CLAIMS

1. A fusion protein that is capable of binding both CD137 and GPC3, wherein the fusion protein comprises at least two subunits in any order, wherein a first subunit comprises a full-length immunoglobulin or an antigen-binding domain thereof and is specific for GPC3, and wherein a second subunit comprises a lipocalin mutein and is specific for CD137.

2. A fusion protein, wherein the fusion protein comprises at least two subunits, wherein a first subunit comprises a full-length immunoglobulin or an antigen-binding domain thereof and is specific for GPC3, and wherein a second subunit comprises a lipocalin mutein and is specific for CD137, wherein the second subunit is linked at the N-terminus to the C-terminus of each heavy chain of the first subunit, optionally via a linker.

3. The fusion protein of claim 1 or 2,
   (a) wherein the fusion protein is capable of binding GPC3 with a K_D value of at most about 1 nM or comparable to or lower than the K_D value of the immunoglobulin or an antigen-binding domain thereof that is included in the first subunit alone;
   (b) wherein the fusion protein is capable of binding CD137 with an EC_{50} value of at most about 3 nM or comparable to or lower than the EC_{50} value of the lipocalin mutein specific for CD137 that is included in the second subunit alone;
   (c) wherein the fusion protein is cross-reactive with cynomolgus GPC3;
   (d) wherein the fusion protein is capable of simultaneously binding CD137 and GPC3 with an EC_{50} values of at most about 10 nM, when said fusion protein is measured in an ELISA assay;
   (e) wherein the fusion protein is capable of binding GPC3 expressing tumor cells;
   (f) wherein the fusion protein is capable of inducing increased secretion of IL-2;
   (g) wherein the fusion protein is capable of inducing increased IL-2 secretion to a higher level than SEQ ID NO: 83 and/or with a better efficiency as compared to SEQ ID NO: 83;
   (h) wherein the fusion protein is capable of inducing lymphocyte-mediated cytotoxicity;
   (i) wherein the fusion protein is capable of inducing enhanced killing of GPC3 expressing tumor cells mediated by T cells than SEQ ID NO: 83 and/or inducing cytotoxic T cell-activation with a better efficacy as compared to SEQ ID NO: 83;
   (j) wherein the fusion protein is capable of co-stimulating T-cell responses in a GPC3-dependent manner; or

(k) wherein the fusion protein is capable of co-stimulating T-cell responses in a tumor microenvironment.

4. The fusion protein of any one of claims 1-3, wherein the fusion protein has a half-life in mice of at least 50 hours, at least 75 hours, at least 100 hours, at least 125 hours, at least 150 hours, at least 175 hours, at least 200 hours, at least 250 hours, or even longer, and/or wherein the fusion protein has a half-life in mice that is longer than that of SEQ ID NO: 83 and/or wherein the fusion protein has an isoelectric point of at least 6.5, at least 6.8, at least 7.1, at least 7.4, at least 7.5, at least 7.7, or even higher, and/or wherein the fusion protein has an isoelectric point higher than that of SEQ ID NO: 83.

5. The fusion protein of any one of claims 1-4, wherein the lipocalin mutein comprises one or more mutated amino acid residues at positions corresponding to positions 28, 36, 40-41, 49, 52, 65, 68, 70, 72-73, 77, 79, 81, 83, 87, 94, 96, 100, 103, 106, 125, 127, 132 and 134 of the linear polypeptide sequence of mature human neutrophil gelatinase-associated lipocalin (hNGAL) (SEQ ID NO: 2), or wherein the lipocalin mutein comprises one or more mutated amino acid residues at positions corresponding to positions 20, 25, 28, 33, 36, 40-41, 44, 49, 52, 59, 68, 70-73, 77-82, 87, 92, 96, 98, 100, 101, 103, 122, 125, 127, 132, and 134 of the linear polypeptide sequence of mature human neutrophil gelatinase-associated lipocalin (hNGAL) (SEQ ID NO: 2), or wherein the lipocalin mutein comprises one or more mutated amino acid residues at positions corresponding to positions 5, 26-31, 33-34, 42, 46, 52, 56, 58, 60-61, 65, 71, 85, 94, 101, 104-106, 108, 111, 114, 121, 133, 148, 150 and 153 of the linear polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1).

6. The fusion protein of any one of claims 1-5, wherein the amino acid sequence of the lipocalin mutein comprises one of the following sets of mutated amino acid residues in comparison with the linear polypeptide sequence of mature hNGAL (SEQ ID NO: 2):

(a) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Lys; Gln 49 → Asn; Tyr 52 → Met; Ser 68 → Gly; Leu 70 → Thr; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Ala; Arg 81 → Ser; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(b) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Arg; Gln 49 → Ile; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Met; Leu 70 → Lys; Arg 72 → Asp; Lys 73 →

Asp; Asp 77 → Met; Trp 79 → Asp; Arg 81 → Trp; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(c) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Arg; Gln 49 → Asn; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Ala; Leu 70 → Ala; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Asp; Arg 81 → Trp; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(d) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Lys; Gln 49 → Asn; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Ala; Leu 70 → Ala; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Asp; Arg 81 → Trp; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(e) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Lys; Gln 49 → Ser; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Gly; Leu 70 → Ser; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Ala; Arg 81 → Met; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(f) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Lys; Gln 49 → Val; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Gly; Leu 70 → Thr; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Arg; Trp 79 → Asp; Arg 81 → Ser; Cys 87 → Ser; Leu 94 → Phe; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(g) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Arg; Gln 49 → His; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Gly; Leu 70 → Thr; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Ala; Arg 81 → Ser; Cys 87 → Ser; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(h) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Lys; Gln 49 → Asn; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Gly; Leu 70 → Thr; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Thr; Trp 79 → Ala; Arg 81 → Ser; Phe 83 → Leu; Cys 87 → Ser; Leu 94 → Phe; Asn 96 → Lys; Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr;

(i) Gln 28 → His; Leu 36 → Gln; Ala 40 → Ile; Ile 41 → Arg; Gln 49 → Ser; Tyr 52 → Met; Asn 65 → Asp; Ser 68 → Ala; Leu 70 → Thr; Arg 72 → Asp; Lys 73 → Asp; Asp 77 → Asn; Trp 79 → Ala; Arg 81 → Ser; Cys 87 → Ser; Asn 96 → Lys;

Tyr 100 → Phe; Leu 103 → His; Tyr 106 → Ser; Lys 125 → Phe; Ser 127 → Phe; Tyr 132 → Glu; and Lys 134 → Tyr.

(j) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Ser; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(k) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Ser; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Lys 98 → Arg; Tyr 100 → Asp; Pro 101 → Leu; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(l) Asn 25 → Tyr; Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Gly; Ser 68 → Asp; Leu 70 → Met; Phe 71 → Leu; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Gln; Phe 92 → Ser; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(m) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Gly; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Tyr 78 → His; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(n) Asn 25 → Asp; Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Gly; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(o) Val 33 → Ile; Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Gly; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(p) Gln 20 → Arg; Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Glu 44 → Val; Gln 49 → His; Tyr 52 → Gly; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Phe 122 → Tyr; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(q) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Ser; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Ile 80 → Asn; Arg 81 → Trp; Thr 82 → Pro; Asn 96 → Phe; Tyr 100 → Asp; Pro 101 → Leu; Leu 103 → Pro; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly;

(r) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Gln 49 → His; Tyr 52 → Gly; Lys 59 → Asn; Ser 68 → Asp; Leu 70 → Met; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → Gln; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly; and

(s) Leu 36 → Met; Ala 40 → Asn; Ile 41 → Leu; Glu 44 → Asp; Gln 49 → His; Tyr 52 → Ser; Ser 68 → Asp; Leu 70 → Met; Phe 71 → Leu; Arg 72 → Leu; Lys 73 → Asp; Asp 77 → His; Trp 79 → Ile; Arg 81 → Trp; Phe 92 → Leu; Asn 96 → Phe; Tyr 100 → Asp; Leu 103 → His; Lys 125 → Ser; Ser 127 → Ile; Tyr 132 → Trp; and Lys 134 → Gly.

7. The fusion protein of any one of claims 1-6, wherein the amino acid sequence of the lipocalin mutein comprises one of the following sets of mutated amino acid residues in comparison with the linear polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1):

(a) Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; and Cys 153 → Ser;

(b) Ala 5 → Thr; Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Lys 65 → Arg; Val 85 → Asp; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Lys 121 → Glu; Ala 133 → Thr; and Cys 153 → Ser;

(c) Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Lys 65 → Asn; Lys 94 → Arg; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Lys 121 → Glu; Ala 133 → Thr; and Cys 153 → Ser;

(d) Ala 5 → Val; Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Lys 65 → Arg; Lys 94 → Glu; Cys 101 →

Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Lys 121 → Glu; Ala 133 → Thr; and Cys 153 → Ser;

(e) Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Thr 42 → Ser; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Ser 150 → Ile; and Cys 153 → Ser;

(f) Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Lys 52 → Glu; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Thr 71 → Ala; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Ala 133 → Thr; Arg 148 → Ser; Ser 150 → Ile; and Cys 153 → Ser; and

(g) Ala 5 → Thr; Arg 26 → Glu; Glu 27 → Gly; Phe 28 → Cys; Pro 29 → Arg; Glu 30 → Pro; Met 31 → Trp; Leu 33 → Ile; Glu 34 → Phe; Gly 46 → Asp; Leu 56 → Ala; Ser 58 → Asp; Arg 60 → Pro; Cys 61 → Ala; Thr 71 → Ala; Cys 101 → Ser; Glu 104 → Val; Leu 105 → Cys; His 106 → Asp; Lys 108 → Ser; Arg 111 → Pro; Lys 114 → Trp; Ser 150 → Ile; and Cys 153 → Ser.

8. The fusion protein of any one of claim 1-7, wherein the amino acid sequence of the lipocalin mutein has at least 85% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 32-38, or wherein the amino acid sequence of the lipocalin mutein has at least 85% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 39-57.

9. The fusion protein of any one of claims 1-8, wherein the second subunit is linked at the N-terminus via a linker to the N- or C-terminus of each heavy chain constant region (CH) of the first subunit or the N- or C-terminus of each light chain constant region (CL) of the first subunit.

10. The fusion protein of any one of claims 1-9, wherein the antibody comprises a heavy chain variable region and a light chain variable region, respectively, as follows: SEQ ID NOs: 78 and 79, SEQ ID NOs: 129 and 79, SEQ ID NOs: 114 and 115, or SEQ ID NOs: 126 and 127, or heavy chain variable region and a light chain variable region that have a sequence having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, at least 97%, at least 98%, or higher sequence identity to the amino acid sequences shown in SEQ ID NOs: 78 and 79, SEQ ID NOs: 129 and 79, SEQ ID NOs: 114 and 115, or SEQ ID NOs: 126 and 127

and/or wherein the heavy chain of the antibody comprises the following set of CDR sequences: GYTFTDYE (HCDR1, SEQ ID NO: 72), LDPKTGDT (HCDR2, SEQ ID NO: 73), TRFYSYTY (HCDR3; SEQ ID NO: 74), and the light chain of the antibody comprises the following set of CDR sequences: of QSLVHSNRNTY (LCDR1, SEQ ID NO: 75), KVS (LCDR2), SQNTHVPPT (LCDR3; SEQ ID NO: 77).

11. The fusion protein of any one of claims 1-15, wherein the antibody has an IgG4 backbone, and particularly has one or more of the following mutations: S228P, N297A, F234A, L235A, M428L, N434S, M252Y, S254T, and T256E.

12. The fusion protein of any one of claims 1-11, wherein the fusion protein comprises the amino acids shown in SEQ ID NOs: 87 and 82, the amino acids shown in SEQ ID NOs: 88 and 82, the amino acids shown in SEQ ID NOs: 81 and 89, the amino acids shown in SEQ ID NOs: 81 and 90, the amino acids shown in SEQ ID NOs: 91 and 82, the amino acids shown in SEQ ID NOs: 92 and 82, the amino acids shown in SEQ ID NOs: 81 and 93, the amino acids shown in SEQ ID NOs: 81 and 94, the amino acids shown in SEQ ID NOs: 95 and 82, or the amino acids shown in SEQ ID NOs: 96 and 82, and particularly wherein the fusion protein comprises the amino acid sequences having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, at least 97%, at least 98%, or higher sequence identity to the amino acid sequences shown in SEQ ID NOs: 87 and 82, SEQ ID NOs: 88 and 82, SEQ ID NOs: 81 and 89, SEQ ID NOs: 81 and 90, SEQ ID NOs: 91 and 82, SEQ ID NOs: 92 and 82, SEQ ID NOs: 81 and 93, SEQ ID NOs: 81 and 94, SEQ ID NOs: 95 and 82, or SEQ ID NOs: 96 and 82.

13. A nucleic acid molecule comprising a nucleotide sequence encoding the fusion protein of any one of claims 1-12.

14. A method of producing the fusion protein according to any one of claims 1-12, wherein the fusion protein is produced starting from the nucleic acid coding for the fusion protein.

15. Use of one or more fusion proteins of any one of claims 1-12 or one or more compositions comprising such fusion protein in the manufacture of a medicament for simultaneously activating downstream signaling pathways of CD137 and engaging GPC3-positive tumor cells, wherein the medicament is to be administered to a tissue comprising a tumor.

16. Use of one or more fusion proteins of any one of claims 1-12 or one or more compositions comprising such fusion protein in the manufacture of a medicament for simultaneously co-stimulating T-cells and engaging GPC3-positive tumor cells, wherein the medicament is to be administered to a tissue comprising a tumor.

17. Use of one or more fusion proteins of any one of claims 1-12 or one or more compositions comprising such fusion protein in the manufacture of a medicament for inducing a localized lymphocyte response in the vicinity of GPC3-positive tumor cells, wherein the medicament is to be administered to a tissue comprising a tumor.

18. Use of one or more fusion proteins of any one of claims 1-12 or one or more compositions comprising such fusion protein in the manufacture of a medicament for inducing increased lymphocyte-mediated cytolysis of GPC3-positive tumor cells, wherein the medicament is to be administered to a tissue comprising a tumor.

19. A pharmaceutical composition comprising one or more fusion proteins of any one of claims 1-12.

20. Use of the fusion protein of any one claims 1-12 or one or more compositions comprising such fusion protein in the manufacture of a medicament for preventing, ameliorating, or treating GPC3-positive cancers .