	
3-80-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens	
3-80-5	NonEnglishQualifier Value Residues	FYEKMQ	6
3-81	Sequences		
3-81-1	Sequence Number [ID]	81	
3-81-2	Molecule Type	AA	
3-81-3	Length	15	

3-81-4	Features Location/Qualifiers	source 1..15 mol_type=protein organism=Homo sapiens	
3-81-5	NonEnglishQualifier Value Residues	CASSLLGQGY NEQFF	15
3-82	Sequences		
3-82-1	Sequence Number [ID]	82	
3-82-2	Molecule Type	AA	
3-82-3	Length	143	
3-82-4	Features Location/Qualifiers	source 1..143 mol_type=protein organism=Homo sapiens	
3-82-5	NonEnglishQualifier Value Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNMSL ELGDSALYFC 120 ASSLLGQGYN EQFFGPGTRL TVL	143
3-83	Sequences		
3-83-1	Sequence Number [ID]	83	
3-83-2	Molecule Type	AA	
3-83-3	Length	179	
3-83-4	Features Location/Qualifiers	source 1..179 mol_type=protein organism=Homo sapiens	
3-83-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTDI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMMA MVKRKDSRG 179	
3-84	Sequences		
3-84-1	Sequence Number [ID]	84	
3-84-2	Molecule Type	AA	
3-84-3	Length	322	
3-84-4	Features Location/Qualifiers	source 1..322 mol_type=protein organism=Homo sapiens	
3-84-5	NonEnglishQualifier Value Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNMSL ELGDSALYFC 120 ASSLLGQGYN EQFFGPGTRL TVLEDLKNVF PPEVAVFEPSEAEISHTQKATLVCLATGFY 180 PDHVELSWWV NGKEVHSGVS TDPQPLKEQP ALNDSRYCLS SRLRVSATFW QNPRNHFRCQ 240 VQFYGLSEND EWTQDRAKPV TQIVSAEAWG RADCGFTSES YQQGVLSATI LYEILLGKAT 300 LYAVLVSALV LMAMVKRKDS RG	322
3-85	Sequences		
3-85-1	Sequence Number [ID]	85	
3-85-2	Molecule Type	AA	
3-85-3	Length	7	
3-85-4	Features Location/Qualifiers	source 1..7 mol_type=protein organism=Homo sapiens	
3-85-5	NonEnglishQualifier Value Residues	TRDTTY	7
3-86	Sequences		
3-86-1	Sequence Number [ID]	86	
3-86-2	Molecule Type	AA	
3-86-3	Length	4	
3-86-4	Features Location/Qualifiers	source 1..4 mol_type=protein organism=Homo sapiens	
3-86-5	NonEnglishQualifier Value Residues	RNSF	4
3-87	Sequences		
3-87-1	Sequence Number [ID]	87	
3-87-2	Molecule Type	AA	
3-87-3	Length	14	
3-87-4	Features Location/Qualifiers	source 1..14 mol_type=protein organism=Homo sapiens	
3-87-5	NonEnglishQualifier Value Residues	CALSNNNAGN MLTF	14
3-88	Sequences		

3-88-1	Sequence Number [ID]	88
3-88-2	Molecule Type	AA
3-88-3	Length	135
3-88-4	Features	source 1..135
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-88-5	NonEnglishQualifier Value Residues	MLTASLLRAV IASICVVSSM AQKVTQAQTE ISVVEKEDVT LDCVYETRDT TYYLFWYKQP 60 PSGELVFLIR RNSFDEQNEI SGRYSWNFQK STSSFNFTIT ASQVVD SAVY FCALSNNNAG 120 NMLTFGGGTR LMVKP 135
3-89	Sequences	
3-89-1	Sequence Number [ID]	89
3-89-2	Molecule Type	AA
3-89-3	Length	141
3-89-4	Features	source 1..141
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-89-5	NonEnglishQualifier Value Residues	HIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RIILLKVGAGF NLLMTLRLWS S 141
3-90	Sequences	
3-90-1	Sequence Number [ID]	90
3-90-2	Molecule Type	AA
3-90-3	Length	276
3-90-4	Features	source 1..276
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-90-5	NonEnglishQualifier Value Residues	MLTASLLRAV IASICVVSSM AQKVTQAQTE ISVVEKEDVT LDCVYETRDT TYYLFWYKQP 60 PSGELVFLIR RNSFDEQNEI SGRYSWNFQK STSSFNFTIT ASQVVD SAVY FCALSNNNAG 120 NMLTFGGGTR LMVKPHIQNP DPAVYQLRDS KSSDKSVCLF TDFDSQTNVS QSKDSDVYIT 180 DKTVLDMRSM DFKSNSAVAW SNKSDFACAN AFNNSIIPED TFFPSPESSC DVKLVEKSFE 240 TDTNLFNQNL SVIGFRILL KVGAGNLLMT LRLWSS 276
3-91	Sequences	
3-91-1	Sequence Number [ID]	91
3-91-2	Molecule Type	AA
3-91-3	Length	5
3-91-4	Features	source 1..5
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-91-5	NonEnglishQualifier Value Residues	PRHDT 5
3-92	Sequences	
3-92-1	Sequence Number [ID]	92
3-92-2	Molecule Type	AA
3-92-3	Length	6
3-92-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-92-5	NonEnglishQualifier Value Residues	FYEKMQ 6
3-93	Sequences	
3-93-1	Sequence Number [ID]	93
3-93-2	Molecule Type	AA
3-93-3	Length	16
3-93-4	Features	source 1..16
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-93-5	NonEnglishQualifier Value Residues	CASSPTGTSG YNEQFF 16
3-94	Sequences	
3-94-1	Sequence Number [ID]	94
3-94-2	Molecule Type	AA
3-94-3	Length	144
3-94-4	Features	source 1..144
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	

3-94-5	Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNMSSL ELGDSALYFC 120 ASSPTGTSGY NEQFFGPGTR LTVL 144
3-95	Sequences	
3-95-1	Sequence Number [ID]	95
3-95-2	Molecule Type	AA
3-95-3	Length	179
3-95-4	Features	source 1..179
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-95-5	NonEnglishQualifier Value	
	Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWVWNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMA MVKRKDSRG 179
3-96	Sequences	
3-96-1	Sequence Number [ID]	96
3-96-2	Molecule Type	AA
3-96-3	Length	323
3-96-4	Features	source 1..323
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-96-5	NonEnglishQualifier Value	
	Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNMSSL ELGDSALYFC 120 ASSPTGTSGY NEQFFGPGTR LTVLEDLKNV FPPEVAVFEP SEAEISHTQK ATLVCLATGF 180 YPDHVELSWW VNGKEVHSGV STDPQPLKEQ PALNDSRYCL SSRLRVSATF WQNPRNHFRG 240 QVQFYGLSEN DEWTQDRAKP VTQIVSAEAW GRADCGFTSE SYQQGVLSAT ILYEILLGKA 300 TLYAVLVSAL VLMAMVKRKD SRG 323
3-97	Sequences	
3-97-1	Sequence Number [ID]	97
3-97-2	Molecule Type	AA
3-97-3	Length	6
3-97-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-97-5	NonEnglishQualifier Value	
	Residues	SSNFYA 6
3-98	Sequences	
3-98-1	Sequence Number [ID]	98
3-98-2	Molecule Type	
3-98-3	Length	
3-98-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-98-5	Residues	000 3
3-99	Sequences	
3-99-1	Sequence Number [ID]	99
3-99-2	Molecule Type	AA
3-99-3	Length	11
3-99-4	Features	source 1..11
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-99-5	NonEnglishQualifier Value	
	Residues	CALNRDDKII F 11
3-100	Sequences	
3-100-1	Sequence Number [ID]	100
3-100-2	Molecule Type	AA
3-100-3	Length	132
3-100-4	Features	source 1..132
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-100-5	NonEnglishQualifier Value	
	Residues	MEKNPLAAPL LILWFHLDV SSILNVEQSP QSLHVQEGDS TNFTCSFPSS NFYALHWYRW 60 ETAKSPEALF VMTLNGDEKK KGRISATLNT KEGYSYLYIK GSQPEDSATY LCALNRDDKI 120 IFGKGTRLHI LP 132
3-101	Sequences	
3-101-1	Sequence Number [ID]	101
3-101-2	Molecule Type	AA
3-101-3	Length	141

3-101-4	Features Location/Qualifiers	source 1..141 mol_type=protein organism=Homo sapiens
3-101-5	NonEnglishQualifier Value Residues	NIQNPDPNAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RILLKLVAGF NLLMTLRLWS S 141
3-102	Sequences	
3-102-1	Sequence Number [ID]	102
3-102-2	Molecule Type	AA
3-102-3	Length	273
3-102-4	Features Location/Qualifiers	source 1..273 mol_type=protein organism=Homo sapiens
3-102-5	NonEnglishQualifier Value Residues	MEKNPLAAPL LILWFHLDVC SSILNVEQSP QSLHVQEGDS TNFTCSFPSS NFYALHWYRW 60 ETAKSPEALF VMTLNGDEKK KGRISATLNT KEGYSYLYIK GSQPEDSATY LCALNRDDKI 120 IFGKGTSLHI LPNIQNPDA VYQLRDSKSS DKSVCCLFTDF DSQTNSVQSK DSDVYITDKT 180 VLDMRSMDFK SNSAVAWSNK SDFACANAFN NSIIPEDTFF PSESSCDVK LVEKSFETDT 240 NLNFQNLSVI GFRILLKVA GFNLLMTLRL WSS 273
3-103	Sequences	
3-103-1	Sequence Number [ID]	103
3-103-2	Molecule Type	AA
3-103-3	Length	5
3-103-4	Features Location/Qualifiers	source 1..5 mol_type=protein organism=Homo sapiens
3-103-5	NonEnglishQualifier Value Residues	MDHEN 5
3-104	Sequences	
3-104-1	Sequence Number [ID]	104
3-104-2	Molecule Type	AA
3-104-3	Length	6
3-104-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens
3-104-5	NonEnglishQualifier Value Residues	SYDVKM 6
3-105	Sequences	
3-105-1	Sequence Number [ID]	105
3-105-2	Molecule Type	AA
3-105-3	Length	14
3-105-4	Features Location/Qualifiers	source 1..14 mol_type=protein organism=Homo sapiens
3-105-5	NonEnglishQualifier Value Residues	CASRLPSRTY EQYF 14
3-106	Sequences	
3-106-1	Sequence Number [ID]	106
3-106-2	Molecule Type	AA
3-106-3	Length	132
3-106-4	Features Location/Qualifiers	source 1..132 mol_type=protein organism=Homo sapiens
3-106-5	NonEnglishQualifier Value Residues	MGIRLLCRVA FCFLAVGLVD VKVTQSSRYL VKRTGEKVFL ECVQMDHEN MFWYRQDPGL 60 GLRLIYFSYD VKMKEKGDIP EGYSVSREKK ERFSLILESA STNQTSMYLC ASRLPSRTYE 120 QYFGPGTRLT VT 132
3-107	Sequences	
3-107-1	Sequence Number [ID]	107
3-107-2	Molecule Type	AA
3-107-3	Length	179
3-107-4	Features Location/Qualifiers	source 1..179 mol_type=protein organism=Homo sapiens
3-107-5	NonEnglishQualifier Value Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWVWNGK EVHSGVSTDP 60 QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTDI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMMA MVKRKDSRG 179

3-108	Sequences	
3-108-1	Sequence Number [ID]	108
3-108-2	Molecule Type	AA
3-108-3	Length	311
3-108-4	Features	source 1..311
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-108-5	NonEnglishQualifier Value	
	Residues	MGIRLLCRVA FCFLAVGLVD VKVTQSSRYL VKRTGEKVFL ECVQDMDHEN MFWYRQDPGL 60 GLRLIYFSYD VKMKEKGDIP EGYSVSREKK ERFSLILESA STNQTSMYLC ASRLPSRTYE 120 QYFGPGTRLT VTEDLKNVFP PEVAVFEPSE AEISHTQKAT LVCLATGFYP DHVELSWWVN 180 GKEVHSGVST DPQPLKEQPA LNSDRYCLSS RLRVSATFWQ NPRNHFRQV QFYGLSENDE 240 WTQDRAKPVT QIVSAEAWGR ADCGFTSESY QQGVLSATIL YEILLGKATL YAVLVSALVL 300 MAMVKRKDSR G 311
3-109	Sequences	
3-109-1	Sequence Number [ID]	109
3-109-2	Molecule Type	AA
3-109-3	Length	6
3-109-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-109-5	NonEnglishQualifier Value	
	Residues	DSAIYN 6
3-110	Sequences	
3-110-1	Sequence Number [ID]	110
3-110-2	Molecule Type	
3-110-3	Length	
3-110-4	Features	
	Location/Qualifiers	
	NonEnglishQualifier Value	
3-110-5	Residues	000 3
3-111	Sequences	
3-111-1	Sequence Number [ID]	111
3-111-2	Molecule Type	AA
3-111-3	Length	11
3-111-4	Features	source 1..11
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-111-5	NonEnglishQualifier Value	
	Residues	CAVNSDYKLS F 11
3-112	Sequences	
3-112-1	Sequence Number [ID]	112
3-112-2	Molecule Type	AA
3-112-3	Length	129
3-112-4	Features	source 1..129
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-112-5	NonEnglishQualifier Value	
	Residues	METLLGLLIL WLQLQWSSK QEVTQIPAAAL SVPEGENLVL NCSFTDSAIY NLQWFRQDPG 60 KGLTSLLLIQ SSQREQTSGR LNASLDKSSG RSTLYIAASQ PGDSATYLCA VNSDYKLSFG 120 AGTTVTVRA 129
3-113	Sequences	
3-113-1	Sequence Number [ID]	113
3-113-2	Molecule Type	AA
3-113-3	Length	141
3-113-4	Features	source 1..141
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
3-113-5	NonEnglishQualifier Value	
	Residues	NIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLSVIGF 120 RILLKLVAGF NLLMTLRLWS S 141
3-114	Sequences	
3-114-1	Sequence Number [ID]	114
3-114-2	Molecule Type	AA
3-114-3	Length	270
3-114-4	Features	source 1..270
	Location/Qualifiers	mol_type=protein organism=Homo sapiens

3-114-5	NonEnglishQualifier Value Residues	METLLGLLIL WLQLQWSSK QEVTQIPAAL SVPEGENLVL NCSFTDSAIY NLQWFRQDPG 60 KGLTSLLLIQ SSQREQTSGR LNASLDKSSG RSTLYIAASQ PGDSATYLCA VNSDYKLSFG 120 AGTTVTVRAN IQNPDPVYQ LRDSKSSDKS VCLFTDFDSQ TNVSQSKDSD VYITDKTVLD 180 MRSMDFKSNS AVAWSNKSDF ACANAFNNSI IPEDTFFPSP ESSCDVKLVE KSFETDTNLN 240 FQNLSVIGFR ILLLKVAGFN LLMTLRLWSS 270
3-115	Sequences	
3-115-1	Sequence Number [ID]	115
3-115-2	Molecule Type	AA
3-115-3	Length	5
3-115-4	Features Location/Qualifiers	source 1..5 mol_type=protein organism=Homo sapiens
3-115-5	NonEnglishQualifier Value Residues	PHRDT 5
3-116	Sequences	
3-116-1	Sequence Number [ID]	116
3-116-2	Molecule Type	AA
3-116-3	Length	6
3-116-4	Features Location/Qualifiers	source 1..6 mol_type=protein organism=Homo sapiens
3-116-5	NonEnglishQualifier Value Residues	FYEKMQ 6
3-117	Sequences	
3-117-1	Sequence Number [ID]	117
3-117-2	Molecule Type	AA
3-117-3	Length	16
3-117-4	Features Location/Qualifiers	source 1..16 mol_type=protein organism=Homo sapiens
3-117-5	NonEnglishQualifier Value Residues	CASSLGLGTG DYGYTF 16
3-118	Sequences	
3-118-1	Sequence Number [ID]	118
3-118-2	Molecule Type	AA
3-118-3	Length	144
3-118-4	Features Location/Qualifiers	source 1..144 mol_type=protein organism=Homo sapiens
3-118-5	NonEnglishQualifier Value Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNSSL ELGDSALYFC 120 ASSLGLGTGD YGYTFGSGTR LTVV 144
3-119	Sequences	
3-119-1	Sequence Number [ID]	119
3-119-2	Molecule Type	AA
3-119-3	Length	177
3-119-4	Features Location/Qualifiers	source 1..177 mol_type=protein organism=Homo sapiens
3-119-5	NonEnglishQualifier Value Residues	EDLNKVPPE VAVFEPSEAE ISHTQKATLV CLATGFFPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRYCLSSRL RVSATFWQNP RNHFRCVQVF YGLSENDEWT QDRAKPVTQI 120 VSAEAWGRAD CGFTSVSYQQ GVLSATILYE ILLGKATLYA VLVSALVLMA MVKRKDF 177
3-120	Sequences	
3-120-1	Sequence Number [ID]	120
3-120-2	Molecule Type	AA
3-120-3	Length	321
3-120-4	Features Location/Qualifiers	source 1..321 mol_type=protein organism=Homo sapiens
3-120-5	NonEnglishQualifier Value Residues	MLSPDLPDSA WNTRLLCHVM LCLLGAVSVA AGVIQSPRHL IKEKRETATL KCYPIPRHDT 60 VYWYQQGPGQ DPQFLISFYE KMQSDKGSIP DRFSAQQFSD YHSELNSSL ELGDSALYFC 120 ASSLGLGTGD YGYTFGSGTR LTVVEDLNKV FPPEVAVFEP SEAEISHTQK ATLVCLATGF 180 FPDHVELSWW VNGKEVHSGV STDPQPLKEQ PALNDSRYCL SSRLRVSATF WQNPRNHFRC 240 QVQFYGLSEN DEWTQDRAKP VTQIVSAEAW GRADCGFTSV SYQQGVLSAT ILYEILLGKA 300 TLYAVLVSAL VLMAMVKRKD F 321
3-121	Sequences	

3-121-1	Sequence Number [ID]	121	
3-121-2	Molecule Type	AA	
3-121-3	Length	6	
3-121-4	Features	source 1..6	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-121-5	Residues	DSAIYN	6
3-122	Sequences		
3-122-1	Sequence Number [ID]	122	
3-122-2	Molecule Type		
3-122-3	Length		
3-122-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-122-5	Residues	000	3
3-123	Sequences		
3-123-1	Sequence Number [ID]	123	
3-123-2	Molecule Type	AA	
3-123-3	Length	15	
3-123-4	Features	source 1..15	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-123-5	Residues	CAVRPTSGGS YIPTF	15
3-124	Sequences		
3-124-1	Sequence Number [ID]	124	
3-124-2	Molecule Type	AA	
3-124-3	Length	133	
3-124-4	Features	source 1..133	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-124-5	Residues	METLLGLLIL WLQLQWSSK QEVTQIPAAL SVPEGENLVL NCSFTDSAIY NLQWFRQDPG 60 KGLTSLLLIQ SSQREQTSGR LNASLDKSSG RSTLYIAASQ PGDSATYLCA VRPTSGGSYI 120 PTFGRGTSLI VHP 133	
3-125	Sequences		
3-125-1	Sequence Number [ID]	125	
3-125-2	Molecule Type	AA	
3-125-3	Length	141	
3-125-4	Features	source 1..141	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-125-5	Residues	YIQNPDAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS DVYITDKTVL DMRSMDFKSN 60 SAVAWSNKSD FACANAFNNS IIPEDTFFPS PESSCDVKLV EKSFETDTNL NFQNLVIGF 120 RILLKLVAGF NLLMTLRLWS S 141	
3-126	Sequences		
3-126-1	Sequence Number [ID]	126	
3-126-2	Molecule Type	AA	
3-126-3	Length	274	
3-126-4	Features	source 1..274	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-126-5	Residues	METLLGLLIL WLQLQWSSK QEVTQIPAAL SVPEGENLVL NCSFTDSAIY NLQWFRQDPG 60 KGLTSLLLIQ SSQREQTSGR LNASLDKSSG RSTLYIAASQ PGDSATYLCA VRPTSGGSYI 120 PTFGRGTSLI VHPYIQNPDP AVYQLRDSKS SDKSVCLFTD FDSQTNVSQS KSDVYITDK 180 TVLDMRSMDF KNSAVAWSN KSDFACANAF NNSIIPEDTF FPSPRESSCDV KLVEKSFETD 240 TNLNFQNLV IGFRILLKV AGFNLLMTLR LWSS 274	
3-127	Sequences		
3-127-1	Sequence Number [ID]	127	
3-127-2	Molecule Type	AA	
3-127-3	Length	5	
3-127-4	Features	source 1..5	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-127-5	Residues	MNHEY	5

3-128	Sequences	
3-128-1	Sequence Number [ID]	128
3-128-2	Molecule Type	AA
3-128-3	Length	6
3-128-4	Features	source 1..6
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-128-5	Residues	SVGAGI6
3-129	Sequences	
3-129-1	Sequence Number [ID]	129
3-129-2	Molecule Type	AA
3-129-3	Length	14
3-129-4	Features	source 1..14
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-129-5	Residues	CASSYVGNTG ELFF14
3-130	Sequences	
3-130-1	Sequence Number [ID]	130
3-130-2	Molecule Type	AA
3-130-3	Length	132
3-130-4	Features	source 1..132
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-130-5	Residues	MSIGLLCCAA LSLWAGPVN AGVTQTPKFQ VLKTGQSMTL QCAQDMNHEY MSWYRQDPGM 60 GLRLIHYSVG AGITDQGEVP NGYNVSRSTT EDFPLRLLSA APSQTSVYFC ASSYVGNTGE 120 LFFGEGSRLT VL132
3-131	Sequences	
3-131-1	Sequence Number [ID]	131
3-131-2	Molecule Type	AA
3-131-3	Length	179
3-131-4	Features	source 1..179
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-131-5	Residues	EDLKNVFPPE VAVFEPSEAE ISHTQKATLV CLATGFYPDH VELSWWVNGK EVHSGVSTDP 60 QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNHFRCQVQF YGLSENDEWT QDRAKPVTTI 120 VSAEAWGRAD CGFTSESYQQ GVLSATILYE ILLGKATLYA VLVSALVLMV MVKRKDSRG 179
3-132	Sequences	
3-132-1	Sequence Number [ID]	132
3-132-2	Molecule Type	AA
3-132-3	Length	311
3-132-4	Features	source 1..311
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-132-5	Residues	MSIGLLCCAA LSLWAGPVN AGVTQTPKFQ VLKTGQSMTL QCAQDMNHEY MSWYRQDPGM 60 GLRLIHYSVG AGITDQGEVP NGYNVSRSTT EDFPLRLLSA APSQTSVYFC ASSYVGNTGE 120 LFFGEGSRLT VLEDLKNVFP PEVAVFEPSE AEISHTQKAT LVCLATGFYP DHVELSWWVN 180 GKEVHSGVST DPQPLKEQPA LNSRVCLSS RLRVSATFWQ NPRNHFRQV QFYGLSENDE 240 WTQDRAKPVTTI VSAEAWGR ADCGFTSESY QQGVLSATIL YEILLGKATL YAVLVLSALVL 300 MAMVKRKDSRG 311
3-133	Sequences	
3-133-1	Sequence Number [ID]	133
3-133-2	Molecule Type	AA
3-133-3	Length	9
3-133-4	Features	source 1..9
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-133-5	Residues	KVLEYVIKV9
3-134	Sequences	
3-134-1	Sequence Number [ID]	134
3-134-2	Molecule Type	AA
3-134-3	Length	9
3-134-4	Features	source 1..9
	Location/Qualifiers	mol_type=protein

3-134-5	NonEnglishQualifier Value Residues	organism=Homo sapiens AVLEYVIKV	9
3-135	Sequences		
3-135-1	Sequence Number [ID]	135	
3-135-2	Molecule Type	AA	
3-135-3	Length	9	
3-135-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-135-5	NonEnglishQualifier Value Residues	KALEYVIKV	9
3-136	Sequences		
3-136-1	Sequence Number [ID]	136	
3-136-2	Molecule Type	AA	
3-136-3	Length	9	
3-136-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-136-5	NonEnglishQualifier Value Residues	KVAEYVIKV	9
3-137	Sequences		
3-137-1	Sequence Number [ID]	137	
3-137-2	Molecule Type	AA	
3-137-3	Length	9	
3-137-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-137-5	NonEnglishQualifier Value Residues	KVLAYVIKV	9
3-138	Sequences		
3-138-1	Sequence Number [ID]	138	
3-138-2	Molecule Type	AA	
3-138-3	Length	9	
3-138-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-138-5	NonEnglishQualifier Value Residues	KVLEAVIKV	9
3-139	Sequences		
3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	AA	
3-139-3	Length	9	
3-139-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-139-5	NonEnglishQualifier Value Residues	KVLEYAIKV	9
3-140	Sequences		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	AA	
3-140-3	Length	9	
3-140-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-140-5	NonEnglishQualifier Value Residues	KVLEYVAKV	9
3-141	Sequences		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	AA	
3-141-3	Length	9	
3-141-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
3-141-5	NonEnglishQualifier Value Residues	KVLEYVIAV	9
3-142	Sequences		
3-142-1	Sequence Number [ID]	142	

3-142-2	Molecule Type	AA	
3-142-3	Length	9	
3-142-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-142-5	Residues	KVLEYVIKA	9
3-143	Sequences		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	AA	
3-143-3	Length	9	
3-143-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-143-5	Residues	ILLPYVSKV	9
3-144	Sequences		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	AA	
3-144-3	Length	9	
3-144-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-144-5	Residues	KALEGFIIV	9
3-145	Sequences		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	AA	
3-145-3	Length	9	
3-145-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-145-5	Residues	KLLEKVRKV	9
3-146	Sequences		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	AA	
3-146-3	Length	9	
3-146-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-146-5	Residues	KLTEYVDKV	9
3-147	Sequences		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	AA	
3-147-3	Length	9	
3-147-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-147-5	Residues	KVLERNNAV	9
3-148	Sequences		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	AA	
3-148-3	Length	9	
3-148-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	
	NonEnglishQualifier Value		
3-148-5	Residues	KVLNKVITV	9
3-149	Sequences		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	AA	
3-149-3	Length	9	
3-149-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein organism=Homo sapiens	

3-149-5	NonEnglishQualifier Value Residues	KVQEQVHKV	9
3-150	Sequences		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	AA	
3-150-3	Length	9	
3-150-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-150-5	NonEnglishQualifier Value Residues	LLLPDVIKV	9
3-151	Sequences		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	AA	
3-151-3	Length	9	
3-151-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-151-5	NonEnglishQualifier Value Residues	NVLEIVQKV	9
3-152	Sequences		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	AA	
3-152-3	Length	9	
3-152-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-152-5	NonEnglishQualifier Value Residues	SVLEPVISV	9
3-153	Sequences		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	AA	
3-153-3	Length	9	
3-153-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-153-5	NonEnglishQualifier Value Residues	SLLMWITQV	9
3-154	Sequences		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	AA	
3-154-3	Length	9	
3-154-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-154-5	NonEnglishQualifier Value Residues	TVLEYVIKV	9
3-155	Sequences		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	AA	
3-155-3	Length	9	
3-155-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-155-5	NonEnglishQualifier Value Residues	KTLEYVIKV	9
3-156	Sequences		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	AA	
3-156-3	Length	9	
3-156-4	Features Location/Qualifiers	source 1..9 mol_type=protein organism=Homo sapiens	
3-156-5	NonEnglishQualifier Value Residues	KVTEYVIKV	9
3-157	Sequences		
3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	AA	

3-157-3	Length	9	
3-157-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
3-157-5	NonEnglishQualifier Value		
	Residues	KVLTYYVIKV	9
3-158	Sequences		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	AA	
3-158-3	Length	9	
3-158-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-158-5	Residues	KVLETYVIKV	9
3-159	Sequences		
3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	AA	
3-159-3	Length	9	
3-159-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-159-5	Residues	KVLEYTIKV	9
3-160	Sequences		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	AA	
3-160-3	Length	9	
3-160-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-160-5	Residues	KVLEYVTKV	9
3-161	Sequences		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	AA	
3-161-3	Length	9	
3-161-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-161-5	Residues	KVLEYVITV	9
3-162	Sequences		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	AA	
3-162-3	Length	9	
3-162-4	Features	source 1..9	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-162-5	Residues	KVLEYVIKT	9