T cell receptors

The present invention relates to T cell receptors (TCRs) which bind the HLA-A2 restricted FMNKFIYEI (158-166) peptide epitope derived from α Fetoprotein (AFP). Certain preferred TCRs of the invention demonstrate excellent binding characteristics and specificity profiles for this AFP epitope.

AFP is expressed during foetal development and is the main component of foetal serum. During development the protein is produced at very high levels by the yolk sac and liver and is later repressed. AFP expression is frequently reactivated in hepatocellular carcinoma (Butterfield *et al*. J Immunol., 2001, Apr 15;166(8):5300-8) and high levels of the protein are used as a diagnostic marker for the disease.

Hepatocellular carcinoma has one of the lowest reported 5 year survival rate of all malignancies in the US, global annual incidence is 1.2 million and is likely to increase due to the pandemic of Hepatitis B and C. Treatment typically involves surgery, however this is only beneficial if carried out in the early stages of the disease. New treatments are therefore desirable.

There are four known epitopes derived from AFP: AFP158, AFP137, AFP325 and AFP542 (Butterfield *et al*. J Immunol., 2001, Apr 15;166(8):5300-8 and Butterfield *et al*. Cancer Res. 1999, 59: 3134-3142). The HLA-A2 restricted AFP158 peptide FMNKFIYEI (SEQ ID No: 1) provides a suitable target for novel immunotherapeutic interventions; this peptide is naturally processed and has been eluted from HepG2 (HLA-A2 positive) liver carcinoma lines and detected by mass spectrometry (Butterfield *et al*. J Immunol., 2001, Apr 15;166(8):5300-8). T cell clones have been raised against AFP158 (and AFP137) (Pichard et al. J Immunother. 2008 Apr;31(3):246-53). However, T cell receptors which recognize this peptide have not been reported.

According to a first aspect of the invention, there is provided a non-naturally occurring and/or purified and/or engineered T cell receptor (TCR) having the property of binding to FMNKFIYEI (SEQ ID No: 1) HLA-A2 complex and comprising at least one TCR alpha chain variable domain and/or at least one TCR beta chain variable domain,

the alpha chain variable domain comprising an amino acid sequence that has at least 90% identity to the sequence of amino acid residues 1- 112 of SEQ ID No: 2, and/or

the beta chain variable domain comprising an amino acid sequence that has at least 90% identity to the sequence of amino acid residues 1- 112 of SEQ ID No: 3.

In some embodiments of the invention, the alpha chain variable domain has at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to amino acid residues 1 to 112 of SEQ ID No: 2.

The beta chain variable domain may have at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to amino acid residues 1 to 112 of SEQ ID No: 3.

TCRs are described using the International Immunogenetics (IMGT) TCR nomenclature, and links to the IMGT public database of TCR sequences. Native alpha-beta heterodimeric TCRs have an alpha chain and a beta chain. Broadly, each chain comprises variable, joining and constant regions, and the beta chain also usually contains a short diversity region between the variable and joining regions, but this diversity region is often considered as part of the joining region. Each variable region comprises three CDRs (Complementarity Determining Regions) embedded in a framework sequence, one being the hypervariable region named CDR3. There are several types of alpha chain variable (Vα) regions and several types of beta chain variable (Vβ) regions distinguished by their framework, CDR1 and CDR2 sequences, and by a partly defined CDR3 sequence. The Vα types are referred to in IMGT nomenclature by a unique TRAV number. Thus "TRAV21" defines a TCR Vα □region having unique framework and CDR1 and CDR2 sequences, and a CDR3 sequence which is partly defined by an amino acid sequence which is preserved from TCR to TCR but which also includes an amino acid sequence which varies from TCR to TCR. In the same way, "TRBV5-1" defines a TCR Vβ□ region having unique framework and CDR1 and CDR2 sequences, but with only a partly defined CDR3 sequence.

The joining regions of the TCR are similarly defined by the unique IMGT TRAJ and TRBJ nomenclature, and the constant regions by the IMGT TRAC and TRBC nomenclature.

The beta chain diversity region is referred to in IMGT nomenclature by the abbreviation TRBD, and, as mentioned, the concatenated TRBD/TRBJ regions are often considered together as the joining region.

The α and β chains of $\alpha\beta$ TCR's are generally regarded as each having two "domains" or "regions", namely variable and constant domains/regions. The terms "domain(s)" and "region(s)" are used interchangeably herein. The variable domain consists of a concatenation of variable region and joining region. In the present specification and claims, the term "TCR alpha variable domain" therefore refers to the concatenation of TRAV and TRAJ regions, and the term TCR alpha constant domain refers to the extracellular TRAC region, or to a C-terminal truncated TRAC sequence. Likewise the term "TCR beta variable domain" refers to the concatenation of TRBV and TRBD/TRBJ regions, and the term TCR beta constant domain refers to the extracellular TRBC region, or to a C-terminal truncated TRBC sequence.

The unique sequences defined by the IMGT nomenclature are widely known and accessible to those working in the TCR field. For example, they can be found in the IMGT public database. The "T cell Receptor Factsbook", (2001) LeFranc and LeFranc, Academic Press, ISBN 0-12-441352-8 also discloses sequences defined by the IMGT nomenclature, but because of its publication date and consequent time-lag, the information therein sometimes needs to be confirmed by reference to the IMGT database.

SEQ ID Nos: 2 and 3 are, respectively, the alpha and beta chain extracellular sequences of what is referred to herein as the “parental” AFP TCR. The parental AFP TCR has the following alpha and beta chain usage:

Alpha chain: TRAV12-2*02/TRAJ41*01/TRAC (the extracellular sequence of the parental AFP TCR alpha chain is given in Figure 1 (SEQ ID No: 2). The CDRs are defined by amino acids 27-32 (CDR1), 50-55 (CDR2) and 90-101 (CDR3) of SEQ ID NO: 2.

Beta chain: TRBV9*01/TRBD2/TRBJ2-7*01/TRBC2 (the extracellular sequence of the parental AFP TCR alpha chain is given in Figure 2 (SEQ ID No: 3). The CDRs are defined by amino acids 27-31 (CDR1), 49-54 (CDR2) and 92-102 (CDR3) of SEQ ID NO: 3.

(Note, the terms ‘*01’ and ‘*02’ indicate there is more than one allelic variant for this sequence, as designated by IMGT nomenclature, and that it is the *01/ *02 variant which is present in the TCR clone referred to above. Note also that the absence of a”*” qualifier means that only one allele is known for the relevant sequence.)

For the purpose of providing a reference TCR against which the binding profile of mutated TCRs of the invention may be compared, it is convenient to use the soluble TCR having the extracellular sequence of the AFP TCR alpha chain given in Figure 3 (SEQ ID No: 4) and the extracellular sequence of the AFP TCR beta chain given in Figure 4 (SEQ ID No: 5). That TCR is referred to herein as the “the reference TCR” or “the reference AFP TCR”. Note that SEQ ID No: 4 is identical to the parental alpha chain extracellular sequence SEQ ID No: 2 except that C159 has been substituted for T159 (i.e. T48 of TRAC). Likewise SEQ ID No: 5 is identical to the parental beta chain extracellular sequence SEQ ID No: 3 except that C169 has been substituted for S169 (i.e. S57 of TRBC2), A187 has been substituted for C187 and D201 has been substituted for N201. These cysteine substitutions relative to the parental AFP alpha and beta chain extracellular sequences enable the formation of an interchain disulfide bond which stabilises the refolded soluble TCR, ie the TCR formed by refolding extracellular alpha and beta chains. Use of the stable disulfide linked soluble TCR as the reference TCR enables more convenient assessment of binding affinity and binding half-life.

TCRs of the invention may be transformed into T cells, rendering them capable of destroying cells presenting AFP HLA-A2 complex, for administration to a patient in the treatment process known as adoptive therapy. For this purpose, it would be desirable if the TCRs had a higher affinity and/or a slower off-rate for the peptide-HLA complex than native TCRs specific for that complex. Dramatic increases in affinity have been associated with a loss of antigen specificity in TCR gene-modified CD8 T cells, which could result in the nonspecific activation of these TCR-transfected CD8 cells. Therefore, TCRs having a somewhat higher affinity and/or a slower off-rate for the peptide-HLA complex than native TCRs specific for that complex, but not a dramatically higher affinity and/or dramatically slower off-rate for the peptide-HLA complex than native TCRs, would be preferred for

adoptive therapy (see Zhao *et al.,* (2007) *J Immunol.* **179:** 5845-54; Robbins *et al.,* (2008) *J Immunol.* **180:** 6116-31; and WO2008/038002).

Embodiments of the invention include TCRs which are mutated relative to the parental AFP TCR. Mutated TCRs may comprise an alpha chain variable domain that includes a mutation in one or more of the amino acids corresponding to: 31Q, 32S, 94D, 95S, 96G, 97Y, and 98A, with reference to the numbering shown in SEQ ID No: 2. For example, the alpha chain variable domain may have one or more of the following mutations:

Residue no.		
31Q	F	Y
32S	A	
94D	Q	
95S	N	
96G	S	
97Y	V	
98A	S	

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

The alpha chain variable domain may comprise an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to residues 1-112 of any one of SEQ ID No: 6, SEQ ID No: 7, SEQ ID No: 8, SEQ ID No: 9, SEQ ID No: 10, SEQ ID No: 11, SEQ ID No: 12, SEQ ID No: 13, SEQ ID No: 14, SEQ ID No: 15, SEQ ID No: 16, SEQ ID No: 17, SEQ ID No: 18, SEQ ID No: 19 and SEQ ID No: 20, and preferably, the amino acid sequence also has at least 90% identity to residues 1-112 of SEQ ID No: 2. The amino acids underlined in Figure 5 may be invariant.

In one embodiment, the TCR comprises an alpha chain variable domain comprising Q1 to H112 of SEQ ID No: 11, SEQ ID No: 12 or SEQ ID No: 13, and/or a beta chain variable domain comprising D1 to T112 of SEQ ID NO: 3.

Mutations can be carried out using any appropriate method including, but not limited to, those based on polymerase chain reaction (PCR), restriction enzyme-based cloning, or ligation independent cloning (LIC) procedures. These methods are detailed in many of the of the standard molecular biology texts. For further details regarding polymerase chain reaction (PCR) and restriction enzyme-based cloning, see Sambrook & Russell, (2001) Molecular Cloning – A Laboratory Manual (3rd Ed.) CSHL Press. Further information on ligation independent cloning (LIC) procedures can be found in Rashtchian, (1995) Curr Opin Biotechnol **6**(1): 30-6.

Also within the scope of the invention are phenotypically silent variants of any TCR disclosed herein. As used herein the term "phenotypically silent variants" is understood to refer to those TCRs which have a K_D and/or binding half-life for the FMNKFIYEI (SEQ ID No: 1) HLA-A2 complex within the ranges of K_Ds and binding half-lives described below. For example, as is known to those

skilled in the art, it may be possible to produce TCRs that incorporate changes in the constant and/or variable domains thereof compared to those detailed above without altering the affinity for the interaction with the FMNKFIYEI (SEQ ID No: 1) HLA-A2 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.

As will 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 binding characteristics of the TCR. All such trivial variants are encompassed by the present invention.

Native TCRs exist in heterodimeric $\alpha\beta$ or $\gamma\delta$ forms. However, recombinant TCRs consisting of αα or $\beta\beta$ homodimers have previously been shown to bind to peptide MHC molecules. Therefore, the TCR of the invention may be a heterodimeric $\alpha\beta$ TCR or may be an $\alpha\alpha$ or $\beta\beta$ homodimeric TCR.

For use in adoptive therapy, an $\alpha\beta$ heterodimeric TCR may, for example, be transfected as full length chains having both cytoplasmic and transmembrane domains. In certain embodiments TCRs of the invention may have an introduced disulfide bond between residues of the respective constant domains, as described, for example, in WO 2006/000830.

TCRs of the invention, particularly alpha-beta heterodimeric TCRs, may comprise an alpha chain TRAC constant domain sequence and/or a beta chain TRBC1 or TRBC2 constant domain sequence. The alpha and beta chain constant domain sequences may be modified by truncation or substitution to delete the native disulfide bond between Cys4 of exon 2 of TRAC and Cys2 of exon 2 of TRBC1 or TRBC2. The alpha and/or beta chain constant domain sequence(s) may also be modified by substitution of cysteine residues for Thr 48 of TRAC and Ser 57 of TRBC1 or TRBC2, the said cysteines forming a disulfide bond between the alpha and beta constant domains of the TCR.

TCRs of the invention may be in single chain format, for example see WO 2004/033685. Single chain formats include $\alpha\beta$ TCR polypeptides of the Vα-L-Vβ, Vβ-L-Vα, Vα-Cα-L-Vβ, Vα-L-Vβ-Cβ, Vα-Cα-L-Vβ–Cβ types, wherein Vα and Vβ are TCR α and β variable regions respectively, Cα and Cβ are TCR α and β constant regions respectively, and L is a linker sequence. In certain embodiments single chain TCRs of the invention may have an introduced disulfide bond between residues of the respective constant domains, as described in WO 2004/033685.

The TCRs of the invention have the property of binding the FMNKFIYEI (SEQ ID No: 1) HLA-A2 complex. Certain TCRs of the invention have been found to be highly suitable for use in adoptive therapy. Such TCRs may have a K_D for the complex of less than the parental AFP TCR, for example from about 1 μM to about 21 μM and/or have a binding half-life (T½) for the complex in the range of from less than 0.5 seconds to about 2 seconds. Increasing the binding affinity of a native TCR often reduces the selectivity of the TCR for its peptide-MHC ligand, and this is

demonstrated in Zhao Yangbing et al., (J. Immunol, 2007 179: 9, p5845-5854). However, certain TCRs of the invention remain selective for the FMNKFIYEI HLA-A2 complex, despite, in some embodiments, having higher binding affinity than the parental AFP TCR (see Example 6).

Binding affinity (inversely proportional to the equilibrium constant K_D) and binding half-life (expressed as T½) can be determined by any appropriate method. It will be appreciated that doubling the affinity of a TCR results in halving the K_D. T½ is calculated as ln2 divided by the off-rate (k_{off}). So doubling of T½ results in a halving in k_{off}. K_D and k_{off} values for TCRs are usually measured for soluble forms of the TCR, i.e. those forms which are truncated to remove cytoplasmic and transmembrane domain residues. Therefore it is to be understood that a given TCR has an improved binding affinity for, and/or a binding half-life for the parental TCR if a soluble form of that TCR has the said characteristics. Preferably the binding affinity or binding half-life of a given TCR is measured several times, for example 3 or more times, using the same assay protocol, and an average of the results is taken. In a preferred embodiment these measurements are made using the Surface Plasmon Resonance (BIAcore) method of Example 3 herein.

In a further aspect, the present invention provides nucleic acid encoding a TCR of the invention. In some embodiments, the nucleic acid is cDNA. In some embodiments, the invention provides nucleic acid comprising a sequence encoding an α chain variable domain of a TCR of the invention. In some embodiments, the invention provides nucleic acid comprising a sequence encoding a β chain variable domain of a TCR of the invention. In some embodiments, the invention provides nucleic acid comprising a sequence encoding both an α chain variable domain of a TCR of the invention and a β chain variable domain of a TCR of the invention. The nucleic acid may be non-naturally occurring and/or purified and/or engineered.

In another aspect, the invention provides a vector which comprises nucleic acid of the invention. Preferably the vector is a TCR expression vector.

The invention also provides a cell harbouring a vector of the invention, preferably a TCR expression vector. The vector may comprise nucleic acid of the invention encoding in a single open reading frame, or two distinct open reading frames, the alpha chain and the beta chain respectively. Another aspect provides a cell harbouring a first expression vector which comprises nucleic acid encoding the alpha chain of a TCR of the invention, and a second expression vector which comprises nucleic acid encoding the beta chain of a TCR of the invention. Such cells are particularly useful in adoptive therapy. The cells may be isolated and/or recombinant and/or non-naturally occurring and/or engineered.

Since the TCRs of the invention have utility in adoptive therapy, the invention includes a non-naturally occurring and/or purified and/or or engineered cell, especially a T-cell, presenting a TCR of the invention. There are a number of methods suitable for the transfection of T cells with nucleic acid (such as DNA, cDNA or RNA) encoding the TCRs of the invention (see for example Robbins et al., (2008) J Immunol. **180**: 6116-6131). T cells expressing the TCRs of the invention will be

suitable for use in adoptive therapy-based treatment of cancers such as those of the pancreas and liver. As will be known to those skilled in the art, there are a number of suitable methods by which adoptive therapy can be carried out (see for example Rosenberg et al., (2008) Nat Rev Cancer **8**(4): 299-308).

As is well-known in the art TCRs of the invention may be subject to post-translational modifications when expressed by transfected cells. Glycosylation is one such modification, which comprises the covalent attachment of oligosaccharide moieties to defined amino acids in the TCR chain. For example, asparagine residues, or serine/threonine residues are well-known locations for oligosaccharide attachment. The glycosylation status of a particular protein depends on a number of factors, including protein sequence, protein conformation and the availability of certain enzymes. Furthermore, glycosylation status (i.e oligosaccharide type, covalent linkage and total number of attachments) can influence protein function. Therefore, when producing recombinant proteins, controlling glycosylation is often desirable. Glycosylation of transfected TCRs may be controlled by mutations of the transfected gene (Kuball J et al. (2009), J Exp Med 206(2):463–475). Such mutations are also encompassed in this invention.

The TCR of the invention may be associated with a detectable label, a therapeutic agent or a PK modifying moiety.

Certain TCRs of the invention may be in soluble form (i.e. having no transmembrane or cytoplasmic domains). For stability, TCRs of the invention, and preferably soluble $\alpha\beta$ heterodimeric TCRs, may have an introduced disulfide bond between residues of the respective constant domains, as described, for example, in WO 03/020763. Some soluble TCRs of the invention are useful for making fusion proteins which can be used for delivering detectable labels or therapeutic agents to antigen presenting cells and tissues containing antigen presenting cells. They may therefore be associated (covalently or otherwise) with a detectable label (for diagnostic purposes wherein the TCR is used to detect the presence of cells presenting the FMNKFIYEI (SEQ ID No 1) HLA-A2 complex; a therapeutic agent; or a PK modifying moiety (for example by PEGylation).

Detectable labels for diagnostic purposes include for instance, fluorescent labels, radiolabels, enzymes, nucleic acid probes and contrast reagents.

Therapeutic agents which may be associated with the TCRs of the invention include immunomodulators, radioactive 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 a TCR 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 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 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, docetaxel, etoposide, gemcitabine, ifosfamide, irinotecan, melphalan, mitoxantrone, sorfimer sodiumphotofrin II, temozolomide, topotecan, trimetreate glucuronate, auristatin E vincristine and doxorubicin;
- peptide cytotoxins, i.e. proteins or fragments thereof with the ability to kill mammalian cells. For example, ricin, diphtheria toxin, pseudomonas bacterial exotoxin A, DNase and RNase;
- 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. For example, 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;
- immuno-stimulants, i.e. immune effector molecules which stimulate immune response. For example, cytokines such as IL-2 and IFN-γ,
- Superantigens and mutants thereof;
- TCR-HLA fusions;
- chemokines such as IL-8, platelet factor 4, melanoma growth stimulatory protein, etc;
- antibodies or fragments thereof, including anti-T cell or NK cell determinant antibodies (e.g. anti-CD3, anti-CD28 or anti-CD16);
- alternative protein scaffolds with antibody like binding characteristics
- complement activators;
- xenogeneic protein domains, allogeneic protein domains, viral/bacterial protein domains, viral/bacterial peptides.

For administration to patients, the TCRs or cells of the invention may be provided in a pharmaceutical composition together with one or more pharmaceutically acceptable carriers or excipients. Cells in accordance with the invention will usually be supplied 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) include instructions for use. It may include a plurality of said unit dosage forms.

The pharmaceutical composition may be adapted for administration by any appropriate route, preferably a parenteral (including subcutaneous, intramuscular, or 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.

TCRs, pharmaceutical compositions, vectors, nucleic acids and cells of the invention may be provided in substantially pure form, for example at least 50%, at least 60%, at least 70%, at least 80%, at least 85 %, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% pure.

Also provided by the invention are:

- a non-naturally occurring and/or purified and/or engineered TCR which binds the FMNKFIYEI peptide presented as a peptide-HLA-A2 complex, or a cell expressing and/or presenting such a TCR, for use in medicine, preferably in a method of treating cancer. The method may comprise adoptive therapy;
- the use of a TCR which binds the FMNKFIYEI peptide presented as a peptide-HLA-A2 complex, or a cell expressing and/or presenting such a TCR, in the manufacture of a medicament for treating cancer;
- a method of treating cancer in a patient, comprising administering to the patient a TCR which binds the FMNKFIYEI peptide presented as a peptide-HLA-A2 complex, or a cell expressing and/or presenting such a TCR.

It is preferred that the TCR which binds the FMNKFIYEI peptide presented as a peptide-HLA-A2 complex is a TCR of the invention.

Preferred features of each aspect of the invention are as for each of the other aspects *mutatis mutandis*. The published documents mentioned herein are incorporated to the fullest extent permitted by law. Citation or identification of any document in this application is not an admission that such document is available as prior art to the present invention.

Description of Figures

Figure 1 (SEQ ID No: 2) gives the amino acid sequence of the extracellular part of the alpha chain of the parental AFP-specific TCR with gene usage TRAV12-2*02/TRAJ41*01/TRAC.

Figure 2 (SEQ ID No: 3) gives the amino acid sequence of the extracellular part of the beta chain of the parental AFP-specific TCR with gene usage TRBV9*01/TRBD2/TRBJ2-7*01/TRBC2.

Figure 3 (SEQ ID No: 4) gives the amino acid sequence of the alpha chain of a soluble TCR (referred to herein as the “reference TCR”). The sequence is the same as that of Figure 1 (SEQ ID No: 2) except that a cysteine (bold and underlined) is substituted for T159 of SEQ ID No: 2 (i.e. T48 of the TRAC constant region).

Figure 4 (SEQ ID No: 5) gives the amino acid sequence of the beta chain of a soluble TCR (referred to herein as the “reference TCR”). The sequence is the same as that of Figure 2 (SEQ ID

No: 3) except that a cysteine (bold and underlined) is substituted for S169 of SEQ ID No: 3 (i.e. S57 of the TRBC2 constant region) and A187 is substituted for C187 and D201 is substituted for N201.

Figure 5 (SEQ ID Nos: 6-20) gives the amino acid sequence of the mutated alpha chains which may be present in TCRs of the invention. The CDR regions are underlined and amino acid changes relative to the parental AFP TCR are shaded.

Figures 6 (SEQ ID No: 21) and (SEQ ID No: 22) gives the DNA sequences encoding the TCR alpha and beta chains shown in Figures 3 and 4 respectively

Figure 7 (SEQ ID No: 23) gives the DNA sequence for the parental AFP TCR gene (alpha chain-2A-beta chain construct with the Porcine teschovirus-1 2A sequence bold and underlined) for transduction of T-cells.

Figure 8 (SEQ ID No: 24) gives the amino acid sequence of the parental AFP TCR for T-cell transduction produced from the DNA sequence of Figure 7. The Porcine teschovirus-1 2A sequence is bold and underlined.

Figure 9 shows the results of an ELISPOT assay in which IFN-γ release of AFP TCR-transduced T-cells in response to a range of target cells was assessed

The invention is further described in the following non-limiting examples.

Examples

Example 1

Cloning of the parental AFP TCR alpha and beta chain variable region sequences into pGMT7-based expression plasmids

The reference AFP TCR variable alpha and TCR variable beta domains were PCR amplified from total cDNA isolated from an AFP T cell clone. In the case of the alpha chain, an alpha chain variable region sequence specific oligonucleotide A1 gaattccatatgcaaaaagaagttgaacaaaattctggacccctc (SEQ ID No: 25) which encodes the restriction site NdeI and an alpha chain constant region sequence specific oligonucleotide A2 ttgtcagtcgacttagagtctctcagctggtacacg (SEQ ID No: 26) which encodes the restriction site SalI are used to amplify the alpha chain variable domain. In the case of the beta chain, a beta chain variable region sequence specific oligonucleotide B1 gaattccatatggattctggagttacacaaaccccaaagcacctg (SEQ ID No: 27) which encodes the restriction site NdeI and a beta chain constant region sequence specific oligonucleotide B2 tagaaaccggtggccaggcacaccagtgtggc (SEQ ID No: 28) which encodes the restriction site Age1 are used to amplify the beta chain variable domain.

The alpha and beta variable domains were cloned into pGMT7-based expression plasmids containing either Cα or Cβ by standard methods described in (Molecular Cloning a Laboratory Manual Third edition by Sambrook and Russell). Plasmids were sequenced using an Applied Biosystems 3730xl DNA Analyzer.

The DNA sequences encoding the TCR alpha chain cut with *NdeI* and *SalI* were ligated into pGMT7 + Cα vector, which was cut with *NdeI* and *XhoI*. The DNA sequences encoding the TCR beta chain cut with *NdeI* and *AgeI* was ligated into separate pGMT7 + Cβ vector, which was also cut with *NdeI* and *AgeI*.

Ligation

Ligated plasmids were transformed into competent *E.coli* strain XL1-blue cells and plated out on LB/agar plates containing 100 μg/ml ampicillin. Following incubation overnight at 37ºC, single colonies are picked and grown in 10 ml LB containing 100 μg/ml ampicillin overnight at 37ºC with shaking. Cloned plasmids were purified using a Miniprep kit (Qiagen) and the plasmids were sequenced using an Applied Biosystems 3730xl DNA Analyzer.

Figures 3 and 4 show respectively the reference AFP TCR α and β chain extracellular amino acid sequences (SEQ ID Nos: 4 and 5 respectively) produced from the DNA sequences of Figures 7 (SEQ ID No: 21) (SEQ ID No: 22) respectively. Note that, relative to the parental TCR, cysteines were substituted in the constant regions of the alpha and beta chains to provide an artificial inter-chain disulphide bond on refolding to form the heterodimeric TCR. The introduced cysteines are shown in bold and underlined.

Example 2

Expression, refolding and purification of soluble parental AFP TCR

The expression plasmids containing the TCR α-chain and β-chain respectively, as prepared in Example 1, were transformed separately into *E.coli* strain BL21pLysS, and single ampicillin-resistant colonies were grown at 37°C in TYP (ampicillin 100 μg/ml) medium to OD_{600} of ~0.6-0.8 before inducing protein expression with 0.5 mM IPTG. Cells were harvested three hours post-induction by centrifugation for 30 minutes at 4000rpm in a Beckman J-6B. Cell pellets were lysed with 25 ml Bug Buster® (Novagen) in the presence of $MgCl_2$ and DNaseI. 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 (50 mM Tris-HCl pH 8.0, 0.5% Triton-X100, 200 mM NaCl, 10 mM NaEDTA) 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: 50 mM Tris-HCl pH 8.0, 1 mM NaEDTA. Finally, the inclusion bodies were divided into 30 mg aliquots and frozen at -70°C. Inclusion body protein yield was quantified by

solubilising with 6 M guanidine-HCl and an OD measurement was taken on a Hitachi U-2001 Spectrophotometer. The protein concentration was then calculated using the extinction coefficient.

Approximately 15mg of TCR β chain and 15mg of TCR α chain solubilised inclusion bodies were thawed from frozen stocks and diluted into 10ml of a guanidine solution (6 M Guanidine-hydrochloride, 50 mM Tris HCl pH 8.1, 100 mM NaCl, 10 mM EDTA, 10 mM DTT), to ensure complete chain denaturation. The guanidine solution containing fully reduced and denatured TCR chains was then injected into 0.5 litre of the following refolding buffer: 100 mM Tris pH 8.1, 400 mM L-Arginine, 2 mM EDTA, 5 M Urea. The redox couple (cysteamine hydrochloride and cystamine dihydrochloride) to final concentrations of 6.6 mM and 3.7 mM respectively, were added approximately 5 minutes before addition of the denatured TCR chains. The solution was left for ~30 minutes. The refolded TCR was dialysed in Spectra/Por ® 1 membrane (Spectrum; Product No. 132670) against 10 L H_2O for 18-20 hours. After this time, the dialysis buffer was changed twice to fresh 10 mM Tris pH 8.1 (10 L) and dialysis was continued at 5 °C ± 3 °C for another ~8 hours.

Soluble TCR 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 in 10 mM Tris pH 8.1 over 50 column volumes using an Akta® purifier (GE Healthcare). Peak fractions were pooled and a cocktail of protease inhibitors (Calbiochem) were added. The pooled fractions were then stored at 4 °C and analysed by Coomassie-stained SDS-PAGE before being pooled and concentrated. Finally, the soluble TCR was purified and characterised using a GE Healthcare Superdex® 75HR gel filtration column pre-equilibrated in PBS buffer (Sigma). 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.

Example 3

Binding characterisation

BIAcore Analysis

A surface plasmon resonance biosensor (BIAcore® 3000) can be used to analyse the binding of a soluble TCR to its peptide-MHC ligand. This is facilitated by producing soluble biotinylated peptide-HLA ("pHLA") complexes which can be immobilised to a streptavidin-coated binding surface (sensor chip). The sensor chips comprise four individual flow cells which enable simultaneous measurement of T-cell receptor binding to four different pHLA complexes. Manual injection of pHLA complex allows the precise level of immobilised class I molecules to be manipulated easily.

Biotinylated class I HLA-A*02 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*02-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 β2-microglobulin was also expressed as inclusion bodies in *E.coli* from an appropriate construct, at a level of ~500 mg/litre bacterial culture.

E. coli cells were lysed and inclusion bodies were 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 β2m into 0.4 M L-Arginine, 100 mM Tris pH 8.1, 3.7 mM cystamine dihydrochloride, 6.6 mM cysteamine hydrochloride, 4 mg/L of the AFP peptide required to be loaded by the HLA-A*02 molecule, by addition of a single pulse of denatured protein into refold buffer at < 5ºC. Refolding was allowed to reach completion at 4ºC for at least 1 hour.

Buffer was exchanged by dialysis in 10 volumes of 10 mM Tris pH 8.1. The protein solution was then filtered through a 1.5μm 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 in 10 mM Tris pH 8.1 using an Akta® purifier (GE Healthcare). HLA-A*02-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.

Biotinylation tagged pHLA molecules were buffer exchanged into 10 mM Tris pH 8.1, 5 mM NaCl using a GE Healthcare 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 μg/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.

The biotinylated pHLA-A*01 molecules were purified using gel filtration chromatography. A GE Healthcare 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 using an Akta® purifier (GE Healthcare). Biotinylated pHLA-A*02 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*02 molecules were stored frozen at –20ºC.

The BIAcore® 3000 surface plasmon resonance (SPR) biosensor 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 BIAcore® experiments were performed at a temperature of 25°C, using PBS buffer (Sigma, pH 7.1-7.5) as the running buffer and in preparing dilutions of protein samples. Streptavidin was immobilised to the flow cells by standard amine coupling methods. The pHLA complexes were immobilised via the biotin tag. The assay was then performed by passing soluble TCR over the surfaces of the different flow cells at a constant flow rate, measuring the SPR response in doing so.

Equilibrium binding constant

The above BIAcore® analysis methods were used to determine equilibrium binding constants. Serial dilutions of the disulfide linked soluble heterodimeric form of the reference AFP TCR were prepared and injected at constant flow rate of 5 μl min^{-1} over two different flow cells; one coated with ~1000 RU of specific HLA-A*02 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 non-linear curve fitting model in order to calculate the equilibrium binding constant, K_D (Price & Dwek, Principles and Problems in Physical Chemistry for Biochemists (2^{nd} Edition) 1979, Clarendon Press, Oxford). The disulfide linked soluble form of the reference AFP TCR (Example 2) demonstrated a K_D of approximately 754 μM. From the same BIAcore® data the T½ was approximately <0.5 s.

Kinetic Parameters

The above BIAcore® analysis methods were also used to determine equilibrium binding constants and off-rates.

For high affinity TCRs (see Example 4 below) K_D was determined by experimentally measuring the dissociation rate constant, k_{off}, and the association rate constant, k_{on}. The equilibrium constant K_D was calculated as k_{off}/k_{on}.

TCR was injected over two different cells one coated with ~1000 RU of FMNKFIYEI HLA-A*02 complex, the second coated with ~1000 RU of non-specific HLA-A2-peptide complex. Flow rate was set at 50 μl/min. Typically 250 μl of TCR at ~ 1 μM concentration was injected. Buffer was then flowed over until the response had returned to baseline or >2 hours had elapsed. Kinetic parameters were calculated using BIAevaluation® software. The dissociation phase was fitted to a single exponential decay equation enabling calculation of half-life.

Example 4

Preparation of mutated TCRs of the invention

Phage display is one means by which libraries of AFP TCR variants can be generated in order to identify higher affinity mutants. The TCR phage display and screening methods described in (Li et al, (2005) Nature Biotech 23 (3): 349-354) were applied to the parental AFP TCR of Example 1.

TCRs with improved binding compared to the parental AFP TCR were identified, having one or more mutations in the alpha chain variable domain amino acid residues 31Q, 32S, 94D, 95S, 96G, 97Y, and 98A (using the numbering shown in SEQ ID No: 2). Specific examples of the amino acid sequences of the variable regions of the alpha chains (SEQ ID Nos: 6 to 20) of higher affinity TCRs are shown in Figure 5. These alpha chains are mutated in CDR1 and/or CDR3.

Expression plasmids containing the TCR α-chain and β-chain respectively for the following TCRs of the invention were prepared as in Example 1:

TCR ID	Alpha Chain SEQ ID No	Beta Chain SEQ ID No
Parental	2	3
ADB327	6	3
ADB329	7	3
ADB330	8	3
ADB331	9	3
ADB328	10	3
ADB352	11	3
ADB350	12	3
ADB332	13	3
ADB351	14	3
ADB349	15	3
ADB353	16	3
ADB326	17	3
ADB333	18	3
ADB334	19	3
ADB335	20	3

The plasmids were transformed separately into *E.coli* strain BL21pLysS, and single ampicillin-resistant colonies grown at 37°C in TYP (ampicillin 100 μg/ml) medium to OD_{600} of ~0.6-0.8 before inducing protein expression with 0.5 mM IPTG. Cells were harvested three hours post-induction by centrifugation for 30 minutes at 4000rpm in a Beckman J-6B. Cell pellets were lysed with 25 ml Bug Buster® (Novagen) in the presence of $MgCl_2$ and DNaseI. 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 (50 mM Tris-HCl pH 8.0, 0.5% Triton-X100, 200 mM NaCl, 10 mM NaEDTA,) 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: 50 mM Tris-HCl pH 8.0, 1 mM NaEDTA. Finally, the inclusion bodies were divided into 30 mg aliquots and frozen at -70°C. Inclusion body protein yield was quantified by

solubilising with 6 M guanidine-HCl and an OD measurement was taken on a Hitachi U-2001 Spectrophotometer. The protein concentration was then calculated using the extinction coefficient.

Approximately 10mg of TCR β chain and 10mg of TCR α chain solubilised inclusion bodies for each TCR of the invention were diluted into 10ml of a guanidine solution (6 M Guanidine-hydrochloride, 50 mM Tris HCl pH 8.1, 100 mM NaCl, 10 mM EDTA, 10 mM DTT), to ensure complete chain denaturation. The guanidine solution containing fully reduced and denatured TCR chains was then injected into 0.5 litre of the following refolding buffer: 100 mM Tris pH 8.1, 400 mM L-Arginine, 2 mM EDTA, 5 M Urea. The redox couple (cysteamine hydrochloride and cystamine dihydrochloride) to final concentrations of 6.6 mM and 3.7 mM respectively, were added approximately 5 minutes before addition of the denatured TCR chains. The solution was left for ~30 minutes. The refolded TCR was dialysed in Spectra/Por® 1 membrane (Spectrum; Product No. 132670) against 10 L H_2O for 18-20 hours. After this time, the dialysis buffer was changed twice to fresh 10 mM Tris pH 8.1 (10 L) and dialysis was continued at 5 °C ± 3 °C for another ~8 hours.

Soluble TCR 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 in 10 mM Tris pH 8.1 over 15 column volumes using an Akta® purifier (GE Healthcare). The pooled fractions were then stored at 4 °C and analysed by Coomassie-stained SDS-PAGE before being pooled and concentrated. Finally, the soluble TCRs were purified and characterised using a GE Healthcare Superdex® 75HR gel filtration column pre-equilibrated in PBS buffer (Sigma). 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.

The affinity profiles of the thus-prepared TCRs for the AFP epitope were assessed using the method of Example 3, and compared with the reference TCR. The results are set forth in the following table:

TCR alpha chain extracellular domain	T½ (s)	KD µM
Parental	<0.5	754
ADB327	<0.5	489
ADB329	<0.5	356
ADB330	<0.5	178
ADB331	<0.5	79.5
ADB328	<0.5	33.3
ADB352	<0.5	20.1
ADB350	0.8	11.0
ADB332	0.7	10.6
ADB351	0.8	8.0
ADB349	1.8	4.55
ADB353	1.5	4.17
ADB326	1.5	1.50
ADB333	3.8	0.71
ADB334	4.3	0.52
ADB335	13.9	0.31

Example 5

Transfection of T-cells with parental and variant AFP TCRs

(a) Lentiviral vector preparation by Express-In mediated transient transfection of 293T cells

A 3rd generation lentiviral packaging system was used to package lentiviral vectors containing the gene encoding the desired TCR. 293T cells were transfected with 4 plasmids (one lentiviral vector containing the TCR alpha chain-P2A-TCR beta chain single ORF gene described in Example 5c (below), and 3 plasmids containing the other components necessary to construct infective but non-replicative lentiviral particles) using Express-In mediated transfection (Open Biosystems).

For transfection take one T150 flask of 293T cells in exponential growth phase, with cells evenly distributed on the plate, and slightly more than 50% confluent. Bring Express-In aliquots to room temperature. Place 3 ml Serum-Free Medium (RPMI 1640 + 10mM HEPES) in a sterile 15 ml conical tube. Add 174 µl of Express-In Reagent directly into the Serum-Free Medium (this provides for a 3.6:1 weight ratio of Reagent to DNA). Mix thoroughly by inverting tubes 3-4 times and incubate at room temperature for 5-20 minutes.

In a separate 1.5 ml microtube, add 15 µg plasmid DNA to premixed packaging mix aliquots (containing 18 µg pRSV.REV (Rev expression plasmid), 18 µg pMDLg/p.RRE (Gag/Pol expression plasmid), 7 µg pVSV-G (VSV glycoprotein expression plasmid), usually ~22 µl, and pipette up and down to ensure homogeneity of the DNA mix. Add ~1 ml of Express-In/Serum-Free Medium to the DNA mix drop wise then pipette up and down gently before transferring back to the remainder of

the Express-In/Serum-Free Medium. Invert tube 3-4 times and incubate at room temperature for 15-30 minutes.

Remove old culture medium from flask of cells. Add Express-In/medium/DNA (3ml) complex to flask direct into the bottom of an upright flask of 293T cells. Slowly, place the flask flat to cover the cells and very gently rock the flask to ensure even distribution. After 1 minute add 22 ml fresh culture medium (R10+HEPES: RPMI 1640, 10% heat-inactivated FBS, 1% Pen/Strep/L-glutamine, 10 mM HEPES) and carefully return to incubator. Incubate overnight at 37^{o}C/5% CO2. After 24 hours, proceed to harvest the medium containing packaged lentiviral vectors.

To harvest the packaged lentiviral vectors, filter the cell culture supernatent through a 0.45micron nylon syringe filter, centrifuge the culture medium at 10,000 g for 18 hours (or 112,000 g for 2 hours), remove most of the supernatant (taking care not to disturb the pellet) and resuspend the pellet in the remaining few ml of supernatant (usually about 2 ml from a 31 ml starting volume per tube). Snap freeze on dry ice in 1 ml aliquots and store at -80^{o}C.

(b) Transduction of T cells with packaged lentiviral vectors containing gene of interest

Prior to transduction with the packaged lentiviral vectors, human T cells (CD8 or CD4 or both depending on requirements) are isolated from the blood of healthy volunteers. These cells are counted and incubated overnight in R10 containing 50 U/ml IL-2 at 1x10^{6} cells per ml (0.5 ml/well) in 48 well plates with pre-washed anti-CD3/CD28 antibody-coated microbeads (Dynabeads® T cell expander, Invitrogen) at a ratio of 3 beads per cell.

After overnight stimulation, 0.5 ml of neat packaged lentiviral vector is added to the desired cells. Incubate at 37^{o}C/5% CO2 for 3 days. 3 days post-transduction count cells and dilute to 0.5x10^{6} cells/ml. Add fresh medium containing IL-2 as required. Remove beads 5-7 days post-transduction. Count cells and replace or add fresh medium containing IL-2 at 2 day intervals. Keep cells between 0.5x10^{6} and 1x10^{6} cells/ml. Cells can be analysed by flow cytometry from day 3 and used for functional assays (e.g. ELISpot for IFNγ release, see Example 6) from day 5. From day 10, or when cells are slowing division and reduced in size, freeze cells in aliquots of at least 4x10^{6} cells/vial (at 1x10^{7} cells/ml in 90% FBS/10% DMSO) for storage.

(c) Parental TCR gene for T-cell transfection by methods (a) and (b) above

Figure 7 is a DNA sequence (SEQ ID No: 23) encoding the parental AFP TCR (codon-optimised for maximal human cell expression). It is a full length alpha chain - Porcine teschovirus-1 2A - full length beta chain single open reading frame construct. The 2A sequence is underlined, and is preceded by nucleotides encoding a furin cleavage site to assist proteolytic removal of the 2A sequence (discussed further below in relation to Fig 8 (SEQ ID No: 24). Peptide bond skipping during protein translation of the mRNA at the 3' end of the 2A sequence produces two proteins: 1) alpha TCR chain-2A fusion, 2) beta TCR chain. SEQ ID No: 23 includes NheI and SalI restriction sites (underlined).

Figure 8 is the amino acid sequence (SEQ ID No: 24) corresponding to Figure 7

In Figure 8:

M1- Q22 is a leader sequence which is removed on maturation of the parental alpha chain TCR;

Q23-S274 corresponds to the parental alpha chain sequence;

Q23-N246 corresponds to the parental alpha chain extracellular domain;

L247-T268 is the alpha chain transmembrane region of the mature TCR;

L269-S274 is the alpha chain intracellular region of the mature TCR;

R277-R280 is the furin cleavage site to assist proteolytic removal, in the Golgi apparatus, of the P2A sequence A285-P303;

G275, S276, S281 to G284, are flexible linkers allowing full function of the furin cleavage and P2A sequences;

R304-V323 is a leader sequence which is removed on maturation of the parental beta chain TCR;

D324-G614 corresponds to the parental beta chain sequence;

D324-E585 corresponds to the parental beta chain extracellular domain;

I586-V607 is the beta chain transmembrane region of the mature TCR;

K608-G614 is the beta chain intracellular region of the mature TCR.

(d) T-cells transfected with parental and high affinity AFP TCRs

Following the procedures described in (a) and (b) above, the parental AFP alpha-2A-beta TCR gene (SEQ ID No: 23 (Figure 7)) was inserted into the pELNSxv lenti vector using the NheI and SalI restriction sites unique to both DNA constructs, and transfected T-cells created.

Similarly, T-cells may be created by transfection with genes identical to SEQ ID No: 23 (Fig 7) except that they encode an alpha chain variable domain having one of SEQ ID Nos: 6 to 20 associated with the variable domain sequence (D1 to T112) of the parental beta chain SEQ ID No: 3;

Example 6

Activation of AFP TCR engineered T cells

The following assay was carried out to demonstrate the activation of TCR-transduced cytotoxic T lymphocytes (CTLs) in response to tumour cell lines. IFN-γ production, as measured using the ELISPOT assay, was used as a read-out for cytotoxic T lymphocyte (CTL) activation.

ELISPOTs

Reagents

Assay media: 10% FCS (Gibco, Cat# 2011-09), 88% RPMI 1640 (Gibco, Cat# 42401), 1% glutamine (Gibco Cat# 25030) and 1% penicillin/streptomycin (Gibco Cat# 15070-063).

Wash buffer: 0.01M PBS/0.05% Tween 20

PBS (Gibco Cat# 10010)

The Human IFNγ ELISPOT kit (BD Bioscience; Cat# 551849) containing capture and detection antibodies and Human IFN-γ PVDF ELISPOT 96 well plates, with associated AEC substrate set (BD Bioscience, Cat# 551951)

Methods

Target cell preparation

The target cells used in this method were natural epitope-presenting cells: HepG2 hepatocellular carcinoma cells which are both HLA-$A2^+$ AFP^+. HEP2 normal human hepatocytes, which are HLA-$A2^+$ AFP^-, were used as a negative control. Sufficient target cells (50,000 cells/well) were washed by centrifugation three times at 1200 rpm, 10 min in a Megafuge® 1.0 (Heraeus). Cells were then re-suspended in assay media at 10^6 cells/ml.

Effector Cell Preparation

The effector cells (T cells) used in this method were peripheral blood lymphocytes (PBL), obtained by negative selection using CD14 and CD25 microbead kits (Miltenyi Biotech Cat# 130-050-201 and 130-092-983 respectively) from freshly isolated peripheral blood mononuclear cells (PBMC) from the venous blood of healthy volunteers. Cells were stimulated with antiCD3/CD28 coated beads (Dynabeads® T cell expander, Invitrogen), transduced with lentivirus carrying the gene encoding the full $\alpha\beta$ TCR of interest (based on the construct described in Example 5 and shown in Figure 7) and expanded in assay media containing 50U/ml IL-2 until between 10 and 13 days post transduction. These cells were then placed in assay media prior to washing by centrifugation at 1200 rpm, 10 min in a Megafuge® 1.0 (Heraeus). Cells were then re-suspended in assay media at a 4X the final required concentration.

Plates were prepared as follows: 100 µl anti-IFN-γ capture antibody was diluted in 10 ml sterile PBS per plate. 100 µl of the diluted capture antibody was then dispensed into each well. The plates were then incubated overnight at 4^oC. Following incubation the plates were washed (programme 1, plate type 2, Ultrawash Plus 96-well plate washer; Dynex) to remove the capture antibody. Plates were then blocked by adding 200 µl of assay media to each well and incubated at room temperature for two hours. The assay media was then washed from the plates (programme

1, plate type 2, Ultrawash Plus 96-well plate washer, Dynex) and any remaining media was removed by flicking and tapping the ELISPOT plates on a paper towel.

The constituents of the assay were then added to the ELISPOT plate in the following order:

50 µl of target cells 10^6 cells/ml (giving a total of 50,000 target cells/well)
50 µl media (assay media)
50 µl effector cells (20,000 TCR-transduced PBL cells/well)

The plates were then incubated overnight (37^oC / 5%CO_2). The next day the plates were washed three times (programme 1, plate type 2, Ultrawash Plus 96-well plate washer, Dynex) with wash buffer and tapped dry on paper towel to remove excess wash buffer. 100 µl of primary detection antibody was then added to each well. The primary detection antibody was diluted into 10ml of dilution buffer (the volume required for a single plate) using the dilution specified in the manufacturer's instructions. Plates were then incubated at room temperature for at least 2 hours prior to being washed three times (programme 1, plate type 2, Ultrawash Plus 96-well plate washer, Dynex) with wash buffer; excess wash buffer was removed by tapping the plate on a paper towel.

Secondary detection was performed by adding 100 µl of diluted streptavidin-HRP to each well and incubating the plate at room temperature for 1 hour. The streptavidin-HRP was diluted into 10ml dilution buffer (the volume required for a single plate), using the dilution specified in the manufacturer's instructions. The plates were then washed three times (programme 1, plate type 2, Ultrawash Plus 96-well plate washer, Dynex) with wash buffer and tapped on paper towel to remove excess wash buffer. Plates were then washed twice with PBS by adding 200 µl to each well, flicking the buffer off and tapping on a paper towel to remove excess buffer. No more than 15 mins prior to use, one drop (20 ul) of AEC chromogen was added to each 1 ml of AEC substrate and mixed. 10ml of this solution was prepared for each plate; 100 µl was added per well. The plate was then protected from light using foil, and spot development monitored regularly, usually occurring within 5 – 20 mins. The plates were washed in tap water to terminate the development reaction, and shaken dry prior to their disassembly into three constituent parts. The plates were then allowed to dry at room temperature for at least 2 hours prior to counting the spots using an Immunospot® Plate reader (CTL; Cellular Technology Limited).

RESULTS

IFNγ release by activated TCR-transduced T cells in response to a variety of AFP-positive and control tumour cell lines was tested by ELISPOT assay (as described above). The number of ELISPOT spots observed in each well was plotted using Graph Pad Prism®.

CD4+, CD8+ or mixed CD4+/CD8+ T cells expressing the WT TCR or one of TCR Nos:1-5 (as described in the table below) were incubated with AFP+ HLA:A2+ tumour cell line HepG2 or with AFP- HLA:A2+ HEP2 normal hepatocytes. A sample containing no T cells was used as a control.

TCR No	TCR α variable domain SEQ ID NO:	TCR β variable domain SEQ ID NO:
1	11	D1 to T112 of SEQ ID No: 3
2	12	D1 to T112 of SEQ ID No: 3
3	13	D1 to T112 of SEQ ID No: 3
4	14	D1 to T112 of SEQ ID No: 3
5	15	D1 to T112 of SEQ ID No: 3

Figure 9 demonstrates that T cells transduced with the TCRs described in the table above are activated in response to AFP positive tumour cells (HepG2). Activation of these variant TCRs is greater than for the WT TCR. Activation by AFP negative normal hepatocytes (HEP2) is minimal demonstrating the specificity of the TCRs for AFP.

Claims:

1. A non-naturally occurring and/or purified and/or engineered T cell receptor (TCR) having the property of binding to FMNKFIYEI (SEQ ID No: 1) HLA-A2 complex and comprising at least one TCR alpha chain variable domain and at least one TCR beta chain variable domain,

the alpha chain variable domain comprising Q1 to H112 of SEQ ID No: 11, SEQ ID No 12, SEQ ID No 13, SEQ ID No 14 or SEQ ID No 15, and

the beta chain variable domain comprising D1 to T112 of SEQ ID No: 3.

2. The TCR of claim 1 having an alpha chain TRAC constant domain sequence and/or a beta chain TRBC1 or TRBC2 constant domain sequence.

3. The TCR of claim 2, wherein, the alpha and/or beta chain constant domain sequence(s) are modified by truncation or substitution to delete the native disulfide bond between Cys4 of exon 2 of TRAC and Cys2 of exon 2 of TRBC1 or TRBC2.

4. The TCR of claim 2 or claim 3, wherein the alpha and/or beta chain constant domain sequence(s) are modified by substitution of cysteine residues for Thr 48 of TRAC and Ser 57 of TRBC1 or TRBC2, the cysteines forming a disulfide bond between the alpha and beta constant domains of the TCR.

5. The TCR of any preceding claim, which is in single chain format of the type Vα-L-Vβ, Vβ-L-Vα, Vα-Cα-L-Vβ, Vα-L-Vβ-Cβ, or Vα-Cα-L-Vβ-Cβ wherein Vα and Vβ are TCR α and β variable regions respectively, Cα and Cβ are TCR α and β constant regions respectively, and L is a linker sequence.

6. The TCR of any one of claims 1-4, which is an alpha-beta heterodimer.

7. The TCR of any preceding claim associated with a detectable label, a therapeutic agent or a PK modifying moiety.

8. Non-naturally occurring and/or purified and/or engineered nucleic acid encoding the TCR of any one of the preceding claims.

9. A non-naturally occurring and/or purified and/or engineered cell presenting a TCR as claimed in any one of claims 1-7.

10. A cell as claimed in claim 9, which is a T-cell.

11. A cell harbouring

(a) a TCR expression vector which comprises nucleic acid as claimed in claim 8 encoding in a single open reading frame, or two distinct open reading frames, the alpha chain and the beta chain respectively; or

(b) a first expression vector which comprises nucleic acid encoding the alpha chain of a TCR as claimed in any of claims 1 to 7, and a second expression vector which comprises nucleic acid encoding the beta chain of a TCR as claimed in any of claims 1 to 7.

12. A pharmaceutical composition comprising a TCR as claimed in any one of claims 1 to 7 or a cell as claimed in claim 10 or claim 11, together with one or more pharmaceutically acceptable carriers or excipients.

13. A TCR as claimed in any one of claims 1 to 7, or a cell as claimed in claim 9, 10 or 11, for use in medicine.

14. The TCR or the cell of claim 13, for use in the treatment of cancer.

15. The TCR or the cell of claim 14, wherein the treatment comprises adoptive therapy.

Abstract

T cell receptors

The present invention relates to T cell receptors (TCRs) which bind the HLA-A2 restricted FMNKFIYEI (158-166) peptide epitope derived from α Fetoprotein (AFP). Certain preferred TCRs of the invention demonstrate excellent binding characteristics and specificity profiles for this AFP epitope. T cell receptors of the invention comprise at least one TCR alpha chain variable domain and/or at least one TCR beta chain variable domain, the alpha chain variable domain comprising an amino acid sequence that has at least 90% identity to the sequence of amino acid residues 1- 112 of SEQ ID No: 2, and/or the beta chain variable domain comprising an amino acid sequence that has at least 90% identity to the sequence of amino acid residues 1- 112 of SEQ ID No: 3.