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(54) Title: HIGH AFFINITY HIV T CELL RECEPTORS

(57) Abstract: The present invention provides TCRs having an affinity (K_D) of less than or equal to $1\mu\text{M}$, and/or an off-rate (k_{off}) of $1 \times 10^{-3} \text{ s}^{-1}$ or slower, for the SLYNTVATL-HLA-A*0201 complex PROVIDED THAT when the said TCR is presented by cell and comprises SEQ ID NOs: 1 and 2, the cell is not a native T cell. Such TCRs are useful, either alone or associated with a therapeutic agent, for targeting HIV infected cells presenting that complex.



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High Affinity HIV T cell receptors

The present invention relates to T-cell receptors (TCRs) having the property of binding to HIV Gag polypeptide-derived SLYNTVATL-HLA-A*0201. The TCRs comprise at least one TCR α chain variable domain and/or at least one TCR β chain variable domain and have a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or has an off-rate (k_{off}) for the SLYNTVATL-HLA-A*0201 complex of $1 \times 10^{-3} \text{ S}^{-1}$ or slower.

Background to the Invention

The Human Immuno-deficiency Virus (HIV) is the causative agent of Acquired Immuno-deficiency Disease Syndrome (AIDS). The virus is an enveloped retrovirus belonging to the lentivirus group. The SLYNTVATL (SEQ ID NO: 16) peptide is derived from the *g17* gene product of the Gag gene, one of nine genes which make up the Human Immuno-deficiency Virus-1 (HIV-1). The peptide is loaded by HLA-A*0201 and presented on the surface of HIV infected cells. Therefore, the SLYNTVATL-HLA-A*0201 complex provides an HIV marker that TCRs can target, for example for the purpose of delivering cytotoxic or immuno-stimulatory agents to the infected cells. However, for that purpose it would be desirable if the TCR had a high affinity and/or a slow off-rate for the peptide-HLA complex.

Brief Description of the Invention

This invention makes available for the first time TCRs having an affinity (K_D) of less than or equal to $1\mu\text{M}$, and/or an off-rate (k_{off}) of $1 \times 10^{-3} \text{ S}^{-1}$ or slower, for the SLYNTVATL-HLA-A*0201 complex PROVIDED THAT when the said TCR is presented by cell and comprises SEQ ID NOs: 1 and 2, the cell is not a native T cell. Such TCRs are useful, either alone or associated with a therapeutic agent, for targeting HIV infected cells presenting that complex.

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Detailed Description of the Invention

The present invention provides a T-cell receptor (TCR) having the property of binding to SLYNTVATL-HLA-A*0201 and comprising at least one TCR α chain variable domain and/or at least one TCR β chain variable domain, wherein said TCR has a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or has an off-rate (k_{off}) for the SLYNTVATL-HLA-A*0201 complex of $1 \times 10^{-3} \text{ s}^{-1}$ or slower, provided that when the said TCR is presented by cell and comprises SEQ ID NOs:1 and 2, the cell is not a native T-cell. The K_D and/or (k_{off}) measurement can be made by any of the known methods. A preferred method is the Surface Plasmon Resonance (Biacore) method of Example 4.

According to one aspect, the present invention provides an isolated T-cell receptor (TCR) having the property of binding to SLYNTVATL-HLA-A*0201 and comprising at least one TCR α chain variable domain and/or at least one TCR β chain variable domain, wherein:

- (i) the TCR α chain variable domain has SEQ ID NO:1 except that at least one complementarity determining region thereof is/are mutated and/or the TCR β chain variable domain has SEQ ID NO:2 except that at least one complementarity determining region thereof is/are mutated; and
- (ii) the TCR has a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or has an off-rate (k_{off}) for the SLYNTVATL-HLA-A*0201 complex of $1 \times 10^{-3} \text{ s}^{-1}$ or slower.

For comparison, the interaction of a disulfide-linked soluble variant of the parental HIV Gag TCR (see SEQ ID NO:9 for TCR α chain and SEQ ID NO:10 for TCR β chain) and the SLYNTVATL-HLA-A*0201 complex has a K_D of approximately 85nM and an off-rate (k_{off}) of $2.21 \times 10^{-2} \text{ s}^{-1}$ as measured by the Biacore-base method of Example 4.

The parental HIV Gag TCR specific for the SLYNTVATL-HLA-A*0201 complex has the following Valpha chain and Vbeta chain gene usage:

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2A

Alpha chain – TRAV 12.2

Beta chain – TRBV 5.6

The parental HIV Gag TCR can be used as a template from which other TCRs of the invention with high affinity and/or a slow off-rate for the interaction between said TCRs and the SLYNTVATL-HLA-A*0201 complex can be produced. Thus, the invention includes TCRs which are mutated relative to the parental HIV Gag TCR α chain variable domain (see Figure 1a and SEQ ID NO:1) and/or β chain variable domain (see Figure 1b and SEQ ID NO:2) in at least one complementarity determining region (CDR) and/or variable domain framework region thereof. It is also contemplated that other hypervariable regions in the variable domains of the TCRs of

the invention, such as the hypervariable 4 (HV4) regions, may be mutated within a high affinity mutant TCR.

5 Phage display provides one means by which libraries of TCR variants can be generated. Methods suitable for the phage display and subsequent screening of libraries of TCR variants each containing a non-native disulfide interchain bond are detailed in (Li *et al.*, (2005) *Nature Biotech* **23** (3): 349-354) and WO 2004/04404.

10 Native TCRs exist in heterodimeric $\alpha\beta$ or $\gamma\delta$ forms. However, recombinant TCRs consisting of a single TCR α or TCR β chain have previously been shown to bind to peptide MHC molecules.

In one embodiment the TCR of the invention comprise both an α chain variable domain and an TCR β chain variable domain.

15 As will be obvious to those skilled in the art the mutation(s) in the TCR α chain sequence and/or TCR β chain sequence may be one or more of substitution(s), deletion(s) or insertion(s). These mutations can be carried out using any appropriate method including, but not limited to, those based on polymerase chain reaction (PCR),
20 restriction enzyme-based cloning, or ligation independent cloning (LIC) procedures. These methods are detailed in many of the standard molecular biology texts. For further details regarding polymerase chain reaction (PCR) mutagenesis and restriction enzyme-based cloning see (Sambrook & Russell, (2001) *Molecular Cloning – A Laboratory Manual* (3rd Ed.) CSHL Press) Further information on LIC procedures can
25 be found in (Rashtchian, (1995) *Curr Opin Biotechnol* **6** (1): 30-6)

It should be noted that any $\alpha\beta$ TCR that comprises similar V α and V β gene usage and therefore amino acid sequence to that of the HIV Gag TCR could make a convenient template TCR. It would then be possible to introduce into the DNA
30 encoding one or both of the variable domains of the template $\alpha\beta$ TCR the changes required to produce the mutated high affinity TCRs of the invention. As will be

obvious to those skilled in the art, the necessary mutations could be introduced by a number of methods, for example site-directed mutagenesis.

5 The TCRs of the invention include those in which one or more of the TCR alpha chain variable domain amino acids corresponding to those listed below are mutated relative to the amino acid occurring at these positions in the sequence provided for the parental HIV Gag TCR alpha chain variable domain in Figure 1a and SEQ ID No: 1.

10 Unless stated to the contrary, the TCR amino acid sequences herein are generally provided including an N-terminal methionine (Met or M) residue. As will be known to those skilled in the art this residue may be removed during the production of recombinant proteins. As will also be obvious to those skilled in the art, it may be possible to truncate the sequences provided at the C-terminus and/or N-terminus thereof, by 1, 2, 3, 4, 5 or more residues, without substantially affecting the pMHC
15 binding characteristics of the TCR, all such trivial variants are encompassed by the present invention.

As used herein the term "variable region" is understood to encompass all amino acids of a given TCR which are not included within the constant domain as encoded by the
20 TRAC gene for TCR α chains and either the TRBC1 or TRBC2 genes for TCR β chains. (T cell receptor Factsbook, (2001) LeFranc and LeFranc, Academic Press, ISBN 0-12-441352-8)

As used herein the term "variable domain" is understood to encompass all amino acids
25 of a given TCR which are encoded by a TRAV gene for TCR α chains and a TRBV gene for TCR β chains. (T cell receptor Factsbook, (2001) LeFranc and LeFranc, Academic Press, ISBN 0-12-441352-8)

As is known to those skilled in the art, part of the diversity of the TCR repertoire is
30 due to variations which occur in the amino acid encoded by the codon at the boundary between the variable region, as defined herein, and the constant domain. For example,

the codon that is present at this boundary in the parental HIV Gag TCR sequence results in the presence of the Histidine (H) residue at the C-terminal of the variable region sequences herein. This Histidine replaces the N-terminal Asparagine (N) residue encoded by the TRAC gene shown in Figure 8a.

5

Embodiments of the invention include mutated TCRs which comprise mutation of one or more of alpha chain variable region amino acids corresponding to: 95T, 96N, 97S, 98G, and 100A, for example the amino acids:

10

95S or G

96A

97H

98D

100S

15

The numbering used above is the same as that shown in Figure 1a and SEQ ID No: 1

20

Embodiments of the invention also include TCRs which comprise mutation of one or more of the TCR beta chain variable region amino acids corresponding to those listed below, are relative to the amino acid occurring at these positions in the sequence provided for the native HIV Gag TCR alpha chain variable region of the native HIV Gag TCR beta chain in Figure 1b and SEQ ID No: 2. The amino acids referred to which may be mutated are: 51Y, 52E, 53E and 54E, for example:

25

51V or A

52R or L

53G

54V

30

The numbering used above is the same as that shown in Figure 1b and SEQ ID No: 2

Further preferred embodiments of the invention are provided by TCRs comprising one of the mutated alpha chain variable region amino acid sequences shown in Fig 6 (SEQ ID Nos: 11 to 13). Phenotypically silent variants of such TCRs also form part of this invention.

5

Additional preferred embodiments of the invention are provided by TCRs comprising one of the mutated beta chain variable region amino acid sequences shown in Figure 7. (SEQ ID Nos: 14 and 15). Phenotypically silent variants of such TCRs also form part of this invention.

10

Native TCRs exist in heterodimeric $\alpha\beta$ or $\gamma\delta$ forms. However, recombinant TCRs consisting of $\alpha\alpha$ or $\beta\beta$ homodimers have previously been shown to bind to peptide MHC molecules. Therefore, one embodiment of the invention is provided by TCR $\alpha\alpha$ or TCR $\beta\beta$ homodimers.

15

Further preferred embodiments are provided by TCRs of the invention comprising the alpha chain variable region amino acid sequence and the beta chain variable region amino acid sequence combinations listed below, phenotypically silent variants of such TCRs also form part of this invention:

20

Alpha chain variable region sequence, SEQ ID NO:	Beta chain variable region sequence, SEQ ID NO:
1	2
1	14
1	15
11	2
12	2
13	2
12	15
13	15

12	14
13	14

In another preferred embodiment TCRs of the invention comprising the variable region combinations detailed above further comprise the alpha chain constant domain amino acid sequence shown in Figure 8a (SEQ ID NO: 19) and one of the beta chain amino acid constant domain sequences shown in Figures 8b and 8c (SEQ ID NOs: 20 and 21) or phenotypically silent variants thereof.

As used herein the term “phenotypically silent variants” is understood to refer to those TCRs which have a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or have an off-rate (k_{off}) of $1 \times 10^{-3} \text{ s}^{-1}$ or slower. For example, as is known to those skilled in the art, it may be possible to produce TCRs that incorporate minor changes in the constant domain and/or variable regions thereof compared to those detailed above without altering the affinity and/or off-rate for the interaction with the SLYNTVATL-HLA-A*0201 complex. Such trivial variants are included in the scope of this invention. Those TCRs in which one or more conservative substitutions have been made also form part of this invention.

In one broad aspect, the TCRs of the invention are in the form of either single chain TCRs (scTCRs) or dimeric TCRs (dTCRs) as described in WO 04/033685 and WO 03/020763.

A suitable scTCR form comprises a first segment constituted by an amino acid sequence corresponding to a TCR α chain variable region, a second segment constituted by an amino acid sequence corresponding to a TCR β chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR β chain constant domain extracellular sequence, and a linker sequence linking the C terminus of the first segment to the N terminus of the second segment.

Alternatively the first segment may be constituted by an amino acid sequence corresponding to a TCR β chain variable region, the second segment may be constituted by an amino acid sequence corresponding to a TCR α chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant domain extracellular sequence

The above scTCRs may further comprise a disulfide bond between the first and second chains, said disulfide bond being one which has no equivalent in native $\alpha\beta$ T cell receptors, and wherein the length of the linker sequence and the position of the disulfide bond being such that the variable domain sequences of the first and second segments are mutually orientated substantially as in native $\alpha\beta$ T cell receptors.

More specifically the first segment may be constituted by an amino acid sequence corresponding to a TCR α chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant domain extracellular sequence, the second segment may be constituted by an amino acid sequence corresponding to a TCR β chain variable region fused to the N terminus of an amino acid sequence corresponding to TCR β chain constant domain extracellular sequence, and a disulfide bond may be provided between the first and second chains, said disulfide bond being one which has no equivalent in native $\alpha\beta$ T cell receptors.

In the above scTCR forms, the linker sequence may link the C terminus of the first segment to the N terminus of the second segment, and may have the formula -PGGG-(SGGGG)_n-P- wherein n is 5 or 6 and P is proline, G is glycine and S is serine.

-PGGG-SGGGSGGGGSGGGGSGGGGSGGGG-P (SEQ ID NO: 17)

-PGGG-SGGGSGGGGSGGGGSGGGGSGGGGSGGGG-P (SEQ ID NO: 18)

A suitable dTCR form of the TCRs of the present invention comprises

a first polypeptide wherein a sequence corresponding to a TCR α chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant domain extracellular sequence, and a second polypeptide wherein a sequence corresponding to a TCR β chain variable region sequence fused to the N terminus a sequence corresponding to a TCR β chain constant domain extracellular sequence, the first and second polypeptides being linked by a disulfide bond which has no equivalent in native $\alpha\beta$ T cell receptors.

The first polypeptide may comprise a TCR α chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant domain extracellular sequence, and a second polypeptide wherein a sequence corresponding to a TCR β chain variable region sequence is fused to the N terminus a sequence corresponding to a TCR β chain constant domain extracellular sequence, the first and second polypeptides being linked by a disulfide bond between cysteine residues substituted for Thr 48 of exon 1 of TRAC*01 and Ser 57 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof. ("TRAC" etc. nomenclature herein as per T cell receptor Factsbook, (2001) LeFranc and LeFranc, Academic Press, ISBN 0-12-441352-8)

The dTCR or scTCR form of the TCRs of the invention may have amino acid sequences corresponding to human $\alpha\beta$ TCR extracellular constant domain and variable region sequences, and a disulfide bond may link amino acid residues of the said constant domain sequences, which disulfide bond has no equivalent in native TCRs. The disulfide bond is between cysteine residues corresponding to amino acid residues whose β carbon atoms are less than 0.6 nm apart in native TCRs, for example between cysteine residues substituted for Thr 48 of exon 1 of TRAC*01 and Ser 57 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof. Other sites where cysteines can be introduced to form the disulfide bond are the following residues in exon 1 of TRAC*01 for the TCR α chain and TRBC1*01 or TRBC2*01 for the TCR β chain:

TCR α chain	TCR β chain	Native β carbon separation (nm)
Thr 45	Ser 77	0.533
Tyr 10	Ser 17	0.359
Thr 45	Asp 59	0.560
Ser 15	Glu 15	0.59

In addition to the non-native disulfide bond referred to above, the dTCR or scTCR form of the TCRs of the invention may include a disulfide bond between residues corresponding to those linked by a disulfide bond in native TCRs.

The dTCR or scTCR form of the TCRs of the invention preferably does not contain a sequence corresponding to transmembrane or cytoplasmic sequences of native TCRs.

TCRs of the invention bind strongly to the SLYNTVATL-HLA-A2*0201. These TCRs also bind to an altered, but still useful, extent to naturally occurring variants of the HIV Gag-derived SLYNTVATL when loaded by HLA-A*0201. Variants of the SLYNTVATL which have been isolated from AIDs patients include the following (Sewell *et al.*, (1997) *Eur J Immunol.* **27**: 2323-2329):

SLENTVATL
 SLENTVAVL
 20 SLSNTVATL
 SSENTVATL
 SLLNTVATL
 SLYNTIATL
 SLYNTIAVL
 25 SLENTIATL
 SLENTIAVL
 SLENFVATL

The mutated amino acids are underlined.

PEGylated TCR Monomers

5 In one particular embodiment a TCR of the invention is associated with at least one polyalkylene glycol chain(s). This association may be caused in a number of ways known to those skilled in the art. In a preferred embodiment the polyalkylene chain(s) is/are covalently linked to the TCR. In a further embodiment the polyethylene glycol chains of the present aspect of the invention comprise at least two polyethylene
10 repeating units.

Multivalent TCR Complexes

15 One aspect of the invention provides a multivalent TCR complex comprising at least two TCRs of the invention. In one embodiment of this aspect, at least two TCR molecules are linked via linker moieties to form multivalent complexes. Preferably the complexes are water soluble, so the linker moiety should be selected accordingly. Furthermore, it is preferable that the linker moiety should be capable of attachment to
20 defined positions on the TCR molecules, so that the structural diversity of the complexes formed is minimised. One embodiment of the present aspect is provided by a TCR complex of the invention wherein the polymer chain or peptidic linker sequence extends between amino acid residues of each TCR which are not located in a variable region sequence of the TCR.

25 Since the complexes of the invention may be for use in medicine, the linker moieties should be chosen with due regard to their pharmaceutical suitability, for example their immunogenicity.

30 Examples of linker moieties which fulfil the above desirable criteria are known in the art, for example the art of linking antibody fragments.

There are two classes of linker that are preferred for use in the production of multivalent TCR molecules of the present invention. A TCR complex of the invention in which the TCRs are linked by a polyalkylene glycol chain provides one
5 embodiment of the present aspect.

The first are hydrophilic polymers such as polyalkylene glycols. The most commonly used of this class are based on polyethylene glycol or PEG, the structure of which is shown below.

10



Wherein n is greater than two. However, others are based on other suitable, optionally substituted, polyalkylene glycols include polypropylene glycol, and copolymers of
15 ethylene glycol and propylene glycol.

Such polymers may be used to treat or conjugate therapeutic agents, particularly polypeptide or protein therapeutics, to achieve beneficial changes to the PK profile of the therapeutic, for example reduced renal clearance, improved plasma half-life,
20 reduced immunogenicity, and improved solubility. Such improvements in the PK profile of the PEG-therapeutic conjugate are believed to result from the PEG molecule or molecules forming a 'shell' around the therapeutic which sterically hinders the reaction with the immune system and reduces proteolytic degradation. (Casey *et al*, (2000) Tumor Targeting 4 235-244) The size of the hydrophilic polymer used may in
25 particular be selected on the basis of the intended therapeutic use of the TCR complex. There are numerous review papers and books that detail the use of PEG and similar molecules in pharmaceutical formulations. For example, see Harris (1992) Polyethylene Glycol Chemistry - Biotechnical and Biomedical Applications, Plenum, New York, NY. or Harris & Zalipsky (1997) Chemistry and Biological Applications
30 of Polyethylene Glycol ACS Books, Washington, D.C.

The polymer used can have a linear or branched conformation. Branched PEG molecules, or derivatives thereof, can be induced by the addition of branching moieties including glycerol and glycerol oligomers, pentaerythritol, sorbitol and lysine.

5 Usually, the polymer will have a chemically reactive group or groups in its structure, for example at one or both termini, and/or on branches from the backbone, to enable the polymer to link to target sites in the TCR. This chemically reactive group or groups may be attached directly to the hydrophilic polymer, or there may be a spacer group/moiety between the hydrophilic polymer and the reactive chemistry as shown
10 below:

Reactive chemistry-Hydrophilic polymer-Reactive chemistry

Reactive chemistry-Spacer-Hydrophilic polymer-Spacer-Reactive chemistry

15

The spacer used in the formation of constructs of the type outlined above may be any organic moiety that is a non-reactive, chemically stable, chain. Such spacers include, by are not limited to the following:

$-(\text{CH}_2)_n-$ wherein $n = 2$ to 5

20

$-(\text{CH}_2)_3\text{NHCO}(\text{CH}_2)_2$

A TCR complex of the invention in which a divalent alkylene spacer radical is located between the polyalkylene glycol chain and its point of attachment to a TCR of the complex provides a further embodiment of the present aspect.

25

A TCR complex of the invention in which the polyalkylene glycol chain comprises at least two polyethylene glycol repeating units provides a further embodiment of the present aspect.

30

There are a number of commercial suppliers of hydrophilic polymers linked, directly or via a spacer, to reactive chemistries that may be of use in the present invention.

These suppliers include Nektar Therapeutics (CA, USA), NOF Corporation (Japan), Sunbio (South Korea) and Enzon Pharmaceuticals (NJ, USA).

- 5 Commercially available hydrophilic polymers linked, directly or via a spacer, to reactive chemistries that may be of use in the present invention include, but are not limited to, the following:

PEG linker Description	Source of PEG	Catalogue Number
TCR Monomer attachment		
5K linear (Maleimide)	Nektar	2D2MOHO1
20K linear (Maleimide)	Nektar	2D2MOPO1
20K linear (Maleimide)	NOF Corporation	SUNBRIGHT ME-200MA
20K branched (Maleimide)	NOF Corporation	SUNBRIGHT GL2-200MA
30K linear (Maleimide)	NOF Corporation	SUNBRIGHT ME-300MA
40K branched PEG (Maleimide)	Nektar	2D3XOTO1
5K-NP linear (for Lys attachment)	NOF Corporation	SUNBRIGHT MENP-50H
10K-NP linear (for Lys attachment)	NOF Corporation	SUNBRIGHT MENP-10T
20K-NP linear (for Lys attachment)	NOF Corporation	SUNBRIGHT MENP-20T
TCR dimer linkers		
3.4K linear (Maleimide)	Nektar	2D2DOFO2
5K forked (Maleimide)	Nektar	2D2DOHOF
10K linear (with orthopyridyl ds-linkers in place of Maleimide)	Sunbio	
20K forked (Maleimide)	Nektar	2D2DOPOF
20K linear (Maleimide)	NOF Corporation	
40K forked (Maleimide)	Nektar	2D3XOTOF
Higher order TCR multimers		
15K, 3 arms, Mal ₃ (for trimer)	Nektar	OJOONO3
20K, 4 arms, Mal ₄ (for tetramer)	Nektar	OJOOP04
40 K, 8 arms, Mal ₈ (for octamer)	Nektar	OJOOTO8

A wide variety of coupling chemistries can be used to couple polymer molecules to protein and peptide therapeutics. The choice of the most appropriate coupling chemistry is largely dependant on the desired coupling site. For example, the following coupling chemistries have been used attached to one or more of the termini of PEG molecules (Source: Nektar Molecular Engineering Catalogue 2003):

N-maleimide
Vinyl sulfone
Benzotriazole carbonate
Succinimidyl propionate
Succinimidyl butanoate
Thio-ester
Acetaldehydes
Acrylates
Biotin
Primary amines

As stated above non-PEG based polymers also provide suitable linkers for multimerising the TCRs of the present invention. For example, moieties containing maleimide termini linked by aliphatic chains such as BMH and BMOE (Pierce, products Nos. 22330 and 22323) can be used.

Peptidic linkers are the other class of TCR linkers. These linkers are comprised of chains of amino acids, and function to produce simple linkers or multimerisation domains onto which TCR molecules can be attached. The biotin / streptavidin system has previously been used to produce TCR tetramers (see WO/99/60119) for in-vitro binding studies. However, streptavidin is a microbially-derived polypeptide and as such not ideally suited to use in a therapeutic.

A TCR complex of the invention in which the TCRs are linked by a peptidic linker derived from a human multimerisation domain provides a further embodiment of the present aspect.

- 5 There are a number of human proteins that contain a multimerisation domain that could be used in the production of multivalent TCR complexes. For example the tetramerisation domain of p53 which has been utilised to produce tetramers of scFv antibody fragments which exhibited increased serum persistence and significantly reduced off-rate compared to the monomeric scFV fragment. (Willuda *et al.* (2001) J. Biol. Chem. 276 (17) 14385-14392) Haemoglobin also has a tetramerisation domain
10 that could potentially be used for this kind of application.

- A multivalent TCR complex of the invention comprising at least two TCRs provides a final embodiment of this aspect, wherein at least one of said TCRs is associated with a
15 therapeutic agent.

- In one aspect a TCR (or multivalent complex thereof) of the present invention may alternatively or additionally comprise a reactive cysteine at the C-terminal or N-terminal of the alpha or beta chains thereof.

20

Diagnostic and therapeutic Use

- In one aspect the TCR of the invention may be associated with a therapeutic agent or detectable moiety. For example, said therapeutic agent or detectable moiety may be
25 covalently linked to the TCR.

In one embodiment of the invention said therapeutic agent or detectable moiety is covalently linked to the C-terminus of one or both TCR chains.

- 30 In one aspect the scTCR or one or both of the dTCR chains of TCRs of the present invention may be labelled with an detectable moiety, for example a label that is

suitable for diagnostic purposes. Such labelled TCRs are useful in a method for detecting a SLYNTVATL-HLA-A*0201 complex which method comprises contacting the TCR ligand with a TCR (or a multimeric high affinity TCR complex) which is specific for the TCR ligand; and detecting binding to the TCR ligand. In tetrameric
5 TCR complexes formed for example, using biotinylated heterodimers, fluorescent streptavidin can be used to provide a detectable label. Such a fluorescently-labelled TCR tetramer is suitable for use in FACS analysis, for example to detect antigen presenting cells carrying the SLYNTVATL-HLA-A*0201 complex for which these high affinity TCRs are specific.

10 Another manner in which the soluble TCRs of the present invention may be detected is by the use of TCR-specific antibodies, in particular monoclonal antibodies. There are many commercially available anti-TCR antibodies, such as α F1 and β F1, which recognise the constant domains of the α and β chains, respectively.

15 In a further aspect a TCR (or multivalent complex thereof) of the present invention may alternatively or additionally be associated with (e.g. covalently or otherwise linked to) a therapeutic agent which may be, for example, a toxic moiety for use in cell killing, or an immune effector molecule such as an interleukin or a cytokine. A
20 multivalent TCR complex of the invention may have enhanced binding capability for a TCR ligand compared to a non-multimeric wild-type or T cell receptor heterodimer of the invention. Thus, the multivalent TCR complexes according to the invention are particularly useful for tracking or targeting cells presenting SLYNTVATL-HLA-A*0201 complexes *in vitro* or *in vivo*, and are also useful as intermediates for the
25 production of further multivalent TCR complexes having such uses. These TCRs or multivalent TCR complexes may therefore be provided in a pharmaceutically acceptable formulation for use *in vivo*.

30 The invention also provides a method for delivering a therapeutic agent to a target cell, which method comprises contacting potential target cells with a TCR or multivalent TCR complex in accordance with the invention under conditions to allow attachment

of the TCR or multivalent TCR complex to the target cell, said TCR or multivalent TCR complex being specific for the SLYNTVATL-HLA-A*0201 complex and having the therapeutic agent associated therewith.

5 In particular, the soluble TCR or multivalent TCR complex of the present invention can be used to deliver therapeutic agents to the location of cells presenting a particular antigen. This would be useful in many situations and, in particular, against HIV infected cells. A therapeutic agent could be delivered such that it would exercise its effect locally but not only on the cell it binds to. Thus, one particular strategy
10 envisages cytotoxic or immuno-stimulatory molecules linked to TCRs or multivalent TCR complexes according to the invention specific for the SLYNTVATL-HLA-A*0201 complex.

Many therapeutic agents could be employed for this use, for instance radioactive
15 compounds, enzymes (perforin for example) or chemotherapeutic agents (cis-platin for example). To ensure that toxic effects are exercised in the desired location the toxin could be inside a liposome linked to streptavidin so that the compound is released slowly. This will prevent damaging effects during the transport in the body and ensure that the toxin has maximum effect after binding of the TCR to the relevant antigen
20 presenting cells.

Other suitable therapeutic agents include:

- small molecule cytotoxic agents, i.e. compounds with the ability to kill mammalian cells having a molecular weight of less than 700 daltons. Such
25 compounds could also contain toxic metals capable of having a cytotoxic effect. Furthermore, it is to be understood that these small molecule cytotoxic agents also include pro-drugs, i.e. compounds that decay or are converted under physiological conditions to release cytotoxic agents. Examples of such agents include cis-platin, maytansine derivatives, rachelmycin, calicheamicin,
30 docetaxel, etoposide, gemcitabine, ifosfamide, irinotecan, melphalan,

- mitoxantrone, sorfimer sodiumphotofrin II, temozolmide, topotecan, trimetreate glucuronate, auristatin E vincristine and doxorubicin;
- peptide cytotoxins, i.e. proteins or fragments thereof with the ability to kill mammalian cells. Including but not limited to, ricin, diphtheria toxin, pseudomonas bacterial exotoxin A, DNAase and RNAase;
 - radio-nuclides, i.e. unstable isotopes of elements which decay with the concurrent emission of one or more of α or β particles, or γ rays. including but not limited to, iodine 131, rhenium 186, indium 111, yttrium 90, bismuth 210 and 213, actinium 225 and astatine 213; chelating agents may be used to facilitate the association of these radio-nuclides to the high affinity TCRs, or multimers thereof;
 - prodrugs, including but not limited to, antibody directed enzyme pro-drugs;
 - immuno-stimulants, i.e. moieties which stimulate immune response. Including but not limited to, cytokines such as IL-2 and IFN, Superantigens and mutants thereof, TCR-HLA fusions and chemokines such as IL-8, platelet factor 4, melanoma growth stimulatory protein, etc, antibodies or fragments thereof, complement activators, xenogeneic protein domains, allogeneic protein domains, viral/bacterial protein domains, viral/bacterial peptides and anti-T cell determinant antibodies (e.g. anti-CD3 or anti-CD28) or antibody analogues such as Nanobodies™ and Affybodies™.

Soluble TCRs or multivalent TCR complexes of the invention may be linked to an enzyme capable of converting a prodrug to a drug. This allows the prodrug to be converted to the drug only at the site where it is required (i.e. targeted by the sTCR).

It is expected that the high affinity SLYNTVATL (SEQ ID NO: 16)-HLA-A*0201 specific TCRs disclosed herein may be used in methods for the diagnosis and treatment of AIDS.

For treatment, therapeutic agent localisation in the vicinity of HIV infected (CD4⁺) cells would enhance the effect of toxins or immunostimulants. For vaccine delivery,

the vaccine antigen could be localised in the vicinity of antigen presenting cells, thus enhancing the efficacy of the antigen. The method can also be applied for imaging purposes.

- 5 One embodiment is provided by a membrane preparation comprising a TCR of the invention. Said membrane preparation may be prepared from cells or may comprise a synthetic membrane.

- 10 Another embodiment is provided by a cell harbouring an expression vector comprising nucleic acid encoding a TCR of the invention. For example, said cell may be a T cell.

Further embodiments of the invention are provided by a pharmaceutical composition comprising:

- 15 a TCR or a multivalent TCR complex of the invention (optionally associated with a therapeutic agent), or a membrane preparation comprising a TCR of the invention, or a plurality of cells harbouring an expression vector comprising nucleic acid encoding a TCR of the invention, together with a pharmaceutically acceptable carrier;

- 20 The invention also provides a method of treatment of AIDS comprising administering to a subject suffering such AIDS an effective amount of a TCR or a multivalent TCR complex of the invention, or a membrane preparation comprising a TCR of the invention, or a plurality of cells harbouring an expression vector comprising nucleic acid encoding a TCR of the invention. In a related embodiment the invention provides
25 for the use of a TCR or a multivalent TCR complex of the invention, or a membrane preparation comprising a TCR of the invention, or a plurality of cells harbouring an expression vector comprising nucleic acid encoding a TCR of the invention, in the preparation of a composition for the treatment of AIDS. Further specific embodiments of these uses and methods of the invention are provided wherein the TCR, or
30 multivalent TCR complex of the invention, or a membrane preparation comprising a TCR of the invention is administered in a form which is associated with a therapeutic

agent. In other preferred embodiments the cells harbouring an expression vector comprising nucleic acid encoding a TCR of the invention are CD8⁺ T cells.

Therapeutic or imaging TCRs in accordance with the invention will usually be supplied
5 as part of a sterile, pharmaceutical composition which will normally include a
pharmaceutically acceptable carrier. This pharmaceutical composition may be in any
suitable form, (depending upon the desired method of administering it to a patient). It
may be provided in unit dosage form, will generally be provided in a sealed container and
may be provided as part of a kit. Such a kit would normally (although not necessarily)
10 include instructions for use. It may include a plurality of said unit dosage forms.

Without wishing to be limited by theory, it is expected that the TCRs of the invention
will provide effective targeting agents capable of delivering therapeutic agents such as
immunostimulants and/or cytotoxic agents to HIV infected (CD4⁺) cells. In particular, it
15 is expected that the administration of the TCRs of the present invention when associated
with immunostimulants and/or cytotoxic agents in combination with conventional anti-
retrovirus drug therapies and/or IL-2 treatment will be able to target HIV infected cells.

The following is a list of anti-retroviral drugs currently approved for use in the US:
20

Agenerase (amprenavir) - protease inhibitor
Combivir - combination of Retrovir (300mg) and Epivir (150mg)
Crixivan (indinavir) - protease inhibitor
Epivir (3tc / lamivudine) - nucleoside analog reverse transcriptase inhibitor
25 Epzicom (a combination of 2 nucleoside reverse transcriptase inhibitors (NRTIs in the
same pill; 600mg of Ziagen (abacavir) and 300mg of Epivir (3TC).
Emtriva [emtricitabine (FTC)]
Fortovase (saquinavir) - protease inhibitor
Fuzeon (enfuvirtide) - Fusion inhibitor
30 Hivid (ddc / zalcitabine) - nucleoside analog reverse transcriptase inhibitor
Invirase (saquinavir) - protease inhibitor

- Kaletra (lopinavir) - protease inhibitor
 Lexiva (Fosamprenavir) - Protease Inhibitor approved 10/20/03
 Norvir (ritonavir) - protease inhibitor
 Rescriptor (delavirdine) - non nucleoside analog reverse transcriptase inhibitor
 5 Retrovir, AZT (zidovudine) - nucleoside analog reverse transcriptase inhibitor
 Reyataz (atazanavir; BMS-232632) - protease inhibitor
 Sustiva (efavirenz) - non nucleoside analog reverse transcriptase inhibitor
 Trizivir (3 non nucleosides in one tablet; abacavir + zidovudine + lamivudine
 Truvada (Emtricitabine + Tenofovir DF)
 10 Videx (ddl / didanosine) nucleoside analog reverse transcriptase inhibitor
 Videx EC; (ddl / didanosine) nucleoside analog reverse transcriptase inhibitor;
 Viracept (nelfinavir) - protease inhibitor
 Viramune (nevirapine) - non nucleoside analog Reverse transcriptase inhibitor
 Viread (tenofovir disoproxil fumarate) Nucleotide Reverse transcriptase inhibitor
 15 (Adenosine Class)
 Zerit (d4t / stavudine) - nucleoside analog reverse transcriptase inhibitor
 Ziagen (abacavir) - nucleoside analog reverse transcriptase inhibitor
- The pharmaceutical composition may be adapted for administration by any appropriate
 20 route, for example parenteral, transdermal or via inhalation, preferably a parenteral
 (including subcutaneous, intramuscular, or, most preferably intravenous) route. Such
 compositions may be prepared by any method known in the art of pharmacy, for example
 by mixing the active ingredient with the carrier(s) or excipient(s) under sterile conditions.
- 25 Dosages of the substances of the present invention can vary between wide limits,
 depending upon the disease or disorder to be treated, the age and condition of the
 individual to be treated, etc. and a physician will ultimately determine appropriate
 dosages to be used.

Additional Aspects

A scTCR or dTCR (which preferably is constituted by constant and variable sequences corresponding to human sequences) of the present invention may be provided in
5 substantially pure form, or as a purified or isolated preparation. For example, it may be provided in a form which is substantially free of other proteins.

The sequence(s) of the nucleic acid or nucleic acids encoding the TCRs of the invention may be altered so as to optimise the level of expression obtained in the host
10 cell. The host cell may be any appropriate prokaryotic or eukaryotic cell. For example, the host cell may be an *E.coli* cell or a human T cell. The alterations made to these genetic sequences are silent, that is they do not alter the amino acid sequence encoded. There are a number of companies which offer such expression optimisation services, including, GeneArt, Germany.

15 The invention also provides a method of producing a high affinity TCR having the property of binding to SLYNTVATL-HLA-A*0201. CHARACTERISED IN THAT the TCR (i) comprises at least one TCR α chain variable domain and/or at least one TCR β chain variable domain and (ii) has a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or an off-rate (k_{off}) for the
20 SLYNTVATL-HLA-A*0201 complex of $1 \times 10^{-3} \text{ s}^{-1}$ or slower, wherein the method comprises:

(a) the production of a TCR comprising the α and β chain variable domains
25 of the parental HIV Gag TCR wherein one or both of the α and β chain variable domains comprise a mutation(s) in one or more of the amino acids identified in claims 7 and 8;

(b) contacting said mutated TCR with SLYNTVATL-HLA-A*0201 under conditions suitable to allow the binding of the TCR to SLYNTVATL-HLA-A*0201;
30

and measuring the K_D and/or k_{off} of the interaction.

Preferred features of each aspect of the invention are as for each of the other aspects *mutatis mutandis*. The prior art documents mentioned herein are incorporated to the fullest extent permitted by law.

5

Examples

The invention is further described in the following examples, which do not limit the scope of the invention in any way.

10

Reference is made in the following to the accompanying drawings in which:

Figure 1a and 1b details the alpha chain variable domain amino acid and beta chain variable domain amino acid sequences of the parental HIV Gag TCR respectively.

15

Figures 2a and 2b show respectively the DNA sequence of soluble versions of the parental HIV Gag TCR α and β chains.

Figures 3a and 3b show respectively the HIV Gag TCR α and β chain extracellular amino acid sequences produced from the DNA sequences of Figures 2a and 2b.

20

Figures 4a and 4b show respectively the DNA sequence of soluble versions of the HIV Gag TCR α and β chains mutated to encode additional cysteine residues to form a non-native disulfide bond. The mutated codon is indicated by shading and The introduced restriction enzyme recognition sites are underlined..

25

Figures 5a and 5b show respectively the HIV Gag TCR α and β chain extracellular amino acid sequences produced from the DNA sequences of Figures 4a and 4b. The introduced cysteine in each chain is indicated by shading.

30

Figure 6 details the alpha chain variable domain amino acid sequences of the high affinity HIV Gag TCR variants.

5 Figure 7 details the beta chain variable domain amino acid sequences of the high affinity HIV Gag TCR variants.

Figure 8a details the amino acid sequence of a soluble portion of TRAC.

10 Figure 8b details the amino acid sequence of a soluble portion of TRBC1.
.

Figure 8c details the amino acid sequence of a soluble portion of TRBC2.

Figure 9 details the DNA sequence of the pEX954 plasmid.

15 Figure 10 details the DNA sequence of the pEX821 plasmid.

Figure 11 details the beta chain amino acid sequences of the parental soluble HIV Gag TCR variant fused via a peptide linker to wild-type human IL-2. The amino acids of the linker and IL-2 are indicated in italics.

20

Figure 12 provides the Biacore response curves generated for the interaction of the soluble disulfide-linked parental HIV Gag TCR and the SLYNTVATL-HLA-A*0201 complex.

25 Figure 13 provides a plasmid map of the pEX954 plasmid.

Figure 14 provides a plasmid map of the pEX821 plasmid.

30 Figure 15a provides the full-length DNA sequence of the parental HIV Gag TCR α chain optimised for expression in human T cells.

Figure 15b provides the full-length DNA sequence of the parental HIV Gag TCR β chain optimised for expression in human T cells.

5 Figure 16a provides the full-length amino acid sequence of the parental HIV Gag TCR α chain.

Figure 16b provides the full-length amino acid sequence of the parental HIV Gag TCR β chain optimised for expression in human T cells.

10 Figures 17a provides FACS analysis data for untransduced control CD8⁺ T cells.

Figure 17b provides FACS analysis data demonstrating expression of the parental HIV Gag TCR on the surface of transduced CD8⁺ T cells.

15 Figures 18a and 18b provide the amino acids sequences of the alpha and beta chains of a soluble disulfide-linked high affinity c11c6 HIV Gag TCR.respectively.

20 Figure 19 demonstrates the ability of soluble disulfide-linked high affinity c11c6 HIV Gag TCRs to inhibit the activation of the SLYNTVATL-HLA-A*0201 reactive OX84 polyclonal T cell line in the presence of To cells infected with HIV as measured by IFN- γ and TNF- α production.

25 Figure 20 demonstrates the ability of soluble disulfide-linked high affinity c11c6 HIV Gag TCRs to inhibit the activation of the SLYNTVATL-HLA-A*0201 reactive OX84 polyclonal T cell line in the presence of SLYNTVATL peptide-pulsed uninfected To cells as measured by IFN- γ and TNF- α production.

Figure 21 demonstrates the ability of soluble disulfide-linked high affinity c11c6 HIV Gag TCRs to stain SLYNTVATL peptide-pulsed T2 cells.

Example 1 – Production of soluble disulfide-linked TCRs comprising the parental HIV Gag TCR variable regions

5 Figures 4a and 4b provide the DNA sequences of soluble disulfide-linked alpha beta chains from a parental TCR which is specific for the SLYNTVATL-HLA-A*0201 complex. These DNA sequences can be synthesis de-novo by a number of contract research companies, for example GeneArt (Germany). Restriction enzyme recognition sites are also added to these DNA sequences in order to facilitate ligation of these
10 DNA sequences into the pGMT7-based expression plasmids, which contain the T7 promoter for high level expression in E.coli strain BL21-DE3(pLysS) (Pan *et al.*, *Biotechniques* (2000) **29** (6): 1234-8)

15 The TCR alpha chain sequences contain introduced *ClaI* and *SalII* restriction enzyme recognition sites and this sequence was ligated into pEX954 (see Figures 9 and 13) cut with *ClaI* and *XhoI*.

20 The TCR beta chain sequences contain introduced *AseI* and *AgeI* restriction enzyme recognition sites and were ligated into pEX821 (see Figures 10 and 14) cut with *NdeI/AgeI*.

Restriction enzyme recognition sites as introduced into DNA encoding the TCR chains

25 *ClaI* - ATCGAT
 SalII - GTCGAC
 AseI - ATTAAT
 AgeI - ACCGGT

Ligation

30 The cut TCR alpha and beta chain DNA and cut vector were ligated using a rapid DNA ligation kit (Roche) following the manufacturers instructions.

Ligated plasmids were transformed into competent E.coli strain XL1-blue cells and plated out on LB/agar plates containing 100mg/ml ampicillin. Following incubation overnight at 37°C, single colonies were picked and grown in 10 ml LB containing
5 100mg/ml ampicillin overnight at 37°C with shaking. Cloned plasmids were purified using a Miniprep kit (Qiagen) and the insert was sequenced using an automated DNA sequencer (Lark Technologies).

Figures 5a and 5b show respectively the soluble disulfide linked parental HIV gag
10 TCR α and β chain extracellular amino acid sequences produced from the DNA sequences of Figures 4a and 4b

*Example 2- Production of high affinity variants of the soluble disulfide linked HIV
Gag TCR*

15 The soluble disulfide-linked native HIV Gag TCR produced as described in Example 1 can be used a template from which to produce the TCRs of the invention which have an increased affinity for the SLYNTVATL (SEQ ID NO: 16) -HLA-A*0201 complex.

20 Phage display is one means by which libraries of HIV Gag TCR variants can be generated in order to identify high affinity mutants. For example, the TCR phage display and screening methods described in (Li *et al.*, (2005) *Nature Biotech* **23** (3): 349-354) can be adapted and applied to HIV Gag TCRs.

25 The amino sequences of the mutated TCR alpha and beta chain variable domains which, when combined with an appropriate TCR chain, demonstrate high affinity for the SLYNTVATL-HLA-A*0201 complex, are listed in Figures 6 and 7 respectively. (SEQ ID Nos: 11-13 and 14-15 respectively) As is known to those skilled in the art the necessary codon changes required to produce these mutated chains can be introduced
30 into the DNA encoding these chains by site-directed mutagenesis. (QuickChangeTM Site-Directed Mutagenesis Kit from Stratagene)

Briefly, this is achieved by using primers that incorporate the desired codon change(s) and the plasmids containing the relevant TCR chain DNA as a template for the mutagenesis:

5

Mutagenesis was carried out using the following conditions : 50ng plasmid template, 1µl of 10mM dNTP, 5 µl of 10x Pfu DNA polymerase buffer as supplied by the manufacturer, 25 pmol of fwd primer, 25 pmol of rev primer, 1µl pfu DNA polymerase in total volume 50 µl. After an initial denaturation step of 2 mins at 95C, the reaction was subjected to 25 cycles of denaturation (95C, 10 secs), annealing (55C 10 secs), and elongation (72C, 8 mins). The resulting product was digested with DpnI restriction enzyme to remove the template plasmid and transformed into E. coli strain XL1-blue. Mutagenesis was verified by sequencing.

15

Example 3 – Expression, refolding and purification of soluble TCR

The expression plasmids containing the mutated α -chain and β -chain respectively as prepared in Examples 1 or 2 were transformed separately into *E.coli* strain BL21pLysS, and single ampicillin-resistant colonies were grown at 37°C in TYP (ampicillin 100µg/ml) medium to OD₆₀₀ of 0.4 before inducing protein expression with 0.5mM IPTG. Cells were harvested three hours post-induction by centrifugation for 30 minutes at 4000rpm in a Beckman J-6B. Cell pellets were re-suspended in a buffer containing 50mM Tris-HCl, 25% (w/v) sucrose, 1mM NaEDTA, 0.1% (w/v) NaAzide, 10mM DTT, pH 8.0. After an overnight freeze-thaw step, re-suspended cells were sonicated in 1 minute bursts for a total of around 10 minutes in a Milsonix XL2020 sonicator using a standard 12mm diameter probe. Inclusion body pellets were recovered by centrifugation for 30 minutes at 13000rpm in a Beckman J2-21 centrifuge. Three detergent washes were then carried out to remove cell debris and membrane components. Each time the inclusion body pellet was homogenised in a Triton buffer (50mM Tris-HCl, 0.5% Triton-X100, 200mM NaCl, 10mM NaEDTA,

30

0.1% (w/v) NaAzide, 2mM DTT, pH 8.0) before being pelleted by centrifugation for 15 minutes at 13000rpm in a Beckman J2-21. Detergent and salt was then removed by a similar wash in the following buffer: 50mM Tris-HCl, 1mM NaEDTA, 0.1% (w/v) NaAzide, 2mM DTT, pH 8.0. Finally, the inclusion bodies were divided into 30 mg aliquots and frozen at -70°C. Inclusion body protein yield was quantitated by solubilising with 6M guanidine-HCl and measurement with a Bradford dye-binding assay (PerBio).

Approximately 30mg of TCR β chain and 60mg of TCR α chain solubilised inclusion bodies were thawed from frozen stocks, samples were then mixed and the mixture diluted into 15ml of a guanidine solution (6 M Guanidine-hydrochloride, 10mM Sodium Acetate, 10mM EDTA), to ensure complete chain de-naturation. The guanidine solution containing fully reduced and denatured TCR chains was then injected into 1 litre of the following refolding buffer: 100mM Tris pH 8.5, 400mM L-Arginine, 2mM EDTA, 5mM reduced Glutathione, 0.5mM oxidised Glutathione, 5M urea, 0.2mM PMSF. The redox couple (2-mercaptoethylamine and cystamine (to final concentrations of 6.6mM and 3.7mM, respectively) were added approximately 5 minutes before addition of the denatured TCR chains. The solution was left for 5 hrs \pm 15minutes. The refolded TCR was dialysed in Spectrapor 1 membrane (Spectrum; Product No. 132670) against 10 L 10 mM Tris pH 8.1 at 5°C \pm 3°C for 18-20 hours. After this time, the dialysis buffer was changed to fresh 10 mM Tris pH 8.1 (10 L) and dialysis was continued at 5°C \pm 3°C for another 20-22 hours.

sTCR was separated from degradation products and impurities by loading the dialysed refold onto a POROS 50HQ anion exchange column and eluting bound protein with a gradient of 0-500mM NaCl over 50 column volumes using an Akta purifier (Pharmacia). Peak fractions were stored at 4°C and analysed by Coomassie-stained SDS-PAGE before being pooled and concentrated. Finally, the sTCR was purified and characterised using a Superdex 200HR gel filtration column pre-equilibrated in HBS-EP buffer (10 mM HEPES pH 7.4, 150 mM NaCl, 3.5 mM EDTA, 0.05% nonidet p40). The peak eluting at a relative molecular weight of approximately 50 kDa was

pooled and concentrated prior to characterisation by BIAcore surface plasmon resonance analysis.

5 *Example 4 – Biacore surface plasmon resonance characterisation of sTCR binding to specific pMHC*

10 A surface plasmon resonance biosensor (Biacore 3000™) was used to analyse the binding of a sTCR to its peptide-MHC ligand. This was facilitated by producing single pMHC complexes (described below) which were immobilised to a streptavidin-coated binding surface in a semi-oriented fashion, allowing efficient testing of the binding of a soluble T-cell receptor to up to four different pMHC (immobilised on separate flow cells) simultaneously. Manual injection of HLA complex allows the precise level of immobilised class I molecules to be manipulated easily.

15 Biotinylated class I HLA-A*0201 molecules were refolded *in vitro* from bacterially-expressed inclusion bodies containing the constituent subunit proteins and synthetic peptide, followed by purification and *in vitro* enzymatic biotinylation (O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). HLA-A*0201-heavy chain was expressed with a C-terminal biotinylation tag which replaces the transmembrane and cytoplasmic domains of the protein in an appropriate construct. Inclusion body expression levels of ~75 mg/litre bacterial culture were obtained. The MHC light-chain or β 2-microglobulin was also expressed as inclusion bodies in *E. coli* from an appropriate construct, at a level of ~500 mg/litre bacterial culture.

25 *E. coli* cells were lysed and inclusion bodies are purified to approximately 80% purity. Protein from inclusion bodies was denatured in 6 M guanidine-HCl, 50 mM Tris pH 8.1, 100 mM NaCl, 10 mM DTT, 10 mM EDTA, and was refolded at a concentration of 30 mg/litre heavy chain, 30 mg/litre β 2m into 0.4 M L-Arginine-HCl, 100 mM Tris pH 8.1, 3.7 mM cystamine, 6.6 mM β -cysteamine, 4 mg/ml of the SLYNTVATL peptide required to be loaded by the HLA-A*0201 molecule, by addition of a single

30

pulse of denatured protein into refold buffer at $< 5^{\circ}\text{C}$. Refolding was allowed to reach completion at 4°C for at least 1 hour.

5 Buffer was exchanged by dialysis in 10 volumes of 10 mM Tris pH 8.1. Two changes of buffer were necessary to reduce the ionic strength of the solution sufficiently. The protein solution was then filtered through a $1.5\mu\text{m}$ cellulose acetate filter and loaded onto a POROS 50HQ anion exchange column (8 ml bed volume). Protein was eluted with a linear 0-500 mM NaCl gradient. HLA-A*0201-peptide complex eluted at approximately 250 mM NaCl, and peak fractions were collected, a cocktail of protease inhibitors (Calbiochem) was added and the fractions were chilled on ice.

10 Biotinylation tagged pMHC molecules were buffer exchanged into 10 mM Tris pH 8.1, 5 mM NaCl using a Pharmacia fast desalting column equilibrated in the same buffer. Immediately upon elution, the protein-containing fractions were chilled on ice and protease inhibitor cocktail (Calbiochem) was added. Biotinylation reagents were then added: 1 mM biotin, 5 mM ATP (buffered to pH 8), 7.5 mM MgCl_2 , and $5\mu\text{g/ml}$ BirA enzyme (purified according to O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). The mixture was then allowed to incubate at room temperature overnight.

20 The biotinylated pHLA-A*0201 molecules were purified using gel filtration chromatography. A Pharmacia Superdex 75 HR 10/30 column was pre-equilibrated with filtered PBS and 1 ml of the biotinylation reaction mixture was loaded and the column was developed with PBS at 0.5 ml/min. Biotinylated pHLA-A*0201 molecules eluted as a single peak at approximately 15 ml. Fractions containing protein were pooled, chilled on ice, and protease inhibitor cocktail was added. Protein concentration was determined using a Coomassie-binding assay (PerBio) and aliquots of biotinylated pHLA-A*0201 molecules were stored frozen at -20°C . Streptavidin was immobilised by standard amine coupling methods.

30 Such immobilised complexes are capable of binding both T-cell receptors and the coreceptor $\text{CD}8\alpha\alpha$, both of which may be injected in the soluble phase. Specific

binding of TCR is obtained even at low concentrations (at least 40µg/ml), implying the TCR is relatively stable. The pMHC binding properties of sTCR are observed to be qualitatively and quantitatively similar if sTCR is used either in the soluble or immobilised phase. This is an important control for partial activity of soluble species
5 and also suggests that biotinylated pMHC complexes are biologically as active as non-biotinylated complexes.

The interactions between HIV Gag sTCR containing a novel inter-chain bond and its ligand/ MHC complex or an irrelevant HLA-peptide combination, the production of
10 which is described above, were analysed on a Biacore 3000™ surface plasmon resonance (SPR) biosensor. SPR measures changes in refractive index expressed in response units (RU) near a sensor surface within a small flow cell, a principle that can be used to detect receptor ligand interactions and to analyse their affinity and kinetic parameters. The probe flow cells were prepared by immobilising the individual HLA-
15 peptide complexes in separate flow cells via binding between the biotin cross linked onto β2m and streptavidin which have been chemically cross linked to the activated surface of the flow cells. The assay was then performed by passing sTCR over the surfaces of the different flow cells at a constant flow rate, measuring the SPR response in doing so.

20

To measure Equilibrium binding constant

Serial dilutions of the parental or mutated HIV Gag sTCR were prepared and injected at constant flow rate of 5 µl min⁻¹ over two different flow cells; one coated with
25 ~1000 RU of specific SLYNTVATL-HLA-A*0201 complex, the second coated with ~1000 RU of non-specific HLA-A2 -peptide complex. Response was normalised for each concentration using the measurement from the control cell. Normalised data response was plotted versus concentration of TCR sample and fitted to a hyperbola in order to calculate the equilibrium binding constant, K_D. (Price & Dwek, Principles and
30 Problems in Physical Chemistry for Biochemists (2nd Edition) 1979, Clarendon Press, Oxford).

To measure Kinetic Parameters

5

For high affinity TCRs K_D was determined by experimentally measuring the dissociation rate constant, k_d , and the association rate constant, k_a . The equilibrium constant K_D was calculated as k_d/k_a .

10

TCR was injected over two different cells one coated with ~300 RU of specific HLA-A2-nyeso peptide complex, the second coated with ~300 RU of non-specific HLA-A2-peptide complex. Flow rate was set at 50 μ l/min. Typically 250 μ l of TCR at ~3 μ M concentration was injected. Buffer was then flowed over until the response had returned to baseline. Kinetic parameters were calculated using Biaevaluation software. The dissociation phase was also fitted to a single exponential decay equation enabling calculation of half-life.

15

Results

20

The interaction between a soluble disulfide-linked native HIV Gag TCR (consisting of the α and β TCR chains detailed in SEQ ID NOs 9 and 10 respectively) and the SLYNTVATL-HLA-A*0201 complex was analysed using the above methods and demonstrated a K_D of 85 nM and an off-rate (k_{off}) of $2.21 \times 10^{-2} \text{ S}^{-1}$. (See Figure 12 for Biacore response curves)

25

The TCRs specified in the following table have a K_D of less than or equal to 1 μ M and/or a k_{off} of $1 \times 10^{-3} \text{ S}^{-1}$ or slower.

Alpha chain variable domain sequence, SEQ ID NO:	Beta chain variable domain sequence, SEQ ID NO:
1	2
1	14

1	15
11	2
12	2
13	2
12	15
13	15
12	14
13	14

Example 5 – Production of a soluble high affinity HIV Gag TCR –WT human IL-2 fusion protein

5

The methods substantially as described in Examples 1 to 3 can be used to produce a soluble high affinity HIV Gag TCR–WT human IL-2 fusion protein. Briefly, the DNA encoding the desired linker and WT human IL-2 are added into the 3' end of the DNA sequence of the soluble disulfide-linked parental HIV Gag TCR beta chain immediately prior to the TAA (“Stop”) codon. Figure 11 provides the amino acid sequence of a fusion protein comprising a disulfide-linked parental HIV Gag TCR beta chain fused to WT human IL-2 via linker sequence. (SEQ ID NO: 24) The linker and IL-2 portion of this fusion protein are indicated in italics. The DNA encoding this construct can then be ligated into pEX821. The soluble parental HIV Gag TCR- IL-2 fusion protein can then be expressed by combining this beta chain fusion protein with the soluble disulfide-linked parental HIV Gag alpha chain TCR chain detailed in Figure 5a (SEQ ID NO: 9) using the methods substantially as described in Example 3.

Example 6 – Recombinant expression of the parental HIV Gag TCR on the surface of T cells.

20

DNA constructs encoding the signal sequence, extracellular, transmembrane and intracellular domains of the parental HIV Gag TCR chains were synthesised (GeneArt, Germany). These TCR α chain and TCR β chain DNA sequences, provided in Figures 15a and 15b respectively, are altered from the parental HIV Gag TCR DNA sequences so as to enhance expression levels of the encoded TCR chains in human T cells whilst maintaining the native amino acid sequence. Figures 16a and 16b provide the full-length amino acid sequences encoded by the DNA sequences of Figures 15a and 15b respectively.

TCR α chain and TCR β chain DNA sequences were then inserted together into a Lentiviral expression vector. This vector contains DNA encoding both the parental HIV Gag TCR α chain and β chain as a single open reading frame with the in-frame Foot and Mouth Disease Virus (FMDV) 2A cleavage factor amino acid sequence (LLNFDLLKLAGDVESNPG (SEQ ID NO: 31)) separating the TCR chains. (de Felipe *et al.*, *Genet Vaccines Ther* (2004) 2 (1): 13) On mRNA translation the TCR α chain is produced with the 2A peptide sequence at its C-terminus and the TCR β chain is produced as a separate polypeptide.

T cells were transduced with the above Lentiviral vector. Briefly, primary T cells were stimulated for 24 hours using anti-CD3/anti-CD28 beads. A concentrated Lentivirus supernatant, expressing the TCR genes, was then incubated with the stimulated T cells to allow viral transduction. The anti-CD3/anti-CD28 beads were then removed and the transduced T cells were cultured until they attained a "resting volume" of 200-300 fL.

Presentation of parental HIV Gag TCRs on the surface of the transduced cells was confirmed by FACS analysis using HLA-A*0201-SLYNTVALT PE tetramer and anti-CD8 monoclonal antibody FITC co-staining.

Results

Figure 17b provides the FACS analysis data which demonstrates the successful expression of the parental HIV Gag TCR on the surface of transduced CD8⁺ T cells.

5 Figure 17a provides FACS analysis data generated using control untransduced T cells.

Example 7 – Inhibition of CTL activation by soluble high affinity HIV Gag TCRs

The following assays were carried out to demonstrate that the soluble high affinity
10 c11c6 HIV Gag TCR was capable of inhibiting activation of a SLYNTVATL-HLA-A*0201 reactive polyclonal T cell line.

*Inhibition of activation of the OX84 SLYNTVATL-HLA-A*0201 reactive polyclonal T cell line in the presence of HIV infected cells*

15 The soluble c11c6 high affinity HIV Gag TCR utilised in this experiment contained the TCR alpha chain variable domain and TCR beta chain variable regions shown in Figure 6c (SEQ ID NO: 13) and Figure 7b (SEQ ID NO: 15) respectively. The full amino acid sequences of the TCR alpha and beta chains of this soluble TCR are
20 provided by Figure 18a (SEQ ID NO: 29) and Figure 18b (SEQ ID NO: 30) respectively.

IFN- γ and TNF- α production was used as the read-outs for CTL activation.

25 *Reagents*

R10 Assay media: 10% FCS (heat-inactivated, Gibco, cat# 10108-165), 88% RPMI 1640 (Gibco, cat# 42401-018), 1% glutamine (Gibco, cat# 25030-024) and 1% penicillin/streptomycin (Gibco, cat# 15070-063).

30

Peptide: (obtained from various sources) initially dissolved in DMSO (Sigma, cat# D2650) at 4mg/ml and frozen.

5 The BD™ Cytometric Bead Array Kit, Human Th1/Th2 cytokine Kit II (BD Biosciences, San Diego, US) contains all the reagents required for the assay.

T cell activation Assay

10 Chronically HIV infected To target cells (HXB2 and HIV3B HIV Lab strains) were washed and re-suspended in R10 media. As a control uninfected To target cells were pulsed with 1nM of SLYNTVATL peptide, for 30 minutes at 37°C, 5%CO₂.

Test Samples:

15 25,000 HIV infected To target cells in R10 media per well of a 96 well U-bottom plate.

2 x 10⁻⁷ M high affinity c11c6 HIV Gag TCR or parental HIV Gag TCR in R10 media per well.

20 5000 OX84 polyclonal effector T cell line in R10 media per well.

Controls:

As above substituting irrelevant soluble TCRs (HLA-A*0201-Tax specific and HLA-A*0201-NY-ESO specific TCRs) or the high affinity HIV Gag TCRs.

25 The plate was then incubated for 4 hours at 37°C, 5% CO₂. The culture supernatant was removed to measure the levels of IFN-γ and TNF-α present using the following method.

30 *IFN-γ and TNF-α assay*

BD™ Cytometric Beads coated with (a) anti-IFN γ capture antibodies and (b) anti-TNF α capture antibodies were prepared according to the manufacturers instructions

A number of assay tubes were then prepared containing the following additions:

5

50 μ l of mixed anti-IFN γ and anti-TNF α BD™ Cytometric Beads in BD Assay Diluent

50 μ l of PE Detection Reagent

10

Followed by either:

50 μ l of the culture supernatant taken from the T cell activation assay wells. (Test Samples)

Or

15

50 μ l of mixed IFN γ and TNF α standards prepared at a range of concentrations by serial dilution of stock standards. (Calibration Standards)

20

The tube were then incubated in the dark for 3 hours prior to being washed with 1ml of BD Wash Buffer and centrifuged. Finally, the beads were re-suspended in 300 μ l of the Wash Buffer and the level of IFN γ and TNF α present was determined by Flow Cytometry according to manufacturer's instructions.

25

*Inhibition of the SLYNTVATL-HLA-A*0201 specific OX84 polyclonal T line in the presence of uninfected SLYNTVATL peptide pulsed To cells*

The same reagents and methods as used for the above CTL activation assay were used except that:

30

2000 OX84 polyclonal effector T cells were used in each T cell activation assay.

Uninfected T2 lymphoblastoid cells, pulsed with 10^{-10} - 10^{-8} M SLYNTVATL peptide were used as the target cells

Results

5

The soluble high affinity c11c6 HIV Gag TCR strongly inhibited activation of the SLYNTVATL-HLA-A*0201 reactive OX84 polyclonal T cell line in the presence of T2 cells infected by HIV as measured by IFN- γ and TNF- α production. (See Figure 19)

10

The soluble high affinity c11c6 HIV Gag TCR strongly inhibited activation of the SLYNTVATL-HLA-A*0201 reactive OX84 polyclonal T cell line in the presence of SLYNTVATL-pulsed uninfected T2 cells as measured by IFN- γ and TNF- α production. (See Figure 20)

15

*Example 8 - Quantification of cell surface SLYNTVATL-HLA-A*0201 antigens on peptide-pulsed T2 cells by fluorescence microscopy using high affinity c11c6 HIV Gag TCR*

20

The number of SLYNTVATL-HLA-A*0201 antigens on peptide-pulsed T2 lymphoblastoid cell was determined (on the assumption that one fluorescence signal relates to a single labelled TCR bound to its cognate pMHC ligand on the surface of the target cell) by single molecule fluorescence microscopy using a soluble high-affinity c11c6 HIV Gag TCR. This was facilitated by using biotinylated TCR to target the antigen-expressing cancer cells and subsequent labelling of cell-bound TCR by streptavidin-R phycoerythrin (PE) conjugates. Individual PE molecules were then imaged by 3-dimensional fluorescence microscopy.

25

30

T2 lymphoblastoid cells were pulsed with the HIV Gag-derived SLYNTVATL peptide, or an irrelevant peptide (SLLMWITQC) at a range of concentrations (10^{-5} – 10^{-10} M) for 90 minutes at 37°C. After pulsing the cells were washed twice with 500 μ l of PBS. Cells were incubated in 200 μ l of TCR solution (100 nM high-affinity c11c6

HIV Gag TCR), in PBS. 0.5% BSA albumin) for 30 min at room temperature. TCR solution was removed, and cells were washed three times with 500 μ l of PBS. Cells were incubated in 200 μ l of streptavidin-PE solution (5 μ g ml⁻¹ streptavidin-PE in PBS containing 0.5% BSA) at room temperature in the dark for 20 min. Streptavidin-PE
5 solution was removed and cells were washed three times with 500 μ l of PBS. Wash media was removed, and cells kept in 400 μ l of R10, without Phenol Red before imaging by fluorescence microscopy.

Fluorescence microscopy. Fluorescent microscopy was carried out using an Axiovert
10 200M (Zeiss) microscope with a 63x Oil objective (Zeiss). A Lambda LS light source containing a 300W Xenon Arc lamp (Sutter) was used for illumination, and light intensity was reduced to optimal levels by placing a 0.3 and a 0.6 neutral density filter into the light path. Excitation and emission spectra were separated using a TRITC/DiI filter set (Chroma). Cells were imaged in three dimensions by z-stack acquisition (21
15 planes, 1 μ m apart). Image acquisition and analysis was performed using Metamorph software (Universal Imaging) as described (Irvine *et al.*, *Nature* **419**: p845-9, and Purbhoo *et al.*, *Nature Immunology* **5**: p524-30).

Results

20

As shown by Figure 21 the above method was used successfully to image high affinity c11c6 HIV Gag TCR bound to SLYNTVATL -HLA-A*0201 antigens on the surface of peptide-pulsed T2 cells. These results show the threshold for counting epitopes on SLYNTVATL peptide-pulsed cells using the high affinity c6c11 HIV Gag TCR is
25 approximately 10⁻⁹ M peptide.

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41A

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

5

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of

10 endeavour to which this specification relates.

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated T-cell receptor (TCR) having the property of binding to SLYNTVATL-HLA-A*0201 and comprising at least one TCR α chain variable domain and/or at least one TCR β chain variable domain, wherein:
 - (i) the TCR α chain variable domain has SEQ ID NO:1 except that at least one complementarity determining region thereof is/are mutated and/or the TCR β chain variable domain has SEQ ID NO:2 except that at least one complementarity determining region thereof is/are mutated; and
 - (ii) the TCR has a K_D for the said SLYNTVATL-HLA-A*0201 complex of less than or equal to $1\mu\text{M}$ and/or has an off-rate (k_{off}) for the SLYNTVATL-HLA-A*0201 complex of $1 \times 10^{-3} \text{ s}^{-1}$ or slower.
2. A TCR as claimed in claim 1 comprising both an α chain variable domain and a TCR β chain variable domain.
3. A T-cell receptor (TCR) as claimed in claim 1 or claim 2, wherein the said K_D and/or k_{off} is/are measured by Surface Plasmon Resonance.
4. A TCR as claimed in any one of the preceding claims, wherein one or more of alpha chain variable region amino acids 95T, 96N, 97S, 98G and 100A using the numbering shown in SEQ ID NO:1 is/are mutated.
5. A TCR as claimed in any one of the preceding claims, wherein one or more of beta chain variable region amino acids 51Y, 52E, 53E and 54E using the numbering shown in SEQ ID NO:2 is/are mutated.
6. A TCR as claimed in any one of claims 1 to 3 comprising one or more of alpha chain variable region amino acids 95S, 95G, 96A, 97H, 98D or 100S using the numbering shown in SEQ ID NO:1.

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7. A TCR as claimed in any one of claims 1 to 3 or 6 comprising one or more of beta chain variable region amino acids 51V, 51A, 52R, 52L, 53G or 54V using the numbering shown in SEQ ID NO:2.

8. A TCR as claimed in any one of claims 1 to 3 comprising one of the alpha chain variable region amino acid sequences shown in SEQ ID NOs:11 to 13.

9. A TCR as claimed in any one of claims 1 to 3 or 8 comprising one of the beta chain variable region amino acid sequences shown in SEQ ID NOs:14 to 15.

10. A TCR as claimed in claim 2 comprising the alpha and beta chain variable region pairings shown in the following table:

Alpha chain variable region sequence, SEQ ID NO:	Beta chain variable region sequence, SEQ ID NO:
1	2
1	14
1	15
11	2
12	2
13	2
12	15
13	15
12	14
13	14

11. A TCR as claimed in any one of the preceding claims, further comprising the alpha chain constant domain amino acid sequence shown in SEQ ID NO:19, and/or one of the beta chain amino acid constant domain sequences shown in SEQ ID NOs:20 and 21, optionally comprising one or more phenotypically silent substitutions.

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12. A TCR as claimed in any one of the preceding claims which is a dimeric TCR comprising:

a first polypeptide, wherein a sequence corresponding to a TCR α chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant domain extracellular sequence, and

a second polypeptide, wherein a sequence corresponding to a TCR β chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR β chain constant domain extracellular sequence,

the first and second polypeptides being linked by a disulfide bond between cysteine residue substituted for Thr 48 of exon 1 of TRAC*01 and Ser 57 of exon 1 of TRBC1*01 or TRBC2*01.

13. A TCR as claimed in any one of the preceding claims which is covalently linked to a therapeutic agent or detectable moiety.

14. A multivalent TCR complex comprising at least two TCRs as claimed in any one of the preceding claims.

15. A cell harbouring an expression vector comprising nucleic acid encoding a TCR as defined in any one of claims 1 to 11.

16. A pharmaceutical composition comprising a TCR as claimed in any one of claims 1 to 13, or a multivalent TCR complex as claimed in claim 14, or a plurality of cell as claimed in claim 15, together with a pharmaceutically acceptable carrier.

17. A TCR as claimed in any one of claims 1 to 13, substantially as hereinbefore described and with reference to any of the Examples and/or figures.

1/24

Figure 1a

10 20
* *
M A Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D

30 40 50
* * *
R G S Q S F F W Y R Q Y S G K S P E L I M F I Y S N G D K

60 70 80
* * *
E D G R F T A Q L N K A S Q Y I S L L I R D S K L S D S A

90 100 110
* * *
T Y L C A V R T N S G Y A L N F G K G T S L L V T P H

(SEQ ID No: 1)

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Figure 1b

10 20
* *
M E A G V T Q S P T H L I K T R G Q Q V T L R C S P K S G

30 40 50
* * *
H D T V S W Y Q Q A L G Q G P Q F I F Q Y Y E E E E R Q R

60 70 80
* * *
G N F P D R F S G H Q F P N Y S S E L N V N A L L L G D S

90 100 110
* * *
A L Y L C A S S D T V S Y E Q Y F G P G T R L T V T

(SEQ ID NO: 2)

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Figure 2a

atggcccagaaggaggtggagcagaattctggaccctcagtggtccagaggagccattgcctctctcaattgcacttaca
gtgaccgaggttcccagtccttcttggtacagacaatatctgggaaaagccctgagttgataatgttcataactccaatgg
tgacaaagaagatggaaggttacagcacagctcaataaagccagccagtataattccctgctcatcagagactccaagctc
agtgattcagccacctacctctgtgcggtgcgcacaaattcgggtatgcactcaactcggcaaaggcacctcgctgttggt
cacaccccatatccagaacctgacctgcccgtgtaccagctgagagactctaaatccagtgacaagtctgtctgcctattca
ccgattttgatttcaaacaaatgtgtcacaagtaaggattctgatgtgtatatcacagacaaaactgtgctagacatgaggtc
tatggacttcaagagcaacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaacaacagcatta
ttccagaagacacctcttccccagcccagaaagttcctaa
(SEQ ID No: 3)

Figure 2b

atggaggctggagtcacacaaagtcccacacacctgatcaaacgagaggacagcaagtgactctgagatgctctcctaa
gtctgggcatgacactgtgtcctggtaccaacaggccctgggtcaggggccccagtttatctttcagtattatgaggaggaag
agagacagagaggcaacttcctgatcgattctcaggtcaccagttccctaactatagctctgagctgaatgtgaacgccttg
ttgctgggggactcggccctctatctctgtgccagcagcgacaccgtctcctacgagcagctactcgggcccgggcaccagg
ctcacggtcacagaggacctgaaaaacgtgtcccaccgaggtcgctgtgtttgagccatcagaagcagagatctccac
acccaaaaggccacactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaa
ggaggtgcacagtggggtcagcacagaccgcagcccctcaaggagcagcccgccctcaatgactccagatacgtctg
agcagccgcctgagggctcggccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctc
tcggagaatgacgagtggaaccaggatagggccaaaccgacaccagatcgtcagcgccgaggcctggggtagagca
gactaa

(SEQ ID No: 4)

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Figure 3a

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

(SEQ ID No: 5)

Figure 3b

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

(SEQ ID No: 6)

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Figure 4a

ccatcgatgggcccagaaggaggtggagcagaattctggacccctcagtggtccagaggagccattgcctcttcaattgc
acttacagtgaccgaggttcccagtccttcttctggtacagacaatattctgggaaaagccctgagttgataatgttcatatactc
caatggtgacaaagaagatggaaggttacagcacagctcaataaagccagccagtataattccctgctcatcagagactcc
aagctcagtgattcagccacctacctctgtgcggtgcgcacaaattccgggtatgcactcaacttcggcaaaggcacctcgc
tgttggtcacaccccatatccagaacctgacctgccgtgtaccagctgagagactctaagtcgagtgacaagtctgtctgc
ctattcaccgattttgattctcaacaaatgtgtcacaaagtaaggattctgatgtgtatatcacagacaaatgtgtgctagacat
gaggtctatggacttcaaggaacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaacaac
agcattattccagaagacaccttcttccccagcccagaaagttcctaa
(SEQ ID No: 7)

Figure 4b

tctctcattaatggaggctggagtcacacaaagtcacacacctgatcaaacgagaggacagcaagtgactctgagatg
ctctcctaagtctgggcatgacactgtgtcctggfaccacaggccctgggtcaggggccccagtttatcttcagtattatga
ggaggaagagagacagagaggcaacttccctgatcgattctcaggtcaccagttccctaactatagctctgagctgaatgtg
aacgccttggtgtgggggactcggccctctatctgtgtccagcagcgacaccgtctcctacgagcagtagtacttcgggccgg
gcaccagg
ctcacggtcacagaggacctgaaaaacgtgttccacccgaggtcgctgtgtttgagccatcagaagcagagatctccac
acccaaaaggccacactgggtgtgcctggccaccggttctaccccgaccacgtggagctgagctgggtgggtgaatgggaa
ggaggtgcacagtggggtctgcacagacccgcagcccctcaaggagcagccgcctcaatgactccagatacgtctg
agcagccgcctgaggggtctggccaccttctggcaggacccccgaaccacttcgctgtcaagtccagttctacgggctc
tcggagaatgacgagtggaaccaggatagggccaaaccgtcaccagatcgtcagcgccgaggcctggggtagagca
gactaa
(SEQ ID No: 8)

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Figure 5a

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

(SEQ ID No: 9)

Figure 5b

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

(SEQ ID No: 10)

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Figure 6a

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

(SEQ ID NO: 11)

Figure 6b

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

(SEQ ID NO: 12)

Figure 6c

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

(SEQ ID NO: 13)

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Figure 7a

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

(SEQ ID NO: 14)

Figure 7b

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

(SEQ ID NO: 15)

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Figure 8a

I Q N P D P A V Y Q L R D S K S S D K S V C L F T
D F D S Q T N V S Q S K D S D V Y I T D K
(SEQ ID NO: 19)

Figure 8b

E D L N K V F P P E V A V F E P S E A E I S H T Q K A T
L V C L A T G F F P D H V E L S W W V N G K E V H S G V
(SEQ ID NO: 20)

Figure 8c

E D L K N V F P P E V A V F E P S E A E I S H T Q K A T
L V C L A T G F Y P D H V E L S W W V N G K E V H S G V
(SEQ ID NO: 21)

10/24

Figure 9

PEX954

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Figure 9 Cont.

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Figure 10

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Figure 10 Cont.

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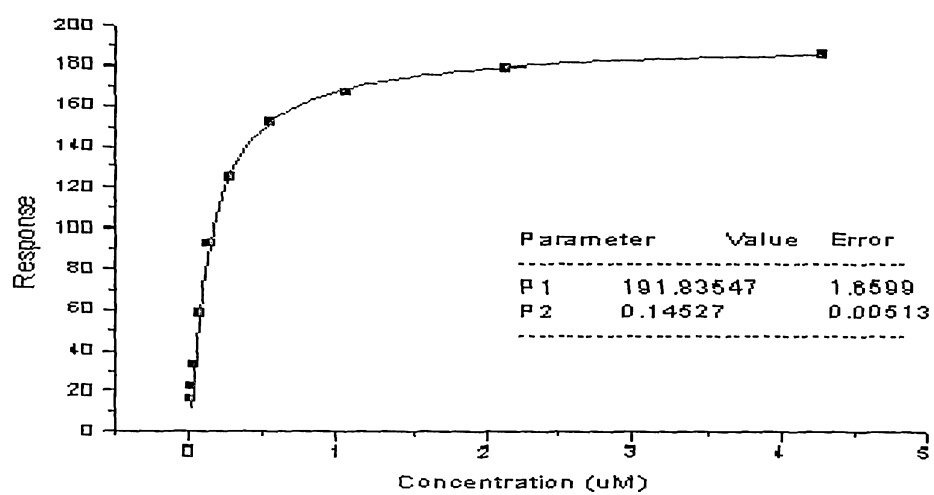
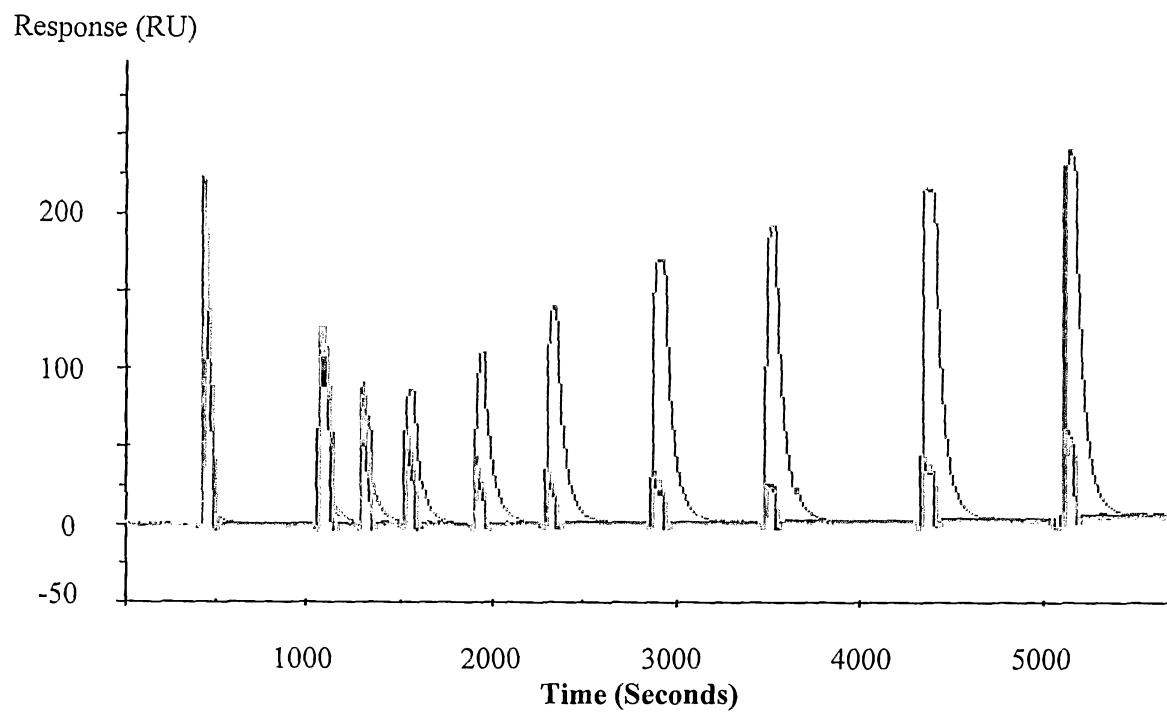
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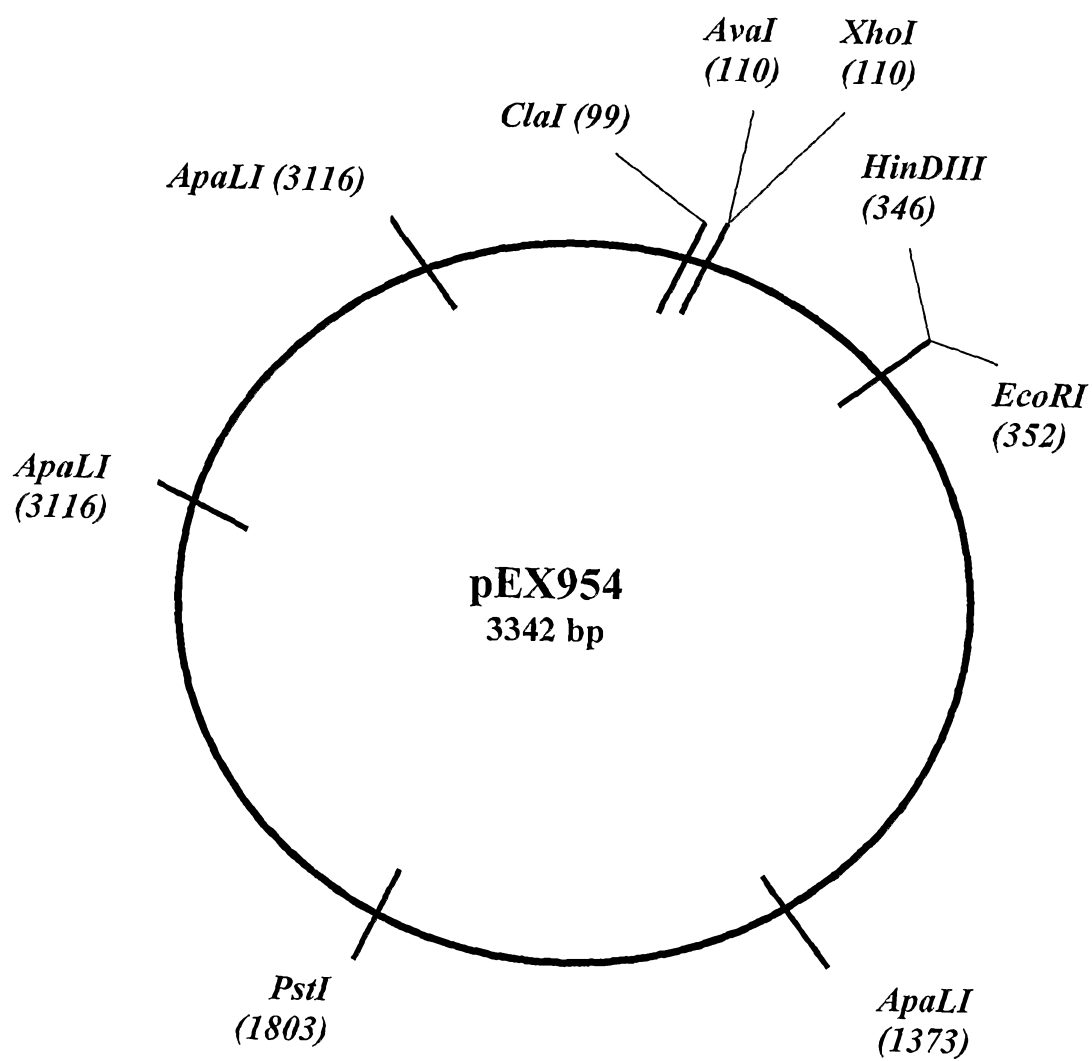
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Figure 12



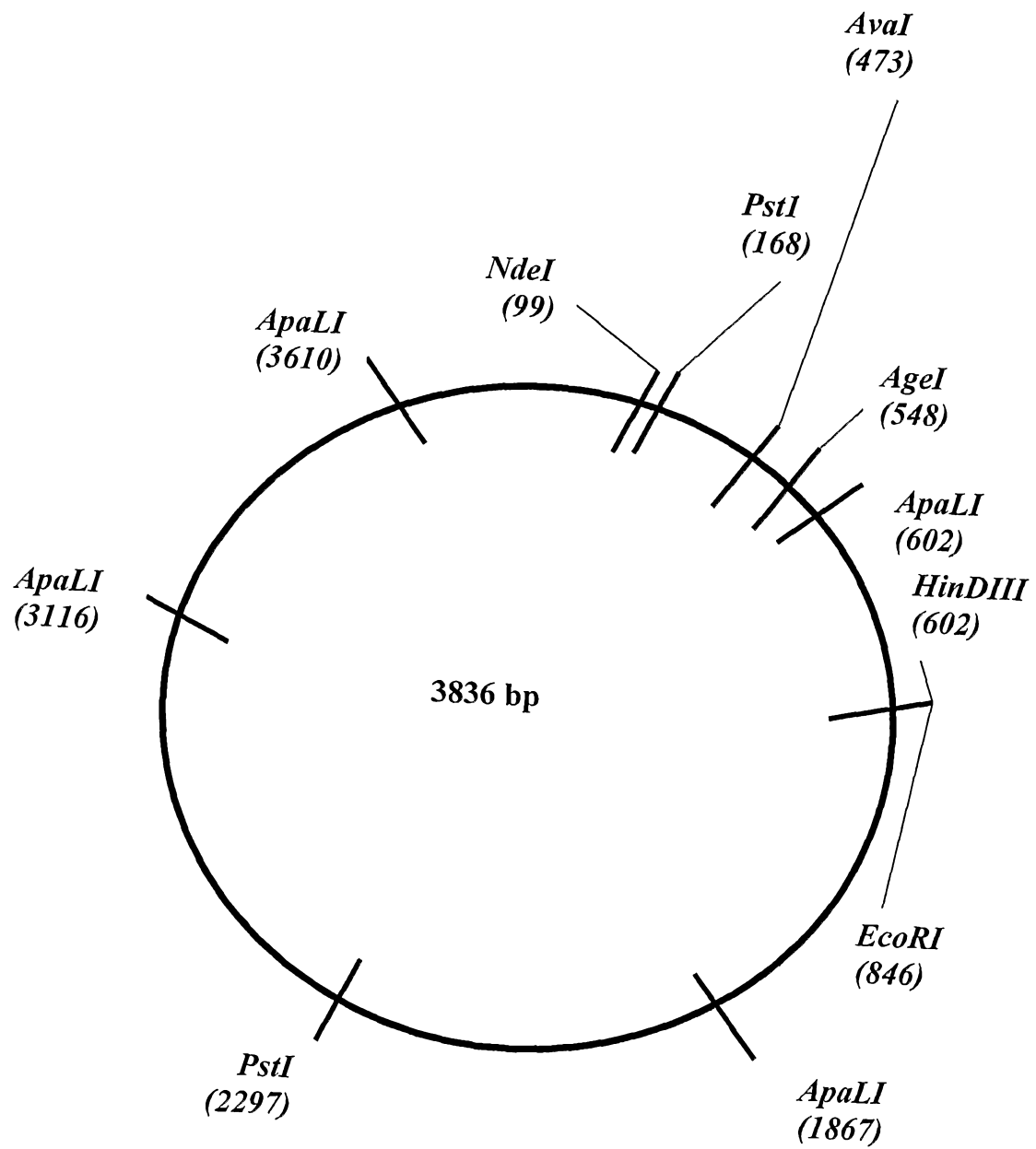
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Figure 13



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Figure 14



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Figure 15a

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Figure 16a

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Figure 16b

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Figure 17a

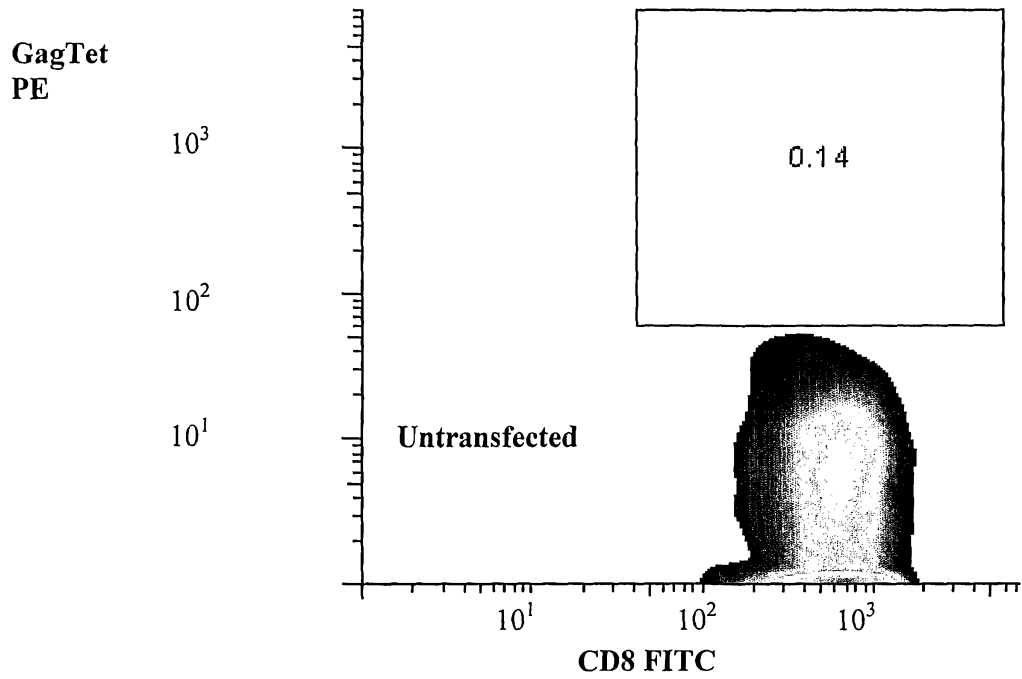
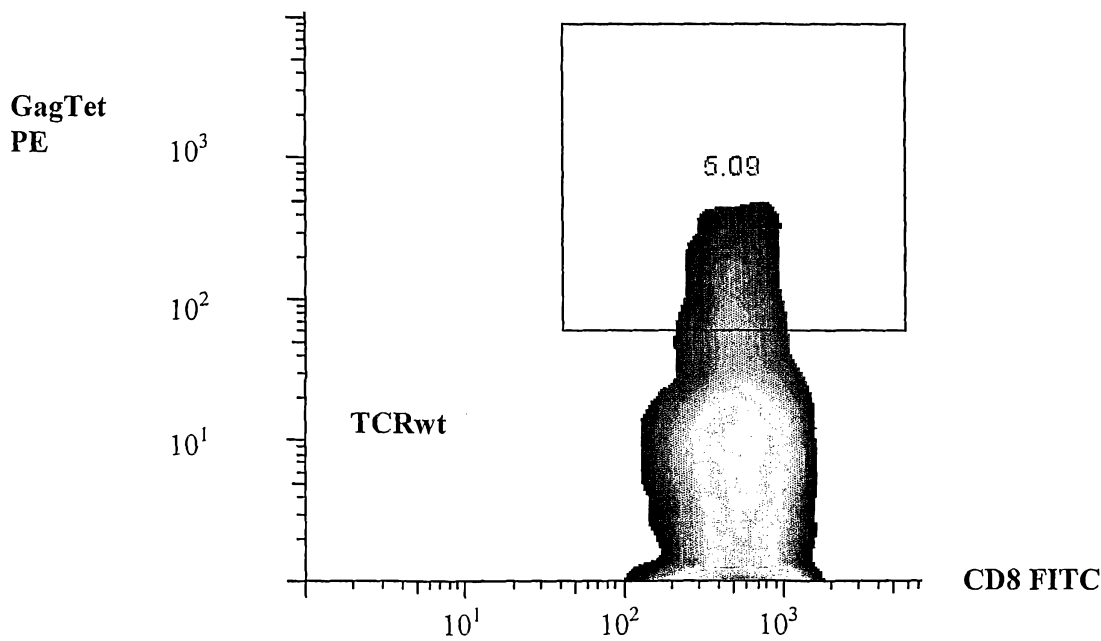


Figure 17b



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Figure 18a

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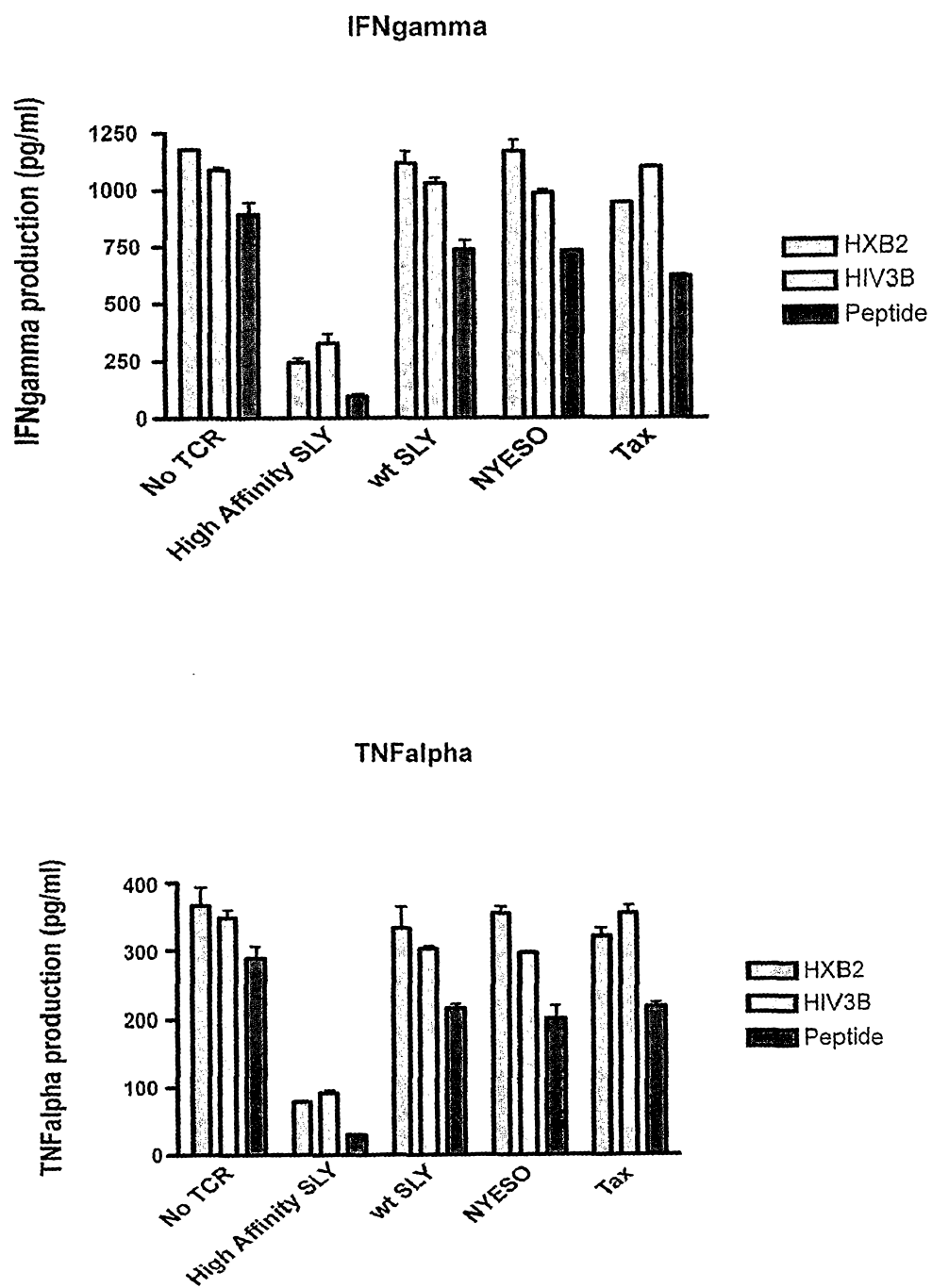
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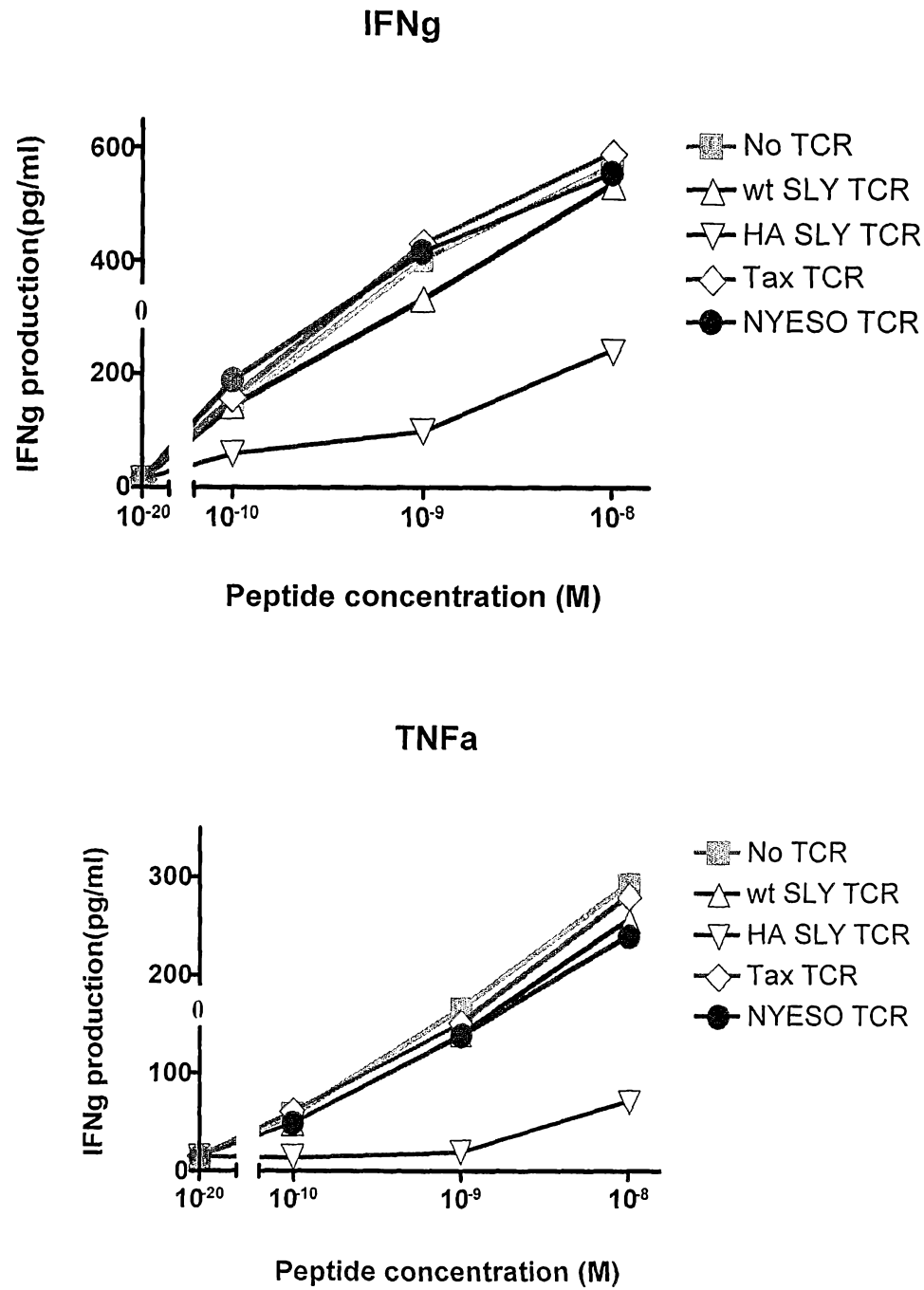
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Figure 19



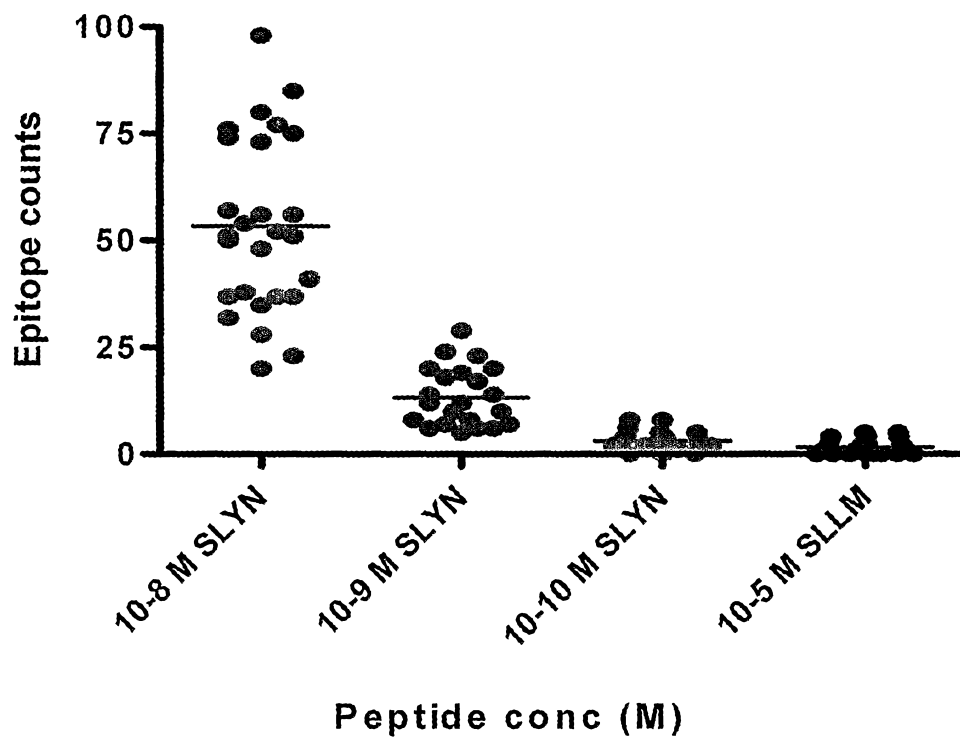
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Figure 20



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Figure 21



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ttccccagcc cagaaagtcc ctaa                                           624

```

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<210> 4
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> dna encoding a truncated portion of the parental gag tcr beta chain

<400> 4
 atggaggctg gagtcacaca aagtcccaca cacctgatca aaacgagagg acagcaagtg 60
 actctgagat gctctcctaa gtctgggcat gacactgtgt cctggtacca acaggccctg 120
 ggtcaggggc cccagtttat ctttcagtat tatgaggagg aagagagaca gagaggcaac 180
 ttccctgata gattctcagg tcaccagttc cctaactata gctctgagct gaatgtgaac 240
 gccttggtgc tgggggactc ggccctctat ctctgtgccg gcagcgacac cgtctcctac 300
 gagcagtact tcggggccggg caccaggctc acggtcacag aggacctgaa aaacgtgttc 360
 ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctccacac ccaaaaggcc 420
 aactggtgtg gcctggccac aggcttctac cccgaccacg tggagctgag ctggtgggtg 480
 aatgggaagg aggtgcacag tggggtcagc acagaccgcg agccctcaa ggagcagccc 540
 gccctcaatg actccagata cgctctgagc agccgcctga gggctctggc caccttctgg 600
 caggaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgac 660
 gagtggaccc aggatagggc caaaccgctc acccagatcg tcagcgccga ggcctggggt 720
 agagcagact aa 732

<210> 5
 <211> 207
 <212> PRT
 <213> Artificial sequence

<220>
 <223> a truncated portion of the parental gag tcr alpha chain

<400> 5

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
 1 5 10 15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
 20 25 30

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
 35 40 45

Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
 50 55 60

Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
 65 70 75 80

Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Thr Asn
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Ser Gly Tyr Ala₁₀₀ Leu Asn Phe Gly₁₀₅ Gly Thr Ser Leu₁₁₀ Val Thr

Pro His Ile₁₁₅ Gln Asn Pro Asp₁₂₀ Ala Val Tyr Gln₁₂₅ Leu Arg Asp Ser

Lys Ser₁₃₀ Ser Asp Lys Ser Val₁₃₅ Cys Leu Phe Thr₁₄₀ Asp Phe Asp Ser Gln

Thr Asn Val Ser Gln₁₅₀ Lys Asp Ser Asp Val₁₅₅ Tyr Ile Thr Asp₁₆₀ Lys

Thr Val Leu Asp Met₁₆₅ Arg Ser Met Asp₁₇₀ Phe Lys Ser Asn Ser Ala₁₇₅ Val

Ala Trp Ser Asn₁₈₀ Lys Ser Asp Phe₁₈₅ Ala Cys Ala Asn Ala₁₉₀ Phe Asn Asn

Ser Ile Ile₁₉₅ Pro Glu Asp Thr Phe₂₀₀ Phe Pro Ser Pro₂₀₅ Glu Ser Ser

<210> 6

<211> 243

<212> PRT

<213> Artificial sequence

<220>

<223> a truncated portion of the parental gag tcr beta chain

<400> 6

Met Glu Ala Gly Val₅ Thr Gln Ser Pro Thr₁₀ His Leu Ile Lys Thr Arg

Gly Gln Gln Val₂₀ Thr Leu Arg Cys₂₅ Ser Pro Lys Ser Gly₃₀ His Asp Thr

Val Ser Trp Tyr Gln Gln Ala Leu₄₀ Gly Gln Gly Pro Gln₄₅ Phe Ile Phe

Gln Tyr Tyr Glu Glu Glu₅₅ Arg Gln Arg Gly Asn₆₀ Phe Pro Asp Arg

Phe Ser Gly His Gln₇₀ Phe Pro Asn Tyr Ser₇₅ Ser Glu Leu Asn Val₈₀ Asn

Ala Leu Leu Leu₈₅ Gly Asp Ser Ala Leu Tyr₉₀ Leu Cys Ala Ser Ser₉₅ Asp

Thr Val Ser Tyr₁₀₀ Glu Gln Tyr Phe Gly₁₀₅ Pro Gly Thr Arg Leu₁₁₀ Thr Val

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Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
115 120 125

Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
130 135 140

Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
145 150 155 160

Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu
165 170 175

Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg
180 185 190

Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg
195 200 205

Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
210 215 220

Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
225 230 235 240

Arg Ala Asp

<210> 7
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a truncated portion of the parental gag tcr alpha chain including an introduced Cys codon and restriction enzyme recognition sequences

<400> 7
ccatcgatgg cccagaagga ggtggagcag aattctggac ccctcagtgt tccagagggg 60
gccattgcct ctctcaattg cacttacagt gaccgaggtt cccagtcctt cttctggtac 120
agacaatatt ctgggaaaag ccctgagttg ataatgttca tatactccaa tggtgacaaa 180
gaagatggaa ggtttacagc acagctcaat aaagccagcc agtatatttc cctgctcatc 240
agagactcca agctcagtga ttcagccacc tacctctgtg cggtgcgcac aaattccggg 300
tatgcactca acttcggcaa aggcacctcg ctgttggtca caccatcatat ccagaaccct 360
gaccctgccg tgtaccagct gagagactct aagtcgagtg acaagtctgt ctgcctattc 420
accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 480
gacaaatgtg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tgtggcctgg 540
agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 600

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acctttcttcc ccagcccaga aagttcctaa 630

<210> 8
<211> 742
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a truncated portion of the parental gag tcr beta chain including an introduced Cys codon and restriction enzyme recognition sequences

<400> 8
tctctcatta atggaggctg gagtcacaca aagtcccaca cacctgatca aaacgagagg 60
acagcaagtg actctgagat gctctcctaa gtctgggcat gacactgtgt cctggtacca 120
acaggccctg ggtcaggggc cccagtttat ctttcagtat tatgaggagg aagagagaca 180
gagaggcaac ttccctgata gattctcagg tcaccagttc cctaactata gctctgagct 240
gaatgtgaac gccttggtgc tgggggactc ggccctctat ctctgtgcca gcagcgacac 300
cgtctcctac gagcagtact tcggggccggg caccaggctc acggtcacag aggacctgaa 360
aaacgtgttc ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctcccacac 420
ccaaaaggcc aacttggtgt gcctggccac cggtttctac cccgaccacg tggagctgag 480
ctggtgggtg aatgggaagg aggtgcacag tggggtctgc acagaccgc agcccctcaa 540
ggagcagccc gccctcaatg actccagata cgctctgagc agccgcctga gggctctggc 600
caccttctgg caggaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc 660
ggagaatgac gagtggaccc aggatagggc caaaccgctc acccagatcg tcagcgccga 720
ggcctgggggt agagcagact aa 742

<210> 9
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> A truncated portion of the parental gag tcr alpha chain including an introduced Cys residue

<400> 9

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
1 5 10 15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
20 25 30

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
35 40 45

Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
50 55 60

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Case 74 PCT Gag TCRs ST25.txt

Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
65 70 75 80

Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Thr Asn
85 90 95

Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
165 170 175

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

<210> 10
<211> 243
<212> PRT
<213> Artificial sequence

<220>
<223> A truncated portion of the parental gag tcr beta chain including
an introduced Cys

<400> 10

Met Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
1 5 10 15

Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
20 25 30

Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
35 40 45

Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
50 55 60

Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
65 70 75 80

Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Asp
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85

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Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
 100 105 110

Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
 115 120 125

Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
 130 135 140

Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
 145 150 155 160

Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu
 165 170 175

Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg
 180 185 190

Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg
 195 200 205

Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
 210 215 220

Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
 225 230 235 240

Arg Ala Asp

<210> 11
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> High affinity mutated GAG TCR alpha chain variable region
 sequence

<400> 11

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
 1 5 10 15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
 20 25 30

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
 35 40 45

Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
 50 55 60

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Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
65 70 75 80

Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Ser Ala
85 90 95

His Gly Tyr Ser Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His

<210> 12
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> High affinity mutated GAG TCR alpha chain variable region
sequence

<400> 12

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
1 5 10 15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
20 25 30

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
35 40 45

Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
50 55 60

Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
65 70 75 80

Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Ser Ala
85 90 95

His Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His

<210> 13
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> High affinity mutated GAG TCR alpha chain variable region

sequence

<400> 13

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
 1 5 10 15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
 20 25 30

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
 35 40 45

Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
 50 55 60

Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
 65 70 75 80

Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Gly Ala
 85 90 95

His Asp Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
 100 105 110

Pro His

<210> 14

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> High affinity mutated GAG TCR beta chain variable region sequence

<400> 14

Met Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
 1 5 10 15

Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
 20 25 30

Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
 35 40 45

Gln Tyr Val Arg Gly Val Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
 50 55 60

Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
 65 70 75 80

Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Asp
 85 90 95

Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
 100 105 110

Thr

<210> 15
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> High affinity mutated GAG TCR beta chain variable region sequence

<400> 15

Met Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
 1 5 10 15

Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
 20 25 30

Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
 35 40 45

Gln Tyr Ala Leu Gly Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
 50 55 60

Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
 65 70 75 80

Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Asp
 85 90 95

Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
 100 105 110

Thr

<210> 16
 <211> 9
 <212> PRT
 <213> Human immunodeficiency virus

<400> 16

Ser Leu Tyr Asn Thr Val Ala Thr Leu
 1 5

<210> 17
 <211> 30
 <212> PRT
 <213> Artificial Sequence

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<220>

<223> Short sCTCR linker

<400> 17

Pro Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Pro
 20 25 30

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<210> 18

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Long sCTCR linker

<400> 18

Pro Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Pro
 35

<210> 19

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated portion of the amino acid sequence encoded by TRAC

<400> 19

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
 1 5 10 15

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
 20 25 30

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 35 40 45

<210> 20

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated portion of the amino acid sequence encoded by TRBC1

<400> 20

Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro

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1 5 10 15
 Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30
 Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45
 Gly Lys Glu Val His Ser Gly Val
 50 55

<210> 21
 <211> 56
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Truncated portion of the amino acid sequence encoded by TRBC2
 <400> 21

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1 5 10 15
 Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30
 Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45
 Gly Lys Glu Val His Ser Gly Val
 50 55

<210> 22
 <211> 3342
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> pEX954 vector

<400> 22
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 gtctgtctgc ctattcaccg attttgattc tcaaacaaat gtgtcacaaa gtaaggattc 180
 tgatgtgtat atcacagaca aatgtgtgct agacatgagg tctatggact tcaagagcaa 240
 cagtgtgtg gcctggagca acaaatctga ctttgcatgt gcaaacgcct tcaacaacag 300
 cattattcca gaagacacct tcttccccag cccagaaagt tcctaagctt gaattccgat 360
 ccggctgcta acaaagcccg aaaggaagct gagttggctg ctgccaccgc tgagcaataa 420
 ctagcataac cccttggggc ctctaaacgg gtcttgaggg gttttttgct gaaaggagga 480
 actatatccg gataattctt gaagacgaaa gggcctcgtg atacgcctat ttttataggt 540

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taatgtcatg	ataataatgg	tttcttagac	gtgaggtggc	acttttcggg	gaaatgtgcg	600
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ataaccctga	taaatgcttc	aataatattt	tgttaaaatt	cgcgttaaatt	ttttgttaaa	720
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tggactccaa	cgtcaaaggg	cgaaaaaccg	tctatcaggg	cgatggccca	ctacgtgaac	900
catcaccta	atcaagtttt	ttggggtcga	ggtgccgtaa	agcactaaat	cggaacccta	960
aagggagccc	ccgatttaga	gcttgacggg	gaaagccggc	gaacgtggcg	agaaaggaag	1020
ggaagaaagc	gaaaggagcg	ggcgctaggg	cgctggcaag	tgtagcggtc	acgctgcgcg	1080
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ggggaaatgt	gcgcggaacc	cctatttggt	tatttttcta	aatacattca	aatatgtatc	1200
cgctcatgag	acaataacct	tgataaatgc	ttcaataata	ttgaaaaagg	aagagtatga	1260
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accacttcaa	gaactctgta	gcaccgccta	catacctcgc	tctgctaata	ctgttaccag	2520
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cggataaggc	gcagcggtcg	ggctgaacgg	ggggttcgtg	cacacagccc	agcttgagac	2640
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<210> 23
 <211> 3836
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pEX821 vector

<400> 23	
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accccaaat	tccaggtcct gaagacagga cagagcatga cactgcagtg tgcccaggat 180
atgaaccatg	aatacatgtc ctggtatcga caagaccag gcattggggct gaggctgatt 240
cattactcag	ttggtgctgg tatcactgac caaggagaag tccccaatgg ctacaatgtc 300
tccagatcaa	ccacagagga tttcccgctc aggtgctgt cggtgctcc ctcccagaca 360
tctgtgtact	tctgtgccag caggccggga ctacgaggag ggcgaccaga gcagtacttc 420
gggcccggca	ccaggctcac ggctcacagag gacctgaaaa acgtgttccc acccgaggtc 480
gctgtgtttg	agccatcaga agcagagatc tcccacaccc aaaaggccac actggtgtgc 540
ctggccaccg	gtttctaccc cgaccacgtg gagctgagct ggtgggtgaa tgggaaggag 600
gtgcacagtg	gggtctgcac agaccgcag cccctcaagg agcagccgc cctcaatgac 660
tccagatacg	ctctgagcag ccgcctgagg gtctcgcca ccttctggca ggacccccgc 720
aaccacttcc	gctgtcaagt ccagttctac gggctctcgg agaattgacga gtggaccag 780
gatagggcca	aaccgctcac ccagatcgtc agcggcgagg cctggggtag agcagactaa 840
gcttgaattc	cgatccggct gctaacaaag cccgaaagga agctgagttg gctgctgcca 900
ccgctgagca	ataactagca taacccttg gggcctctaa acgggtcttg aggggttttt 960

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tgctgaaagg	aggaactata	tccggataat	tcttgaagac	gaaagggcct	cgtgatacgc	1020
ctatTTTTat	aggTTaatgt	catgataata	atggtttctt	agacgtcagg	tggcactttt	1080
cggggaaatg	tgcgcggaac	ccctatttgt	ttatTTTTct	aaatacattc	aaatatgtat	1140
ccgctcatga	gacaataacc	ctgataaatg	cttcaataat	attttgttaa	aattcgcgtt	1200
aaatTTTTgt	taaatacagct	cattTTTTta	ccaataggcc	gaaatcggca	aaatccctta	1260
taaataaaaa	gaatagaccg	agataggggt	gagtgttggt	ccagtttgga	acaagagtcc	1320
actattaaag	aacgtggact	ccaacgtcaa	agggcgaaaa	accgtctatc	agggcgatgg	1380
cccactacgt	gaaccatcac	cctaatacag	ttttttgggg	tcgaggtgcc	gtaaagcact	1440
aaatcggaac	cctaaaggga	gccccgatt	tagagcttga	cggggaaagc	cggcgaacgt	1500
ggcgagaaag	gaagggaaga	aagcgaaagg	agcgggcgct	agggcgctgg	caagtgtagc	1560
ggtcacgctg	cgcgtaacca	ccacaccgcg	cgcgcttaat	gcgccgctac	agggcgcgctc	1620
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ttgccttcct	gtttttgctc	accagaaaac	gctggtgaaa	gtaaaagatg	ctgaagatca	1860
gttgggtgca	cgagtgggtt	acatcgaact	ggatctcaac	agcggtaaga	tccttgagag	1920
ttttcgcccc	gaagaacgtt	ttccaatgat	gagcactttt	aaagttctgc	tatgtggcgc	1980
ggtattatcc	cgtgttgacg	ccgggcaaga	gcaactcggg	cgccgcatac	actattctca	2040
gaatgacttg	gttgagtact	caccagtcac	agaaaagcat	cttacggatg	gcatgacagt	2100
aagagaatta	tgcagtgtcg	ccataaccat	gagtgataac	actgcggcca	acttacttct	2160
gacaacgatac	ggaggaccga	aggagctaac	cgctTTTTtg	cacaacatgg	gggatcatgt	2220
aactcgcctt	gatcgttggg	aaccggagct	gaatgaagcc	ataccaaacg	acgagcgtga	2280
caccacgatg	cctgcagcaa	tggcaacaac	gttgcgcaaa	ctattaactg	gcgaactact	2340
tactctagct	tcccggcaac	aattaataga	ctggatggag	gcggataaag	ttgcaggacc	2400
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gcgtgggtct	cgcggtatca	ttgcagcact	ggggccagat	ggtaagccct	cccgtatcgt	2520
agttatctac	acgacgggga	gtcaggcaac	tatggatgaa	cgaaatagac	agatcgctga	2580
gataggtgcc	tactgatta	agcattggta	actgtcagac	caagtttact	catatatact	2640
ttagattgat	ttaaaacttc	atttttaatt	taaaaggatc	taggtgaaga	tcctTTTTga	2700
taatctcatg	acaaaaatcc	cttaacgtga	gttttcgttc	cactgagcgt	cagaccccgt	2760
agaaaagatc	aaaggatctt	cttgagatcc	ttttttctg	cgcgtaatct	gctgcttgca	2820
aacaaaaaaa	ccaccgctac	cagcgggtgg	ttgtttgccg	gatcaagagc	taccaactct	2880
ttttccgaag	gtaactggct	tcagcagagc	gcagatacca	aatactgtcc	ttctagtgtg	2940
gccgtagtta	ggccaccact	tcaagaactc	tgtagcaccg	cctacatacc	tcgctctgct	3000

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```

aatcctgtta ccagtggctg ctgccagtgg cgataagtcg tgtcttaccg ggttggactc 3060
aagacgatag ttaccggata aggcgcagcg gtcgggctga acgggggggtt cgtgcacaca 3120
gcccagcttg gagcgaacga cctacaccga actgagatac ctacagcgtg agctatgaga 3180
aagcgccacg cttcccgaag ggagaaaggc ggacaggtat ccggttaagcg gcagggtcgg 3240
aacaggagag cgcacgaggg agcttccagg gggaaacgcc tggatatctt atagtctgtg 3300
cgggtttcgc cacctctgac ttgagcgtcg atttttgtga tgctcgtcag gggggcggag 3360
cctatggaaa aacgccagca acgcggcctt ttacgggttc ctggcctttt gctggccttt 3420
tgctcacatg ttcttttctg cgttatcccc tgattctgtg gataaccgta ttaccgcctt 3480
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ccgcaatggt gcaactctcag tacaatctgc tctgatgccg catagttaag ccagtataca 3660
ctccgctatc gctacgtgac tgggtcatgg ctgcgccccg acaccgcca acaccgctg 3720
acgcgccctg acgggcttgt ctgctcccgg catccgctta cagacaagct gtgaccgtct 3780
ccgggagctg catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg aggcag 3836

```

<210> 24
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Truncated soluble parental GAG TCR beta chain containing an introduced Cys residue linked to WT IL-2 via a peptide linker

<400> 24

Met Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
 1 5 10 15

Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
 20 25 30

Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
 35 40 45

Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
 50 55 60

Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
 65 70 75 80

Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Asp
 85 90 95

Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
 100 105 110

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Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu
		115					120								125
Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys
	130					135					140				
Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val
145					150					155					160
Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu
				165					170					175	
Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Ala	Leu	Ser	Ser	Arg
			180					185					190		
Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asp	Pro	Arg	Asn	His	Phe	Arg
		195					200					205			
Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln
	210					215					220				
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly
225					230					235					240
Arg	Ala	Asp	Pro	Gly	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln
				245					250					255	
Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly
			260					265					270		
Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys
		275					280					285			
Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu
	290					295					300				
Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser
305					310					315					320
Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val
				325					330					335	
Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr
			340					345					350		
Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr
		355					360					365			
Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr						
	370					375									

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<210> 25
 <211> 822
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding the full-length parental GAG TCR alpha chain codon optimised for human expression

<400> 25
 atgatgaaga gcctgagggt gctgctggtg atcctgtggc tgcagctgtc ctgggtgtgg 60
 agccagcaga aggaggtgga gcagaatagc ggccctctga gcgtgcccga gggcgccatc 120
 gccagcctga actgtaccta cagcgacaga ggcagccaga gcttcttctg gtacaggcag 180
 tacagcggca agagccccga gctgattatg ttcattctaca gcaacggcga caaggaggac 240
 ggcagattca ccgcccagct gaacaaggcc agccagtaca tcagcctgct gatccgggat 300
 agcaagctgt ccgacagcgc cacctacctg tgtgccgtga gaaccaatag cggctacgcc 360
 ctgaatttctg gcaagggcac cagcctgctg gtgaccccc acatccagaa tcctgacccc 420
 gccgtgtacc agctgagaga cagcaagagc agcgacaaga gcgtgtgtct gttcaccgac 480
 ttcgacagcc agaccaacgt gtcccagagc aaggacagcg acgtgtacat caccgacaag 540
 accgtgctgg acatgaggag catggacttc aagagcaaca gcgccgtggc ctggagcaac 600
 aagagcgact tcgcctgtgc caacgccttc aacaacagca tcatccccga ggacaccttt 660
 ttccccagcc ctgagagcag ctgtgacgtg aaactgggtg agaagagctt cgagaccgac 720
 accaacctga acttccagaa cctgagcgtg atcggcttca gaatcctgct gctgaagggtg 780
 gccggattca acctgctgat gaccctgaga ctgtggagca gc 822

<210> 26
 <211> 930
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding the full-length parental GAG TCR beta chain codon optimised for human expression

<400> 26
 atgggacccg gcctgctgtg ctgggccctg ctgtgcctgc tgggagccgg actggtggac 60
 gccggagtga cccagagccc caccacctg attaagacca ggggccagca ggtgaccctg 120
 agatgtagcc ctaagagcgg ccacgatacc gtgtcctggt atcagcaggc cctgggccag 180
 ggaccccagt tcattctcca gtactacgag gaggaggaga ggcagagagg caacttcccc 240
 gacagattca gcggccacca gttccccaat tacagcagcg agctgaacgt gaatgcctg 300
 ctgctgggcg acagcgccct gtacctgtgt gccagcagcg acacagttag ctacgagcag 360
 tacttcggcc ctggcaccag actgaccgtg accgaggacc tgaagaacgt gttccctcct 420
 gaggtggccg tgttcgagcc cagcgaggcc gagatcagcc acaccagaa ggccaccctg 480
 gtgtgtctgg ccaccggctt ctaccccgac cacgtggagc tgtcctgggt ggtgaacggc 540
 aaggaggtgc acagcggcgt gtccaccgac cccagcccc tgaaggagca gcccgcctg 600

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aacgatagca ggtactgcct gagcagcagg ctgagagtga gcgccacctt ctggcagaac 660
 ccccggaacc acttcagatg ccaggtgcag ttctacggcc tgagcgagaa cgacgagtgg 720
 acccaggata gagccaagcc cgtgaccag atcgtgtccg ccgaggcctg gggcagagcc 780
 gactgtggct tcaccagcga gagctaccag cagggcgtgc tgtccgccac catcctgtac 840
 gagatcctgc tgggcaaggc cacactgtac gccgtgctgg tgtccgccct ggtgctgatg 900
 gctatggtga agcgggaaggc cagcagggggc 930

<210> 27
 <211> 274
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Full-length parental GAG TCR alpha chain
 <400> 27

Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
 1 5 10 15
 Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro
 20 25 30
 Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
 35 40 45
 Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys
 50 55 60
 Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
 65 70 75 80
 Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu
 85 90 95
 Leu Ile Arg Asp Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala
 100 105 110
 Val Arg Thr Asn Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser
 115 120 125
 Leu Leu Val Thr Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 130 135 140
 Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 145 150 155 160
 Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 165 170 175

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Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser

<210> 28
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> Full-length parental GAG TCR beta chain

<400> 28

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Asp Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu
115 120 125

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```

Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
130          135          140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145          150          155          160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
          165          170          175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
          180          185          190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
          195          200          205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210          215          220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225          230          235          240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
          245          250          255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
          260          265          270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275          280          285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290          295          300

Arg Lys Asp Ser Arg Gly
305          310

```

<210> 29
 <211> 207
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Alpha chain of a soluble high affinity c11c6 GAG TCR containing
 an introduced Cys residue

<400> 29

```

Met Ala Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro
1          5          10          15

Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser
20          25          30

```

Case 74 PCT Gag TCRs ST25.txt

Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu
35 40 45
Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr
50 55 60
Ala Gln Leu Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp
65 70 75 80
Ser Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Gly Ala
85 90 95
His Asp Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110
Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125
Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140
Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160
Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
165 170 175
Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190
Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

<210> 30
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Beta chain of a soluble high affinity c11c6 GAG TCR containing an introduced Cys residue

<400> 30

Met Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
1 5 10 15
Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
20 25 30
Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
35 40 45

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Case 74 PCT Gag TCRs ST25.txt

Gln Tyr Ala Leu Gly Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
50 55 60

Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
65 70 75 80

Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Asp
85 90 95

Thr Val Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
100 105 110

Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
115 120 125

Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
130 135 140

Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
145 150 155 160

Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu
165 170 175

Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg
180 185 190

Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg
195 200 205

Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
210 215 220

Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
225 230 235 240

Arg Ala Asp

<210> 31
<211> 18
<212> PRT
<213> Foot-and-mouth disease virus

<400> 31

Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1 5 10 15

Pro Gly