CLAIMS:

1. A chimeric antigen receptor including an antigen-recognition domain for recognising a dysfunctional $P2X_7$ receptor, a transmembrane domain and a linker domain for linking the antigen-recognition domain and the transmembrane domain, wherein the linker domain consists of between 70 to 180 amino acids, and wherein the dysfunctional $P2X_7$ receptor has a reduced capacity to bind ATP compared to an ATP-binding capacity of a functional $P2X_7$ receptor.

2. The chimeric antigen receptor according to claim 1, wherein the linker domain consists of:

a) between 90 to 160 amino acids; or

b) between 110 to 130 amino acids; or

c) between 115 to 125 amino acids; or

d) between 117 to 121 amino acids.

3. The chimeric antigen receptor according to claim 1 or 2, wherein the linker domain consists of about 119 amino acids.

4. The chimeric antigen receptor according to any one of claims 1 to 3, wherein the linker domain comprises:

a) an amino acid sequence homologous to an immunoglobulin hinge region; or

b) an amino acid sequence homologous to a hinge region selected from CD4, CD8, CD3, CD7 or CD28 regions.

5. The chimeric antigen receptor according to any one of claims 1 to 4, wherein the linker domain comprises an amino acid sequence homologous to an immunoglobulin hinge region of IgG, IgD, IgA, or the Constant Heavy (CH) 2 region of IgM or IgE, or a functional variant thereof having at least 50%, 60%, 70%, 80%, 90%, 93%, 96% or 99% sequence identity thereto.

6. The chimeric antigen receptor according to any one of claims 1 to 5, wherein the linker domain comprises an amino acid sequence homologous to a hinge region

from an IgG isotype immunoglobulin, or a functional variant thereof having at least 50%, 60%, 70%, 80%, 90%, 93% or 96% sequence identity thereto.

7. The chimeric antigen receptor according to any one of claims 1 to 5, wherein the linker domain comprises an amino acid sequence homologous to the hinge region of the IgG1, IgG2 or IgG4 subclass of immunoglobulin or a functional variant thereof having at least 50%, 60%, 70%, 80%, 90% or 93% sequence identity thereto.

8. The chimeric antigen receptor according to any one of claims 1 to 7, wherein the linker domain comprises an amino acid sequence homologous to a hinge region from an IgG isotype immunoglobulin including a CXXC motif.

9. The chimeric antigen receptor according to claim 8, wherein the CXXC motif is selected from the group of CPPC, CPRC or CPSC

10. The chimeric antigen receptor according to any one of claims 1 to 9, wherein the linker domain comprises one or more amino acid sequences that is at least 50%, 60%, 70%, 80%, 90%, 93% or 96% identical to or is identical to:

a) a constant heavy (CH) region of an immunoglobulin;

b) a CH1 region, a CH2 region, a CH3 region and/or a CH4 region of an immunoglobulin;

c) a CH2 region and/or a CH3 region of an IgG isotype immunoglobulin;

11. The chimeric antigen receptor according to any one of claims 1 to 10, wherein the linker domain consists of:

a) one or more immunoglobulin hinge region(s) and/or one or more CH region(s) of an immunoglobulin;

b) an IgG hinge region and one or more CH region(s) of an immunoglobulin; or

c) an IgG hinge region and/or a CH2 or CH3 region of an immunoglobulin.

12. The chimeric antigen receptor according to any one of claims 1 to 11, wherein the linker domain comprises an amino acid sequence according to any one of SEQ ID NOs: 9 to 17, or a functional variant thereof having at least 50%, 60%, 70%, 80%, 90%,

93% or 96% sequence identity thereto.

13. The chimeric antigen receptor according to claims 1 to 12, wherein the chimeric antigen receptor does not comprise an amino acid sequence in the linker domain that substantially binds to an Fc receptor.

14. The chimeric antigen receptor according to any one of claims 1 to 13, wherein the chimeric antigen receptor when expressed in a CD8+ T cell has a cytotoxicity *in vitro* against target cells expressing a dysfunctional P2X7 receptor of at least 20%, at a ratio of CAR expressing CD8+T cells : target cells of 30:1 or greater.

15. The chimeric antigen receptor according to any one of claims 1 to 14, wherein when expressed in a CD3+ T cell, the T cell demonstrates activity against as least 2 different cancer types, at least 3 different cancer types, at least 4 different cancer types, at least 5 different cancer types, at least 6 different cancer types, at least 7 different cancer types, at least 8 different cancer types, at least 9 different cancer types, at least 10 different cancer types.

16. The chimeric antigen receptor according to any one of claims 1 to 15, wherein the antigen-recognition domain recognises an epitope associated with an adenosine triphosphate (ATP)-binding site of the P2X7 receptor.

17. The chimeric antigen receptor according to any one of claims 1 to 16, wherein the dysfunctional $P2X_7$ receptor has a conformational change that renders the receptor dysfunctional.

18. The chimeric antigen receptor according to claim 17, wherein the conformational change is a change of an amino acid from a trans-conformation to a cis-conformation; or wherein the amino acid that has changed from a trans-conformation to a cis-conformation is proline at amino acid position 210 of the dysfunctional $P2X_7$ receptor; or wherein the antigen-recognition domain recognises an epitope that includes one or more amino acid residues spanning from glycine at amino acid position 200 to cysteine at amino acid position 216 of the dysfunctional $P2X_7$ receptor.; or

wherein the antigen-recognition domain recognises an epitope that includes proline at amino acid position 210 of the dysfunctional $P2X_7$ receptor.

19. The chimeric antigen receptor according to any one of claims 1 to 18, wherein the antigen-recognition domain comprises an amino acid sequence homologous to the amino acid sequence of an antigen binding domain of an antibody that binds to a dysfunctional $P2X_7$ receptor, or wherein the antigen-recognition domain comprises the complementary determining regions of the heavy chain and/or light chain of an antibody that binds to a dysfunctional $P2X_7$ receptor.

20. The chimeric antigen receptor according to any one of claims 1 to 19, wherein the transmembrane domain comprises all or part of the transmembrane domain of CD8 or CD28.

21. A nucleic acid molecule or construct comprising a nucleotide sequence encoding the chimeric antigen receptor according to any one of claims 1 to 20.

22. An *ex vivo* genetically modified cell, the cell comprising the chimeric antigen receptor according to any one of claims 1 to 20; and/or the cell comprising the nucleic acid molecule according to claim 21 or the nucleic acid construct according to claim 21.

23. The *ex vivo* genetically modified cell according to claim 22, wherein the cell is selected from: a leukocyte; a Peripheral Blood Mononuclear Cell (PBMC); a lymphocyte; a T cell; a CD4+ T cell; a CD8+ T cell; a gamma delta T cell; a natural killer cell; a natural killer T cell; a macrophage.