

comprising at least two intracellular signaling domains, wherein the at least two intracellular signaling domains are selected from the group consisting of an intracellular signaling domain from Fc epsilon receptor Ig (FCER1G), a PI3K recruitment domain, an intracellular signaling domain from CD40 and an intracellular signaling domain from TRIF, wherein the antigen binding domain comprises an antibody or a fragment thereof having a heavy chain variable domain (VH) comprising a CDR3 sequence selected from the sequences GGFGSSYWYFDV (SEQ ID NO: 153) or FYSYTY (SEQ ID NO: 154).

[0041] In some embodiments, the antigen binding domain comprises a GPC3 binding domain or a TROP2 binding domain. In some embodiments, the antigen binding domain comprises a heavy chain variable domain (VH) comprising a VH CDR1, CDR2, and CDR3, and a light chain variable domain (VL) comprising a VL CDR1, CDR2 and CDR3; wherein the VH CDR1, CDR2 and CDR3 comprises a sequence listed in Table 1A; and the VL CDR1, CDR2 and CDR3 comprises a sequence listed in Table 1A. In some embodiments, the antigen binding domain has a VH with at least 80% sequence identity to a VH of an antigen binding domain of Table 1A, and a VL with at least 80% sequence to a VL of an antigen binding domain of Table 1A. In some embodiments, the CFP further comprises a signal peptide. In some embodiments, the signal peptide comprises a sequence MWLQSLLLGLTVACSIS (SEQ ID NO: 7). In some embodiments, the extracellular domain comprises a sequence with at least 90% sequence identity to a sequence of Table 1C. In some embodiments, the CFP comprises a CD89 transmembrane domain comprising a sequence that has at least 90% sequence identity to SEQ ID NO: 11 (Table 1D). In some embodiments, an intracellular signaling domain of the at least two intracellular signaling domains comprises a sequence with at least 80% sequence identity to a sequence of Table 2. In some embodiments, the CFP comprises an intracellular domain that comprises a sequence with at least 80% sequence identity to a sequence of Table 3. In some embodiments, the CFP comprises a sequence having at least 80% sequence identity to a sequence of Table 4.

[0042] In one aspect, provided herein is a composition comprising a recombinant polynucleic acid, wherein the recombinant polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), wherein the CFP has a sequence with at least 95% sequence identity to a sequence of Table 4. In some embodiments, the CFP has a sequence with at least 98%, 99% or 100% sequence identity to a sequence of Table 4. In some embodiments, the intracellular domain comprises at least one additional intracellular signaling domain. In some embodiments, the antigen binding domain comprises an antibody or a fragment thereof. In some embodiments, the antigen binding domain comprises an scFv. In some embodiments, the antigen binding domain comprises the extracellular domain comprises a hinge domain connecting the antigen binding domain and the transmembrane domain. In some embodiments, the recombinant polynucleic acid is an mRNA. In some embodiments, the recombinant polynucleic acid is associated with one or more lipids. In some embodiments, the recombinant polynucleic acid is encapsulated in a liposome.

is associated with a lipid nanoparticle, or within lipid nanoparticle; (c) the recombinant polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), wherein the CFP is an anti-GPC3 CFP and has a sequence with at least 95% sequence identity to SEQ ID NO: 36 or 152; and (d) the recombinant polynucleic acid comprises a sequence with at least 80% sequence identity to SEQ ID NO: 142 or the portion of SEQ ID NO: 142 that does not contain the 5' UTR and/or 3' UTR. Also provided herein is a pharmaceutical composition comprising a recombinant polynucleic acid, wherein: (a) the recombinant polynucleic acid is RNA; (b) the recombinant polynucleic acid is associated with a lipid nanoparticle, or within lipid nanoparticle; (c) the recombinant polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), wherein the CFP is an anti-GPC3 CFP and has a sequence with at least 95% sequence identity to SEQ ID NO: 36 or 152; and (d) the recombinant polynucleic acid comprises a sequence with at least 80% sequence identity to SEQ ID NO: 142 or the portion of SEQ ID NO: 142 that does not contain the 5' UTR and/or 3' UTR. In one aspect, provided herein is a method of treating cancer in a subject in need thereof comprising administering to the subject the pharmaceutical composition described in this paragraph and elsewhere in the specification, wherein the cancer is any one of a lung cancer, liver cancer, prostate cancer, lymphoma or hepatocellular carcinoma (HCC), non-small cell lung cancers (NSCLC), breast cancer, cervical cancer, colon cancer, gastric cancer, bladder cancer, thyroid cancer, osteosarcoma, lung squamous cell carcinoma, ovarian yolk sac tumor, melanoma, and urothelial carcinoma.

[0053] In one aspect, provided herein is a method of expressing a CFP specific for myeloid cell expression in vivo, the method comprising (i) preparing a therapeutically acceptable aqueous formulation of a composition comprising the composition of any one of the compositions described above; (ii) administering to a subject the therapeutically acceptable aqueous formulation systemically; wherein upon isolating and testing a suitable tissue sample from the subject at a suitable time following administration, expression of the CFP is detected in a myeloid cell in the tissue sample. In some embodiments, the suitable tissue sample may be peripheral blood. In some embodiments, the suitable time for testing may be 2, 3, or 4 days after administering.

[0053a] In one aspect, provided herein is a composition comprising a polynucleic acid, wherein the polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), the CFP comprising:

- (a) an extracellular domain;
- (b) a transmembrane domain operatively linked to the extracellular domain; and
- (c) a transmembrane domain operatively linked to the extracellular domain; and

wherein the CFP comprises a sequence having at least 95% sequence identity to SEQ ID NO: 36.

[0053b] In another aspect, provided herein is a composition comprising a polynucleic acid, wherein the polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), the CFP comprising:

- (a) an extracellular domain;

(b) a transmembrane domain operatively linked to the extracellular domain; and

(c) an intracellular domain operatively linked to the transmembrane domain;

wherein the CFP comprises a sequence having at least 95% sequence identity to SEQ ID NO: 26.

[0053c] In another aspect, provided herein is use of the pharmaceutical composition as described herein in the manufacture of a medicament for treatment of cancer.

[0053d] In another aspect, provided herein is the pharmaceutical composition as described herein for use in therapy.

INCORPORATION BY REFERENCE

[0054] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0055] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings.

QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO. 43) and

QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAKNTLYLQMSSLPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO. 44).

[0120] In some embodiments, the anti-CD70 binding domain comprises a heavy chain complementarity determining region 3 (CDR3) that is the CDR3 of the VH sequence of SEQ ID NO: 43. In some embodiments, the anti-CD70 VH domain CDR3 has a sequence: GPYGLDNALDA (SEQ ID NO: 155). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises a heavy chain complementarity determining region 1 (CDR1) that is the CDR1 of the VH sequence of SEQ ID NO: 43. In some embodiments, the anti-CD70 VH domain CDR1 has a sequence: INAMG (SEQ ID NO: 156). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises a heavy chain complementarity determining region 2 (CDR2) that is the CDR2 of the VH sequence of SEQ ID NO: 43. In some embodiments, the anti-CD70 VH domain CDR2 has a sequence: AITSGGSPTYADSVKG (SEQ ID NO: 157).

[0121] In some embodiments, the anti-CD70 binding domain comprises a heavy chain complementarity determining region 3 (CDR3) that is the CDR3 of the VH sequence of SEQ ID NO: 44. In some embodiments, the anti-CD70 VH domain CDR3 has a sequence: SLRSSPSSRWFGS (SEQ ID NO: 158). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises a heavy chain complementarity determining region 1 (CDR1) that is the CDR1 of the VH sequence of SEQ ID NO: 44. In some embodiments, the anti-CD70 VH domain CDR1 has a sequence: DYAIA (SEQ ID NO: 159). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises a heavy chain complementarity determining region 2 (CDR2) that is the CDR2 of the VH sequence of SEQ ID NO: 44. In some embodiments, the anti-CD70 VH domain CDR2 has a sequence: AISWSGGTTHYADSVKG (SEQ ID NO: 160).

[0122] The table below lists the respective CDRs according to three numbering CDR formats, Chothia, Kabat and IMGT:

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
43	Anti-CD70 heavy chain variable domain (VH) sequence	QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS		
	CDR1	RSIFSIN (SEQ ID NO: 161)	INAMG (SEQ ID NO: 156)	RSIFSINA (SEQ ID NO: 162)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR2	TSGGS (SEQ ID NO: 163)	AITSGGSPTYADSVK G (SEQ ID NO: 157)	ITSGGSP (SEQ ID NO: 164)
	CDR3	GPYGLDNALDA (SEQ ID NO: 155)	GPYGLDNALDA (SEQ ID NO: 155)	ATGPYGLDNALDA (SEQ ID NO: 165)
44	Anti-CD70 heavy chain variable domain (VH) sequence	QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGK EREFVAAISWSGGTTHYADSVKGRFTISRDNAKNTLYLQMSSLK PEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS		
	CDR1	GFTFDDY (SEQ ID NO: 166)	DYAIA (SEQ ID NO: 159)	GFTFDDYA (SEQ ID NO: 167)
	CDR2	SWSGGT (SEQ ID NO: 168)	AISWSGGTTHYADS VKG (SEQ ID NO: 160)	ISWSGGTT (SEQ ID NO: 169)
	CDR3	SLRSSPSSRWFGS (SEQ ID NO: 158)	SLRSSPSSRWFGS (SEQ ID NO: 158)	AKSLRSSPSSRWFGS (SEQ ID NO: 170)

[0123] In some embodiments, the VH of the anti-CD70 antigen binding fragment comprises at least about 70% sequence identity to any one of the sequences selected from the group consisting of SEQ ID NOs. 43 and 44. In some embodiments, the VH of the anti-CD70 antigen binding fragment comprises at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to SEQ ID NO: 43, or SEQ ID NO: 44. In some embodiments, the VH is a single domain antibody domain. In some embodiments, the VH is a VHH.

[0124] In some embodiments the target protein is GPC3. Glypican belongs to heparan sulfate proteoglycans family with similar structures, including: a 60-70 kD core protein, which is linked to the surface of the cell membrane by a glycosylphosphatidylinositol anchor (GPI), and the carboxy terminus is modified with a heparan sulfate side chain. The GPC3 gene is located on the long arm of the X chromosome at position 26, and contains 11 exons. The transcript is 2130 bp, encoding 580 amino acids, and the molecular weight of the protein is about 70 kDa. It is implicated in various liver cancers. The expression of GPC3 correlates with prognosis of hepatocellular cancers (HCC). In addition GPC3 is highly expressed in lung squamous cell carcinoma, ovarian yolk sac tumor, melanoma, and urothelial carcinoma. In one aspect, provided herein is a CFP that targets GPC⁺ cells in cancer, and can be developed as a therapeutic for HCC, lung squamous cell carcinoma, ovarian yolk sac tumor, melanoma, and urothelial carcinoma. In some embodiments, the antigen binding domain comprises an anti-GPC3 antibody or antigen binding domain or fragment thereof, wherein the antigen binding domain comprises a heavy chain variable domain (VH) comprising a heavy chain complementarity determining region 3 (HC CDR3) of any one of the sequences selected from

the group consisting of ATACADTTQYAYDY (SEQ ID NO: 171), ATACADTTLYEYDY (SEQ ID NO: 172), ATACVDTTQYEYDY (SEQ ID NO: 173), ATACADATQHEYDY (SEQ ID NO: 174), ATACADTTQYDYDY (SEQ ID NO: 175), ATACADTTQYEYDY (SEQ ID NO: 176), ATACADTTTHYEYDY (SEQ ID NO: 177), ATACVITTLYEYDY (SEQ ID NO: 178), ATACAETTLYEYDY (SEQ ID NO: 179), ATACADTTQHEYDY (SEQ ID NO: 180), ATACVDTTTHYEYDY (SEQ ID NO: 181), ATACASTTLYEYDY (SEQ ID NO: 182), ATACVVTTLYEYDY (SEQ ID NO: 183), ATACGGATGPYDY (SEQ ID NO: 184), ATACAGAIGPYDY (SEQ ID NO: 185), ATACVVVGQNDY (SEQ ID NO: 186), ATACVVVGDRNDY (SEQ ID NO: 187), ATDCAGGTSTPYDY (SEQ ID NO: 188), ATDCAGGTATPYDY (SEQ ID NO: 189), ATACVVADRNEYDY (SEQ ID NO: 190), ATSCVVVTKNEYDY (SEQ ID NO: 191), ATACSGLTHEYDY (SEQ ID NO: 192), ATTCSGLTHEYDY (SEQ ID NO: 193), ATACANWSSLGPYDY (SEQ ID NO: 194), ATACANWSTLGPYDY (SEQ ID NO: 195), ATACSDPRVYEYDY (SEQ ID NO: 196), ATTCASPEKYEYDY (SEQ ID NO: 197), ATHCGGTSWGTSYDY (SEQ ID NO: 198), ATHCGGSSWSNEYDY (SEQ ID NO: 199), YARYSGRTY (SEQ ID NO: 200), ASSAWPAGPKHQVEYDY (SEQ ID NO: 201), ATACGSLVGMYDY (SEQ ID NO: 202), ATACGSAVHEYDY (SEQ ID NO: 203), ATDCVGFSGNWFDY (SEQ ID NO: 204), ATACASPVIYEYDY (SEQ ID NO: 205), ATDCAGGVGHEYDY (SEQ ID NO: 206), ATDCSLHGSDYPYDY (SEQ ID NO: 207) and AVRIYSGSFDNTLAYDY (SEQ ID NO: 208). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 1 (HC CDR1) of any one of the sequences selected from the group: GFPLAYYA (SEQ ID NO: 209), GFSLDYA (SEQ ID NO: 210), GFPLDYA (SEQ ID NO: 211), GFTLDYA (SEQ ID NO: 212), GFSLNYA (SEQ ID NO: 213), GFTLAYA (SEQ ID NO: 214), GFTLGYYA (SEQ ID NO: 215), GFPLNYA (SEQ ID NO: 216), GFPLHYA (SEQ ID NO: 217), GFSLGYA (SEQ ID NO: 218), GFPLGYA (SEQ ID NO: 219), GFPLEYA (SEQ ID NO: 220), GSDFRADA (SEQ ID NO: 221), GRTFSSYG (SEQ ID NO: 222), GFSLAYA (SEQ ID NO: 223) and GLTFRSVG (SEQ ID NO: 224). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 2 (HC CDR2) of any one of the sequences selected from the group: ISNSDGST (SEQ ID NO: 225), ISASDGST (SEQ ID NO: 226), ISSSDGST (SEQ ID NO: 227), ISSSDGNT (SEQ ID NO: 228), ISSADGST (SEQ ID NO: 229), ISSSGGST (SEQ ID NO: 230), ISSGDGST (SEQ ID NO: 231), ISAGDGNT (SEQ ID NO: 232), ISSDDST (SEQ ID NO: 233), ISSNDGST (SEQ ID NO: 234), ISSPDGST (SEQ ID NO: 235), ISSRTGGT (SEQ ID NO: 236), ISAGDGSST (SEQ ID NO: 237), ISSSDGSSDGNT (SEQ ID NO: 238), ISSGDGNT (SEQ ID NO: 239), ISSGDGKT (SEQ ID NO: 240), ISSSDGGT (SEQ ID NO: 241), ISSRTGST (SEQ ID NO: 242), ISSRTGNT (SEQ ID NO: 243), ISSSDGHSST (SEQ ID NO: 244), ISSSDGNT (SEQ ID NO: 245), ISASNGNT (SEQ ID NO: 246), ISSGSDGNT (SEQ ID NO: 247), ISASDGNT (SEQ ID NO: 248), IDSITSI (SEQ ID NO: 249), ISWSGGSTIAASVGST (SEQ ID NO: 250), ISSSDGSDGNT (SEQ ID NO: 251) and ASPSGVIT (SEQ ID NO: 252). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof comprises with 70-100% sequence identity to any one of the sequences selected from the group consisting of SEQ ID NOs: 45-134, listed in Table 5. In some embodiments, the VH is a single domain antibody domain.

In some embodiments, the VH is a VHH. Some exemplary anti-GPC3 VHH domain sequences are listed in Table 5.

[0125] In some embodiments, the anti-GPC3 antigen binding domain comprises a VH domain having a CDR1, a CDR2 and a CDR3 wherein the CDR1 has the amino acid sequence: DYEMH (SEQ ID NO: 253), CDR2 has the amino acid sequence: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); and the CDR3 has the amino acid sequence: FYSYTY (SEQ ID NO: 154).

[0126] In some embodiments the anti-GPC3 antigen binding domain is an scFv having a VH domain, comprising the CDR1, CDR2 and CDR3 domains, wherein the CDR1 sequence is DYEMH (SEQ ID NO: 253); the CDR2 sequence is: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); the CDR3 sequence is: FYSYTY (SEQ ID NO: 154); and a VL domain, comprising the CDR1, CDR2 and CDR3 domains, wherein the CDR1 sequence is RSSQSLVHSNRNTYLH (SEQ ID NO: 255); the CDR2 sequence is: KVSNRFS (SEQ ID NO: 256); the CDR3 sequence is: SQNTHVPPT (SEQ ID NO: 257).

[0127] In some embodiments, provided herein is a CFP, having an antigen binding domain comprising a CDR1, CDR2 and CDR3 as described above, a transmembrane domain and an intracellular domain, wherein the transmembrane domain comprises the sequence of CD89 TMD, for example, SEQ ID NO. 11; and one or more intracellular domains described herein, for example, in Table 2. Exemplary CFP sequences may be found in Table 4. Moreover, the CFP domains may be swapped or rearranged by using general molecular biology skills and techniques using exemplary guidance from Table 4.

[0128] Accordingly, in some embodiments, the antigenic target on a cancer cell is CD5. The CFP capable of binding a CD5 antigen may comprise an extracellular antigen binding domain having a sequence:

EIQLVQSGGGLVKPGGSRISCAASGYTFTNYGMNWVRQAPGKGLEWMGWINTHTGEPTY
ADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGTTVTVSSGG
GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFGQKPGKAPKTLIY
RANRLESGVPSRFSSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK (SEQ
ID NO: 258), or a sequence that is at least 90% identical to the above sequence. The CDR
sequences in accordance to Kabat numbering scheme are underlined, for example, the VH CDR1
sequence is NYGMN (SEQ ID NO: 259), the CDR2 sequence is WINTHTGEPTYADSFKG (SEQ
ID NO: 260), and the CDR3 sequence is RGYDWYFDV (SEQ ID NO: 261); and the VL CDR1
sequence is RASQDINSYLS (SEQ ID NO: 262), the CDR2 sequence is RANRLES (SEQ ID NO:
263), and the CDR3 sequence is QQYDESPWT (SEQ ID NO: 264).

[0129] In some embodiments, the antigenic target on a cancer cell is HER2. The CFP capable of binding a HER2 antigen may comprise an extracellular antigen binding domain having a sequence:

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSSASFLYSGVPSRF
SGSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGGQGTKVEIKRTGSTSGSGKPGSGEGSE
VQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYA
DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTTLTVSS
(SEQ ID NO: 265), or a sequence that is at least 90% identical to the above sequence. The CDR
sequences in accordance to Kabat numbering scheme are underlined, for example, the VL CDR1
sequence is RASQDVNTAVA (SEQ ID NO: 266), the CDR2 sequence is SASFLYS (SEQ ID NO:
267), and the CDR3 sequence is QQHYTTPPT (SEQ ID NO: 268); and the VH CDR1 sequence is
DTYIH (SEQ ID NO: 269), the CDR2 sequence is RIYPTNGYTRYADSVKG (SEQ ID NO: 270),
and the CDR3 sequence is WGGDGFYAMDV (SEQ ID NO: 271).

[0130] In some embodiments, the antigenic target on a cancer cell is Trophoblast cell surface antigen 2 (TROP2). TROP2 is a membrane glycoprotein and regulates cell growth, proliferation, self-renewal, survival and invasion. It is highly upregulated in various cancers, including non-small cell lung cancers (NSCLC), breast cancer, cervical cancer, colon cancer, gastric cancer, bladder cancer, prostate cancer, thyroid cancer, osteosarcoma, among others. FDA and EPA approved sacituzumab govitan for treating triple negative breast cancer patients. The transmembrane glycoprotein trophoblast cell surface

antigen-2 (Trop-2) is widely expressed in various epithelial cancers as well as in specific normal tissue. Trop-2 is also known as tumor-associated calcium signal transducer 2 (TACSTD2), membrane component chromosome 1 surface marker 1 (M1S1), gastrointestinal antigen 733-1 (GA733-1), and epithelial glycoprotein-1 (EGP-1). TROP2 is an attractive therapeutic target in various cancers. The instant patent application focuses on the approach of employing engineered myeloid cells to target TROP2 and eradicate TROP2+ cancer cells by enhanced phagocytosis and further, by activating the immune cells against TROP2+ cells. Provided herein is a CFP capable of binding a TROP2 antigen, and may comprise an extracellular antigen binding domain having a sequence: QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNVWKQAPGQGLKWMGWINTYTGPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYWFFDVWGGQSLVTVSSGGGGSGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFLTISSLPEDFAVYYCQQHYITPLTEGAGTKVEIKR (SEQ ID NO: 3), or a sequence that is at least 90% identical to the above sequence.

[0131] Any one of the sequences described above may comprise an N-terminal signal peptide sequence, for example, MWLQSLLLLGTVAC SIS (SEQ ID NO: 7), and a mature protein expressed on a myeloid cell may or may not comprise the signal sequence.

[0132] In addition, any one of the recombinant nucleic acids may comprise one or more linker sequences, one or more self-cleavage peptide sequences such as T2A, or P2A.

[0133] In some embodiments, the targeted antigen is an autoantigen or fragment thereof, such as Dsg1 or Dsg3. In some embodiments, the antigen binding domain comprises a receptor domain or an antibody domain wherein the antibody domain binds to an auto antigen, such as Dsg1 or Dsg3.

[0134] In some embodiments, the transmembrane domain and the antigen binding domain are operatively linked through a linker. In some embodiments, the transmembrane domain and the antigen binding domain are operatively linked through a linker such as a hinge region of CD8 α , IgG1 or IgG4.

[0135] In some embodiments, the extracellular domain comprises a multimerization scaffold.

[0136] In some embodiments, the transmembrane domain comprises a CD8 transmembrane domain. In some embodiments, the transmembrane domain comprises a CD28 transmembrane domain. In some embodiments, the transmembrane domain comprises a CD68 transmembrane domain. In some embodiments, the transmembrane domain comprises a CD2 transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR γ transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR α transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR β transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR ϵ transmembrane domain. In some embodiments, the transmembrane domain comprises a transmembrane domain from a syntaxin, such as syntaxin 3 or syntaxin 4 or syntaxin 5. In some embodiments, the transmembrane domain

enhanced NF-kappa B activation, or interferon activation in the cell expressing the chimeric protein, compared to an identical cell that does not express a chimeric protein.

[0154] In some embodiments, the myeloid cells are specifically targeted for delivery. Myeloid cells can be targeted using specialized biodegradable polymers, such as PLGA (poly(lactic-co-glycolic) acid and/or polyvinyl alcohol (PVA). In some embodiments, one or more compounds can be selectively incorporated in such polymeric structures to affect the myeloid cell function. In some embodiments, the targeting structures are multilayered, e.g., of one or more PLGA and one or more PVA layers. In some embodiments, the targeting structures are assembled in an order for a layered activity. In some embodiments, the targeted polymeric structures are organized in specific shaped components, such as labile structures that can adhere to a myeloid cell surface and deliver one or more components such as growth factors and cytokines, such as to maintain the myeloid cell in a microenvironment that endows a specific polarization. In some embodiments, the polymeric structures are such that they are not phagocytosed by the myeloid cell, but they can remain adhered on the surface. In some embodiments the one or more growth factors may be M1 polarization factors, such as a cytokine. In some embodiments the one or more growth factors may be an M2 polarization factor, such as a cytokine. In some embodiments, the one or more growth factors may be a macrophage activating cytokine, such as IFN γ . In some embodiments the polymeric structures are capable of sustained release of the one or more growth factors in an in vivo environment, such as in a solid tumor.

[0155] In some embodiments, the recombinant nucleic acid comprises a sequence encoding a homeostatic regulator of inflammation. In some embodiments, the homeostatic regulator of inflammation is a sequence in an untranslated region (UTR) of an mRNA. In some embodiments, the sequence in the UTR is a sequence that binds to an RNA binding protein. In some embodiments, translation is inhibited or prevented upon binding of the RNA binding protein to the sequence in an untranslated region (UTR). In some embodiments, the sequence in the UTR comprises a consensus sequence of WWWU(AUUUA)UUUW (SEQ ID NO: 272), wherein W is A or U. In some embodiments, the recombinant nucleic acid is expressed on a bicistronic vector.

[0156] In some embodiments, the target cell is a mammalian cell. In some embodiments, the target cell is a human cell. In some embodiments, the target cell comprises a cell infected with a pathogen. In some embodiments, the target cell is a cancer cell. In some embodiments, the target cell is a cancer cell that is a lymphocyte. In some embodiments, the target cell is a cancer cell that is an ovarian cancer cell. In some embodiments, the target cell is a cancer cell that is a breast cell. In some embodiments, the target cell is a cancer cell that is a pancreatic cell. In some embodiments, the target cell is a cancer cell that is a glioblastoma cell.

[0157] In some embodiments, the recombinant nucleic acid is DNA. In some embodiments, the recombinant nucleic acid is RNA. In some embodiments, the recombinant nucleic acid is mRNA. In some embodiments, the recombinant nucleic acid is an unmodified mRNA. In some embodiments, the

TABLE 1A. Exemplary Chimeric Fusion Protein Antigen Binding Domains

SEQ ID NO	Antigen Binding Domain	Sequence	CDR sequences
1	Anti-Trop-2 VH domain	QVQLQQSGSELKKPGASVKVS CKASGYTFTNYGMNWVKQAP GQGLKWMGWINTYTGEPTYT DDFKGRFAFSLDTSVSTAYLQI SSLKADDTAVYFCARGGFGSS YWYFDVWGQGS LVTVSS	Chothia: CDR1: GYTFTNY (SEQ ID NO: 273), CDR2: NTYTGE (SEQ ID NO: 274), CDR3: GGFGSSYWYFDV (SEQ ID NO: 153) Kabat: CDR1: NYGMN (SEQ ID NO: 259), CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275), CDR3: GGFGSSYWYFDV (SEQ ID NO: 153) IMGT: CDR1: GYTFTNYG (SEQ ID NO: 276), CDR2: INTYTGE (SEQ ID NO: 277), CDR3: ARGGFGSSYWYFDV (SEQ ID NO: 278)
2	Anti-TROP2 VL domain	DIQLTQSPSSLSASVGDRVSITC KASQDVSIAVA WYQQKPGKAP KLLIYSASYRYTGVPDRFSGSG SGTDFTLTISLQPEDFAVYYC QQHYITPLTFGAGTKVEIKR	Chothia: CDR1: KASQDVSIAVA (SEQ ID NO: 279), CDR2: SASRYT (SEQ ID NO: 280), CDR3: QQHYITPLT (SEQ ID NO: 281) Kabat: CDR1: KASQDVSIAVA (SEQ ID NO: 279), CDR2: SASRYT (SEQ ID NO: 280), CDR3: QQHYITPLT (SEQ ID NO: 281) IMGT: CDR1: QDVSI (SEQ ID NO: 282), CDR2: SAS, CDR3: QQHYITPLT (SEQ ID NO: 281)
3	Anti-Trop-2 binding domain (scFv)	QVQLQQSGSELKKPGASVKVS CKASGYTFTNYGMNWVKQAP GQGLKWMGWINTYTGEPTYT DDFKGRFAFSLDTSVSTAYLQI SSLKADDTAVYFCARGGFGSS YWYFDVWGQGS LVTVSSGGG GSGGGSGGGGSDIQLTQSPSS LSASVGDRVSITCKASQDVSI VAWYQQKPGKAPKLLIYSASY RYTGVPDRFSGSGSGTDFTLTIS SLQPEDFAVYYCQQHYITPLTF GAGTKVEIKR	
4	Anti-GPC3 binding domain variable	QVQLVQSGAEVKKPGASVKVS CKASGYTFTDYEMHWVRQAP GQGLEWMGALDPKGTDTAYS QKFKGKATLTADKSTSTAYME LSSLTSED TAVYYCTRFYSYTY WGQGT LVTVSS	Chothia: CDR1: GYTFTDY (SEQ ID NO: 283), CDR2: DPKTGD (SEQ ID NO: 284), CDR3: FYSYTY (SEQ ID NO: 154)

SEQ ID NO	Antigen Binding Domain	Sequence	CDR sequences
	heavy (VH) chain		Kabat: CDR1: DYEMH (SEQ ID NO: 253), CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254), CDR3: FYSYTY (SEQ ID NO: 154) IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285), CDR2: LDPKTGDT (SEQ ID NO: 286), CDR3: TRFYSYTY (SEQ ID NO: 287)
5	Anti-GPC3 binding domain variable light (VL) chain	DVVMQTQSPLSLPVTGPGEPA SISCRSSQSLVHSNRNTYLHWY LQKPGQSPQLLIYKVS NRFSGVPDRFSGSGSGTDFTLKISR V EAEDVGVYYCSQNT HVPPTFGQGTKLEIK	Chothia: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255), CDR2: KVS NRFS (SEQ ID NO: 256), CDR3: SQNTHVPPT (SEQ ID NO: 257) Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255), CDR2: KVS NRFS (SEQ ID NO: 256), CDR3: SQNTHVPPT (SEQ ID NO: 257) IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288), CDR2: KVS, CDR3: SQNTHVPPT (SEQ ID NO: 257)
6	Anti-GPC3 binding domain (scFv)	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYEMHWVRQ APGQGLEWMGALDPKTGDT AYSQKFKGKATLTADKSTST AYMELSSLTSED TAVYYCTRFYSYTYWGQGT LVTVSSGGG GSGGGGSGGGGSDVVM TQSP LSLPVTPGEPASISCRSSQSLV HSNRNTYLHWY LQKPGQSPQLLIYKVS NRFSGVPDRFSGSG SGTDFTLKISRVEAEDVGVYY CSQNT HVPPTFGQGTKLEIK	VH: Chothia: CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat: CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154). IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) VL: Chothia: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS NRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS NRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257).

SEQ ID NO	Antigen Binding Domain	Sequence	CDR sequences
			IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257)

TABLE 1B. Exemplary Chimeric Fusion Protein Signal Peptide Sequences

SEQ ID NO	CFP/ Domain	Sequence
7	GMCSF Signal peptide	MWLQSLLLLGTVAC SIS

TABLE 1C. Exemplary Chimeric Fusion Protein Extracellular/Hinge Domains

SEQ ID NO	CFP/ Domain	Sequence
8	CD89 extracellular (hinge)	DSIHQDYTTQN
9	Linker	SGGGGAAADYKDDDDKGS
10	Linker-CD89 hinge	SGGGGAAADYKDDDDKGS DSIHQDYTTQN

TABLE 1D. Exemplary Chimeric Fusion Protein Transmembrane Domains

SEQ ID NO	CFP/ Domain	Sequence
11	CD89 TMD	LIRMAVAGLVLVALLAILV

TABLE 4. Exemplary Chimeric Fusion Protein Sequences

[0162] Exemplary sequences of chimeric fusion protein domains and/or fragments thereof are shown, that are meant to be non-limiting for the disclosure. Underlines denote the CDR sequences in sequential order of CDR1, CDR2 and CDR3 for the respective variable heavy (VH) and variable light (VL) chains in accordance to the Kabat numbering system.

SEQ ID NO	CFP/ Domain	Sequence	CDR sequences
26	TROP2-CD89	QVQLQQSGSELKKPGASVKVSK ASGYTFTNYGMNWVKQAPGQGL KWMGWINTYTGEPTYTDDFKGRF AFSLDTSVSTAYLQISSLKADDTA VYFCARGGGFGSSYWFYFDVWGQGS LVTVSSGGGGSGGGSGGGGSDIQ LTQSPSSLSASVGDRVSITCKASQD VSIATAWYQQKPGKAPKLLIYSAS YRYTGVPDRFSGSGSGTDFTLTIS LQPEDFAVYYCQQHYITPLTFGAG TKVEIKRSGGSDSIHQDYTTQNL RMAVAGLVLLALLILVENWWSH TALNKEASADVAEPSWSQQMCQP GLTFARTPSVCK	<u>VH</u> : Chothia : CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGGFGSSYWFYFDV (SEQ ID NO: 153). Kabat : CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGGFGSSYWFYFDV (SEQ ID NO: 153); IMGT : CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGFGSSYWFYFDV (SEQ ID NO: 278) <u>VL</u> : Chothia : CDR1: KASQDVSIATA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat : CDR1: KASQDVSIATA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT : CDR1: QDVSIATA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
27	TROP2-CD89	QVQLQQSGSELKKPGASVKVSK ASGYTFTNYGMNWVKQAPGQGL KWMGWINTYTGEPTYTDDFKGRF AFSLDTSVSTAYLQISSLKADDTA VYFCARGGGFGSSYWFYFDVWGQGS LVTVSSGGGGSGGGSGGGGSDIQ LTQSPSSLSASVGDRVSITCKASQD VSIATAWYQQKPGKAPKLLIYSAS YRYTGVPDRFSGSGSGTDFTLTIS LQPEDFAVYYCQQHYITPLTFGAGTK	<u>VH</u> : Chothia : CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGGFGSSYWFYFDV (SEQ ID NO: 153). Kabat : CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGGFGSSYWFYFDV (SEQ ID NO: 153); IMGT : CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGFGSSYWFYFDV (SEQ ID NO: 278)

		VEIKRSGGGGAAADYKDDDDKG SDSIHQDYTTQNLIRMAVAGLVL VALLAILVENWHSHTALNKEAS ADVAEPSWSQQMCQPGLTFART PSVCK	VL: Chothia: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT: CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
28	TROP2- CD89- FcR	QVQLQQSGSELKKPGASVKVSCAS GYTFTNYGMNWVKQAPGQGLKWM GWINTYTGEPTYTDDFKGRFAFSLD TSVSTAYLQISSLKADDTAVYFCAR GGFGSSYWYFDVWGQGS LTVSSG GGGSGGGSGGGGSDIQLTQSPSSL ASVGDRVSITCKASQDVSIABAWYQ QKPGKAPKLLIYSASYRYTGVPDRFS GSGSGTDFTLTISSLQPEDFAVYYCQ QHYITPLTFGAGTKVEIKRSGGGGA AADYKDDDDKGSDSIHQDYTTQNL IRMAVAGLVLVALLAILVRLKIQVRK AAITSYEKSDGVYTGLSTRNQETYE TLKHEKPPQ	VH: Chothia: CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGFGSSYWYFDV (SEQ ID NO: 153). Kabat: CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGFGSSYWYFDV (SEQ ID NO: 153); IMGT: CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGFGSSYWYFDV (SEQ ID NO: 278) VL: Chothia: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT: CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
29	TROP2- CD89- FcR- PI3K	QVQLQQSGSELKKPGASVKVSCAS GYTFTNYGMNWVKQAPGQGLKWM GWINTYTGEPTYTDDFKGRFAFSLD TSVSTAYLQISSLKADDTAVYFCAR GGFGSSYWYFDVWGQGS LTVSSG GGGSGGGSGGGGSDIQLTQSPSSL ASVGDRVSITCKASQDVSIABAWYQ QKPGKAPKLLIYSASYRYTGVPDRFS GSGSGTDFTLTISSLQPEDFAVYYCQ QHYITPLTFGAGTK	VH: Chothia: CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGFGSSYWYFDV (SEQ ID NO: 153). Kabat: CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGFGSSYWYFDV (SEQ ID NO: 153); IMGT: CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGFGSSYWYFDV (SEQ ID NO: 278)

		VEIKRSGGGGAAADYKDDDDKGS SIHQDYTTQNLIRMAVAGLVALL AILVRLKIQVRKAAITSYEKSDGVYT GLSTRNQETYETLKHEKPPQGSYED MRGILYAAPQLRSIRGQPGPNHEED ADSYENM	<u>VL</u> : Chothia : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT : CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
30	TROP2- CD89- CD40	QVQLQQSGSELKKPGASVKVSK ASGYTFTNYGMNWVKQAPGQGL KWMGWINTYTGEPTYTDDFKGRF AFSLDTSVSTAYLQISSLKADDTA VYFCARGGGSSYWFYFDVWGQGS LVTVSSGGGGSGGGSGGGSDIQ LTQSPSSLSASVGDRVSITCKASQD VSIABAWYQQKPGKAPKLLIYSAS YRYTGVPDRFSGSGSGTDFLTIS LQPEDFAVYYCQQHYITPLTFGAG TKVEIKRSGGGGAAADYKDDDDK GSDSIHQDYTTQNLIRMAVAGLV VALLAILVKKVAKKPTNKAPHPK QEPQEINFDDLPGSNTAAPVQETL HGCQPVTDQEDGKESRISVQERQ	<u>VH</u> : Chothia : CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGGSSYWFYFDV (SEQ ID NO: 153). Kabat : CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGGSSYWFYFDV (SEQ ID NO: 153); IMGT : CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGGGSSYWFYFDV (SEQ ID NO: 278) <u>VL</u> : Chothia : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT : CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
31	TROP2- CD89- CD40- FcR	QVQLQQSGSELKKPGASVKVSKAS GYTFTNYGMNWVKQAPGQGLKWM GWINTYTGEPTYTDDFKGRFAFSLD TSVSTAYLQISSLKADDTAVYFCAR GGFGSSYWFYFDVWGQGS LVTVSSG GGGSGGGSGGGSDIQLTQSPSSLS ASVGDRVSITCKASQDVSIABAWYQ QKPGKAPKLLIYSASRYTGVPDRFS GSGSGTDFLTISLQPEDFAVYYCQ QHYITPLTFGAGTK	<u>VH</u> : Chothia : CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGGSSYWFYFDV (SEQ ID NO: 153). Kabat : CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGGSSYWFYFDV (SEQ ID NO: 153); IMGT : CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGGGSSYWFYFDV (SEQ ID NO: 278)

		VEIKRSGGGGAAADYKDDDDKGS DSIHQDYTTQNLIRMAVAGLVVLA LLAILVKKVAKKPTNKAPHPKQEP QEINFPDDLPGSNTAAPVQETLHG CQPVQTQEDGKESRISVQERQGSRL KIQVRKAAITSYEKSDGVYTGLST RNQETYETLKHEKPPQ	VL: Chothia: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT: CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
32	TROP2- CD89- TRIF	QVQLQQSGSELKKPGASVKVSCAS GYTFTNYGMNWVKQAPGQGLKWM GWINTYTGEPTYTDDFKGRFAFSLD TSVSTAYLQISSLKADDTAVYFCAR GGFGSSYWFYFDVWGQGLVTVSSG GGGSGGGSGGGSDIQLTQSPSSL ASVGDRVSITCKASQDVSIABAWYQ QKPGKAPKLLIYSASYRYTGVPDRFS GSGSGTDFTLTISLQPEDFAVYYCQ QHYITPLTFGAGTKVEIKRSGGGGA AADYKDDDDKGSDSIHQDYTTQNL IRMAVAGLVVALLAILVRGSIRTLQ SNLGCLPPSSALPSGTRSLRPIDGVS DWSQGCSLRSTGSPASLASNLEISQ PTMPFSLHRSHPGSKLCDDPQASL VPEPVPGGCQEPEEMSWPPSGEIASP PELPSSPPGLPEVAPDATSTGLPDT AAPETSTNYPVECTEGSAGPQSLPL ILEPVKNPCSVKDQTPQLSVEDTTS PNTKPCPPTPTTPETSPPPPPPPSSTP CSAHLTPSSLFPSSLE	VH: Chothia: CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGFGSSYWFYFDV (SEQ ID NO: 153). Kabat: CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGFGSSYWFYFDV (SEQ ID NO: 153); IMGT: CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277); CDR3: ARGFGSSYWFYFDV (SEQ ID NO: 278) VL: Chothia: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat: CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT: CDR1: QDVSA (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
33	TROP2- CD89- FcR- TRIF	QVQLQQSGSELKKPGASVKVSCAS GYTFTNYGMNWVKQAPGQGLKWM GWINTYTGEPTYTDDFKGRFAFSLD TSVSTAYLQISSLKADDTAVYFCAR GGFGSSYWFYFDVWGQGLVTVSSG GGGSGGGSGGGSDIQLTQSPSSL ASVGDRVSITCKASQDVSIABAWYQ QKPGKAPKLLIYSASYRYTGVPDRFS GSGSGTDFTLTIS	VH: Chothia: CDR1:GYTFTNY (SEQ ID NO: 273); CDR2: NTYTGE (SEQ ID NO: 274); CDR3: GGFGSSYWFYFDV (SEQ ID NO: 153). Kabat: CDR1: NYGMN (SEQ ID NO: 259); CDR2: WINTYTGEPTYTDDFKG (SEQ ID NO: 275); CDR3: GGFGSSYWFYFDV (SEQ ID NO: 153); IMGT: CDR1: GYTFTNYG (SEQ ID NO: 276); CDR2: INTYTGE (SEQ ID NO: 277);

		SLQPEDFAVYYCQQHYITPLTFGAG TKVEIKRSGGGGAAADYKDDDDKG SDSIHQDYTTQNLIRMAVAGLVVLA LLAILVRLKIQVRKAAITSYEKSDGV YTGLSTRNQETYETLKHEKPPQGSG SIRTLQSNLGCLPPSSALPSGTRSLPR PIDGVSDWSQGCSLRSTGSPASLASN LEISQSPTMPFLSLHRSPHGPKLCD DPQASLVPEPVPGGCQEPEEMSWPP SGEIASPPELPSSPPPGLPEVAPDATS TGLPDTPAAPETSTNYPVECTEGSAG PQSLPLPILEPVKNPCSVKDQTPQLS VEDTTSPNTKPCPPTPTTPETSPPPPP PPPSSTPCSAHLTPSSLPSSLE	CDR3: ARGGFGSSYWFVDV (SEQ ID NO: 278) <u>VL</u> : Chothia : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281). Kabat : CDR1: KASQDVSIABA (SEQ ID NO: 279); CDR2: SASYRYT (SEQ ID NO: 280); CDR3: QQHYITPLT (SEQ ID NO: 281); IMGT : CDR1: QDVSI (SEQ ID NO: 282); CDR2: SAS; CDR3: QQHYITPLT (SEQ ID NO: 281)
34	GPC3- CD89	QVQLVQSGAEVKKPGASVKVSCKA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGKATLT ADKSTSTAYMELSSLTSEDVAVYYC TRFYSTYWGQGTLLVTVSSGGGGS GGGGSGGGGSDVVMQSPSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYKVSNRFSQVPDR FSGSGSGTDFTLKISRVEAEDVGVYY CSQNTHPPTFGQGTLEIKSGGGG AAADYKDDDDKGSDSIHQDYTTQN LIRMAVAGLVVALLAILVENWVSH TALNKEASADVAEPSWSQQMCQPG LTFARTPSVCK	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSTY (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257)
35	GPC3- CD89	QVQLVQSGAEVKKPGASVKVSCK ASGYTFTDYEMHWVRQAPGQGLE WMGALDPKTGDTAYSQKFKGKA TLTADKSTSTAYMELSSLTSEDV VYYCTRFYSTYWGQGTLLVTVSS GGGGSGGGGSGGGGSDVVMQSP LSLPVTPGEPASISCRSSQSLVHSN RNTYLHWYLQKPGQSPQLLIY	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSTY (SEQ ID NO: 287)

		KVSNRFSGVPDRFSGSGSGTDFTL KISRVEAEDVGVIYCSQNTHPPT FGQGTKLEIKSGGSDSIHQDYTT QNLIRMAVAGLVLLVALLAILVEN WHSHTALNKEASADVAEPSWSQQ MCQPGLTFARTPSVCK	<u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
36	GPC3- CD89	QVQLVQSGAEVKKPGASVKVSCKA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGRVTLT ADKSTSTAYMELSSLTSEDVAVYYC TRFYSYTYWGQGTLLTVSSGGGGS GGGGSGGGGSDVVMQSPSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYKVSNRFSGVPDR FSGSGSGTDFTLKISRVEAEDVGVIY CSQNTHPPTFGQGTKLEIKSGGSD SIHQDYTTQNLIRMAVAGLVLLVALL AILVENWHSHTALNKEASADVAEPS WSQQMCQPGLTFARTPSVCK	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287). <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
37	GPC3- CD89- FeR	QVQLVQSGAEVKKPGASVKVSCKA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGKATLT ADKSTSTAYMELSSLTSEDVAVYYC TRFYSYTYWGQGTLLTVSSGGGGS GGGGSGGGGSDVVMQSPSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYKVSNRFSGVPDR FSGSGSGTDFTLKISRVEAEDVGVIY CSQNTHPPTFGQGTKLEIKSGGGG AAADYKDDDDKGSIDYTTQN LIRMAVAGLVLLVALLAILVRLKIQV RKAATSYEKSDGVYTGLSTRNQET YETLKHEKPPQ	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257);

			IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
38	GPC3- CD89- FcR- PI3K	QVQLVQSGAEVKKPGASVKVSCK ASGYTFTDYEMHWVRQAPGQGLE WMGALDPKTGDTAYSQKFKGKA TLTADKSTSTAYMELSSLTSEDTA VYYCTRFYSYTYWGQGLTVTVSS GGGGSGGGSGGGGSDVVMQTSP LSLPVTPGEPASISCRSSQSLVHSN RNTYLHWYLQKPGQSPQLLIYKVS NRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCSQNTHVPPTFGQ GTKLEIKSGGGGAAADYKDDDDK GSDSIHQDYTTQNLIRMAVAGLVL VALLAILVRLKIQVRKAAITSYEKS DGVYTGLSTRNQETYETLKHEKPP QGSYEDMRGILYAAPQLRSIRGQP GPNHEEDADSYENM	VH: Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat: CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) VL: Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
39	GPC3- CD89- CD40	QVQLVQSGAEVKKPGASVKVSCK ASGYTFTDYEMHWVRQAPGQGLE WMGALDPKTGDTAYSQKFKGKA TLTADKSTSTAYMELSSLTSEDTA VYYCTRFYSYTYWGQGLTVTVSS GGGGSGGGSGGGGSDVVMQTSP LSLPVTPGEPASISCRSSQSLVHSN RNTYLHWYLQKPGQSPQLLIYKVS NRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCSQNTHVPPTFGQ GTKLEIKSGGGGAAADYKDDDDK GSDSIHQDYTTQNLIRMAVAGLVL VALLAILVKKVAKKPTNKAPHPK QEPQEINFPDDLPGSNTAAPVQETL HGCQPVTQEDGKESRISVQERQ	VH: Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat: CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) VL: Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).

40	GPC3- CD89- CD40- FcR	QVQLVQSGAEVKKPGASVKVSK ASGYTFTDYEMHWVRQAPGQGLE WMGALDPKTGDTAYSQKFKGKA TLTADKSTSTAYMELSSLTSEDTA VYYCTRFYSYTYWGQGTLLTVSS GGGGSGGGSGGGGSDVVMQTSP LSLPVTPGEPASISCRSSQSLVHSN RNTYLHWYLQKPGQSPQLLIYKVS NRFSGVDPDRFSGSGSGTDFTLKISR VEAEDVGVYYCSQNTHPPTFGQ GTKLEIKSGGGGAAADYKDDDDK GSDSIHQDYTTQNLIRMAVAGLVL VALLAILVKKVAKKPTNKAPHPK QEPQEINFPDDLPGSNTAAPVQETL HGCQPVTQEDGKESRISVQERQGS RLKIQVRKAAITSYEKSDGVYTGL STRNQETYETLKHEKPPQ	VH: Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat: CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) VL: Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
41	GPC3- CD89- TRIF	QVQLVQSGAEVKKPGASVKVSK ASGYTFTDYEMHWVRQAPGQGLE WMGALDPKTGDTAYSQKFKGKA TLTADKSTSTAYMELSSLTSEDTA VYYCTRFYSYTYWGQGTLLTVSS GGGGSGGGSGGGGSDVVMQTSP LSLPVTPGEPASISCRSSQSLVHSN RNTYLHWYLQKPGQSPQLLIYKVS NRFSGVDPDRFSGSGSGTDFTLKISR VEAEDVGVYYCSQNTHPPTFGQ GTKLEIKSGGGGAAADYKDDDDK GSDSIHQDYTTQNLIRMAVAGLVL VALLAILVRGSIRTLQSNLGCLPPS SALPSGTRSLRPIDGVSDWSQGCS LRSTGSPASLASNLEISQSPTMPFLS LHRSPHGPSKLCDDPQASLVPEPV PGGCQEPEEMSWPPSGEIASPPELP SSPPPGLPEVAPDATSTGLPDTPAA PETSTNYPVECTEGSAGPQSLPLPI LEPVKNPCSVKDQTPQLQSVEDTT SPNTKPCPPTPTTPETSPPPPPPPSS TPCSAHLTPSSLFPSSLE	VH: Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat: CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT: CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFYSYTY (SEQ ID NO: 287) VL: Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat: CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVSNRFS (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT: CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).

42	GPC3- CD89- FcR- TRIF	QVQLVQSGAEVKKPGASVKVSCKA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGKATLT ADKSTSTAYMELSSLTSEDVAVYYC TRFY ~~SYTY~~ WGQGTLLTVSSGGGGG GGGGSGGGGSDVVMTQSPLSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYK ~~VSNRFS~~ GV PDRFSGSGSGTDFTLKISRVEAEDVGVYY CSQNT ~~HVPPT~~ FGQGTKEIKSGGGG AAADYKDDDDKGS ~~DSIHQDYTTQN~~ LIRMAVAGLVLVALLAILVRLKIQV RKA ~~AITSYEKSDGVYTGLSTRNQET~~ YETLKHEKPPQGS ~~SIRTLQSNLGCL~~ PPSSALPSGTRSLRPIDGVSDWSQG CSLRSTGSPASLASNLEISQSPTMPFL SLHRSPHGPSKLCDDPQASLVPEPVP GGCQEPEEMSWPPSGEIASPELPSSP PPGLPEVAPDATSTGLPDTPAAPETS TNYPVECTEGSAGPQSLPLPILEPVK NPCSVKDQTPLQLSVEDTTSPNTKPC PPTPTTPETSPPPPPPPPSSTPCSAHLT PSSLFPSSLE	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFY ~~SYTY~~ (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
135	GPC3- CD89- FcR- PI3K	QVQLVQSGAEVKKPGASVKVSCKA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGRVTLT ADKSTSTAYMELSSLTSEDVAVYYC TRFY ~~SYTY~~ WGQGTLLTVSSGGGGG GGGGSGGGGSDVVMTQSPLSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYK ~~VSNRFS~~ GV PDRFSGSGSGTDFTLKISRVEAEDVGVYY CSQNT ~~HVPPT~~ FGQGTKEIKSGGGG AAADYKDDDDKGS ~~DSIHQDYTTQN~~ LIRMAVAGLVLVALLAILVRLKIQV RKA ~~AITSYEKSDGVYTGLSTRNQET~~ YETLKHEKPPQGSYEDMRGILYAAP QLRSIRGQPGPNHEEDADSYENM	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFY ~~SYTY~~ (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).

136	GPC3- CD89- CD40- FcR	QVQLVQSGAEVKKPGASVKVSCA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGRVTLT ADKSTSTAYMELSSLTSEDVAVYYC TRFY ~~SYTY~~ WGQGTLLTVSSGGGGS GGGGSGGGGSDVVMQTQSPLSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYKVS ~~NRFS~~ GVDPDR FSGSGSGTDFTLKISRVEAEDVGVYY CSQNT ~~HVPPT~~ FGQGTKEIKSGGGG AAADYKDDDDKGSDSIHQDYTTQN LIRMAVAGLVLVALLAILVKKVAKK PTNKAPHPKQEPQEINFPDDLPGSNT AAPVQETLHGCQPV ~~TQED~~ GKESRIS VQERQGSRLKIQRKAAITSYEKSD GVYTGLSTRNQETYETLKHEKPPQ	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFY ~~SYTY~~ (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).
137	GPC3- CD89- FcR- TRIF	QVQLVQSGAEVKKPGASVKVSCA SGYTFTDYEMHWVRQAPGQGLEW MGALDPKTGDTAYSQKFKGRVTLT ADKSTSTAYMELSSLTSEDVAVYYC TRFY ~~SYTY~~ WGQGTLLTVSSGGGGS GGGGSGGGGSDVVMQTQSPLSLPVT GEPASISCRSSQSLVHSNRNTYLHW YLQKPGQSPQLLIYKVS ~~NRFS~~ GVDPDR FSGSGSGTDFTLKISRVEAEDVGVYY CSQNT ~~HVPPT~~ FGQGTKEIKSGGGG AAADYKDDDDKGSDSIHQDYTTQN LIRMAVAGLVLVALLAILVRLKIQV RKAAITSYEKSDGVYTGLSTRNQET YETLKHEKPPQGSGSIRTLQSNLGC LPSSALPSGTRSLRPIDGVSDWSQG CSLRSTGSPASLASNLEISQSPTMPFL SLHRSPHGPKLCDDPQASLVPEPVP GGCQEPEEMSWPPSGEIASPELPSSP PPGLPEVAPDATSTGLPDTPAAPETS TNYPVECTEGSAGPQSLPLPILEPVK NPCSVKDQTPLQLSVEDTTSPTNKPC PPTPTTPETSPPPPPPPPSSTPCSAHLT PSSLFPSSLE	<u>VH</u> : Chothia CDR1: GYTFTDY (SEQ ID NO: 283); CDR2: DPKTGD (SEQ ID NO: 284); CDR3: FYSYTY (SEQ ID NO: 154). Kabat : CDR1: DYEMH (SEQ ID NO: 253); CDR2: ALDPKTGDTAYSQKFKG (SEQ ID NO: 254); CDR3: FYSYTY (SEQ ID NO: 154); IMGT : CDR1: GYTFTDYE (SEQ ID NO: 285); CDR2: LDPKTGDT (SEQ ID NO: 286); CDR3: TRFY ~~SYTY~~ (SEQ ID NO: 287) <u>VL</u> : Chothia CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257). Kabat : CDR1: RSSQSLVHSNRNTYLH (SEQ ID NO: 255); CDR2: KVS ~~NRFS~~ (SEQ ID NO: 256); CDR3: SQNTHVPPT (SEQ ID NO: 257); IMGT : CDR1: QSLVHSNRNTY (SEQ ID NO: 288); CDR2: KVS; CDR3: SQNTHVPPT (SEQ ID NO: 257).

[0163] In some embodiments, exemplary chimeric fusion proteins (CFPs) may comprise a sequence that is at least 80% identical to any one of the sequences of SEQ ID NOs 26-42, 135-137 of Table 4. In some embodiments, exemplary chimeric fusion proteins (CFPs) may comprise a sequence that is at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89% identical to any one of the sequences of SEQ ID NOs 26-42, 135-137. In some embodiments, exemplary chimeric fusion proteins (CFPs) may comprise a sequence that is 90% identical to any one of the sequences of SEQ ID NOs 26-42, 135-137 of Table 4. In some embodiments, exemplary chimeric fusion proteins (CFPs) may comprise a sequence that is 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of the sequences of SEQ ID NOs 26-42, 135-137.

[0164] In some embodiments provided herein is a chimeric fusion protein comprising (i) an extracellular antigen binding domain capable of binding a TROP2 antigen; further comprising a TMD of CD89, wherein the extracellular antigen binding domain is an scFv, and comprises a variable heavy chain CDR3 having a sequence GGFGSSYWYFDV (SEQ ID NO: 153); and wherein optionally further comprises a variable light chain CDR3 having a sequence QQHYITPLT (SEQ ID NO: 281).

[0165] In some embodiments provided herein is a chimeric fusion protein comprising (i) an extracellular antigen binding domain capable of binding a GPC3 antigen; further comprising a TMD of CD89, wherein the extracellular antigen binding domain is an scFv, and comprises a variable heavy chain (VH) CDR3 having a sequence FYSYTY (SEQ ID NO: 154).

[0166] In some embodiments, exemplary chimeric fusion proteins (CFPs) may comprise a binding domain that binds to cancer antigen GPC3, wherein the binding domain is a VHH, and may comprise any one of the variable domains listed in Table 5. The CFP may comprise a binding domain that is an scFv, that binds to GPC3 antigen, and comprises any one of the variable domains listed the table below (Table 5). An exemplary CFP may comprise an extracellular antigen binding domain comprising any one or more variable domains listed in Table 5, fused to a transmembrane domain (TMD) described in the specification. In some embodiments, the CFP comprising a GPC3 binding domain comprising one or more VH domains listed in Table 5, a TMD having a sequence of, for example, CD89, as described elsewhere in the specification, and any intracellular domains or combination of intracellular domains described herein. In some embodiments, the CFP comprises a GPC3 binding domain comprising one or more VH domains listed in Table 5, a hinge domain, a TMD having a sequence of, for example, CD89, as described elsewhere in the specification, and one or more intracellular signaling domains or combination of intracellular signaling domains for example, but not limited to, CD40 ICD, TRIF ICD, PI3K recruitment domain ICD, etc., as described herein. One of skill in the art may use standard molecular biology cloning techniques and basic reverse engineering of recombinant technology to arrive at the constructs encompassed within the scope contemplated herein.

[0167] Table 5: Exemplary anti-GPC3 binding variable heavy chain (VH) domain sequences for CFP extracellular domains.

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
45	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVHSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREVSCISS SDGNTYYADAVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATACADTT QHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)
46	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVHSGGSLRLSCAASGFPLDYAIGWFRQAPGKEREVSCISS ADGSTYYADSVKGRFTISRDNKNTVYLMNSLGPEDTAVYYCATACADTT QYDYDYWGQGTQVTVSS		
	CDR1	GFPLDYA (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SSADGS (SEQ ID NO: 295)	CISSADGSTYYADSVK G (SEQ ID NO: 296)	ISSADGST (SEQ ID NO: 229)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)
47	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVHSGGSLRLSCAASGFTLDYYAIGWFRAPGKEREVSCISS GDGKTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATACAGAI GPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSGDGK (SEQ ID NO: 299)	CISSGDGKTYADSVK G (SEQ ID NO: 300)	ISSGDGKT (SEQ ID NO: 240)
	CDR3	ACAGAIGPYDY (SEQ ID NO: 301)	ACAGAIGPYDY (SEQ ID NO: 301)	ATACAGAIGPYDY (SEQ ID NO: 185)
48	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVPPGGSRLRLSCAASGFPLDYAIGWFRQAPGKEREVSCISS ADGSTYYADSVKGRFTISRDNKNTVYLMNSLGPEDTAVYYCATACADTT QYDYDYWGQGTQVTVSS		
	CDR1	GFPLDYA (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SSADGS (SEQ ID NO: 295)	CISSADGSTYYADSVK G (SEQ ID NO: 296)	ISSADGST (SEQ ID NO: 229)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
49	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQAGGSLRLSCAASGFSLGYYAIGWFRQAPGKEREVSCISSDGHSSSTYYADSVKGRFTISRDNAKNTVYLMNNLKPEDTAVYYCATDCAGGTATPYDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSSDGHSS (SEQ ID NO: 303)	CISSSDGHSSSTYYADSVKG (SEQ ID NO: 304)	ISSSDGHSS (SEQ ID NO: 244)
	CDR3	DCAGGTATPYDY (SEQ ID NO: 305)	DCAGGTATPYDY (SEQ ID NO: 305)	ATDCAGGTATPYDY (SEQ ID NO: 189)
50	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYGMGWFRQAPGKEREFVAAISWSGGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCASSAWPAGPKHQVEYDYWGQGTQVTVSS		
	CDR1	GRTFSSY (SEQ ID NO: 306)	SYGMG (SEQ ID NO: 307)	GRTFSSYG (SEQ ID NO: 222)
	CDR2	SWSGGS (SEQ ID NO: 308)	AISWSGGSTYYADSVKG (SEQ ID NO: 309)	ISWSGGST (SEQ ID NO: 310)
	CDR3	SAWPAGPKHQVEYDY (SEQ ID NO: 311)	SAWPAGPKHQVEYDY (SEQ ID NO: 311)	ASSAWPAGPKHQVEYDY (SEQ ID NO: 201)
51	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQAGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREVACISSRTGSTYYADSVKGRFTISRDNAKNTVALQMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
52	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQDGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREVSCISASDGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACAETTLYEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SASDGS (SEQ ID NO: 316)	CISASDGSTYYADSVKG (SEQ ID NO: 317)	ISASDGST (SEQ ID NO: 226)
	CDR3	ACAETTLYEYDY (SEQ ID NO: 318)	ACAETTLYEYDY (SEQ ID NO: 318)	ATACAETTLYEYDY (SEQ ID NO: 179)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
53	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGESLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDG STYYADSVKGRFTISRDNKNTVYVYLMNSLKPEDTAVYYCATACANWSTLGPYD YWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACANWSTLGPYDY (SEQ ID NO: 321)	ACANWSTLGPYDY (SEQ ID NO: 321)	ATACANWSTLGPYDY (SEQ ID NO: 195)
54	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGESLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDG NTYYADSVKGRFTISRDNKNTVYVYLMNRLKPEDTAVYYCATACADTTQYEYDY WGQGTQVTVSS		
	CDR1	GFTLAYY (SEQ ID NO: 322)	YYAIG (SEQ ID NO: 290)	GFTLAYYA (SEQ ID NO: 214)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADSVKG (SEQ ID NO: 323)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYDY (SEQ ID NO: 176)
55	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGSLRLSCAASGSDFRADAMGWYRQAPGKEREPVAIDSITS IYYVDSVEGRFTISRDNKNTVYVYLMNTSLKPEDTAVYYCYARYSGRTYWGRGTQ VTSS		
	CDR1	GSDFRAD (SEQ ID NO: 325)	ADAMG (SEQ ID NO: 326)	GSDFRADA (SEQ ID NO: 221)
	CDR2	SITS (SEQ ID NO: 327)	IDSITSIYYVDSVEG (SEQ ID NO: 328)	DSITSI (SEQ ID NO: 329)
	CDR3	RYSGRTY (SEQ ID NO: 330)	RYSGRTY (SEQ ID NO: 330)	YARYSGRTY (SEQ ID NO: 200)
56	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASD GSTYYADSVKGRFTISRDNKNTVYVYLMNSLRPEDTAVYYCATACADTTLYEYD YWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SASDGS (SEQ ID NO: 316)	CISASDGSTYYADSVKG (SEQ ID NO: 317)	ISASDGST (SEQ ID NO: 226)
	CDR3	ACADTTLYEYDY (SEQ ID NO: 331)	ACADTTLYEYDY (SEQ ID NO: 331)	ATACADTTLYEYDY (SEQ ID NO: 172)
57	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDG NTYYADAVKGRFAISRDNKNTVYVYLMNSLKPEDTAVYYCATACSDPRVYEYDY WGQGTQVTVSS		

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACSDPRVYEYDY (SEQ ID NO: 332)	ACSDPRVYEYDY (SEQ ID NO: 332)	ATACSDPRVYEYDY (SEQ ID NO: 196)
58	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGNTYYADAVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)
59	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGNTYYADAVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACVDTTHYEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACVDTTHYEYDY (SEQ ID NO: 333)	ACVDTTHYEYDY (SEQ ID NO: 333)	ATACVDTTHYEYDY (SEQ ID NO: 181)
60	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGNTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADSVKG (SEQ ID NO: 323)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADATQHEYDY (SEQ ID NO: 334)	ACADATQHEYDY (SEQ ID NO: 334)	ATACADATQHEYDY (SEQ ID NO: 174)
61	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNANKNTVYLMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)
62	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYDY (SEQ ID NO: 176)
63	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
64	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRAPGKEREGVSCISSDGNTYYADAVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)
65	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYAIGWFRQAPGKEREGVSCISAGDGSSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACASTTLYEYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SAGDGSS (SEQ ID NO: 336)	CISAGDGSSTYYADSVK G (SEQ ID NO: 337)	ISAGDGSST (SEQ ID NO: 237)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	ACASTTLYEYDY (SEQ ID NO: 338)	ACASTTLYEYDY (SEQ ID NO: 338)	ATACASTTLYEYDY (SEQ ID NO: 182)
66	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYAIGWFRQAPGKERE GVSCISSADGSTYYADSVKGRFTISRDNNAKNAVYLQMNSLGPEDTAVY YCATA CADTTQYDYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SSADGS (SEQ ID NO: 295)	CISSADGSTYYADSVKG (SEQ ID NO: 296)	ISSADGST (SEQ ID NO: 229)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)
67	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYAIGWFRQAPGKERE GVSCISSADGSTYYADSVKGRFTISRDNNAKNTVYLQMNSLGPEDTAVY CATA CADTTQYDYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SSADGS (SEQ ID NO: 295)	CISSADGSTYYADSVKG (SEQ ID NO: 296)	ISSADGST (SEQ ID NO: 229)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)
68	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYAIGWFRQAPGKERE GVSCISSADGSTYYADSVKGRFTISRDNNAKNTVYLQMNSLKPEDTAVY CATA CVDTTQYDYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SSADGS (SEQ ID NO: 295)	CISSADGSTYYADSVKG (SEQ ID NO: 296)	ISSADGST (SEQ ID NO: 229)
	CDR3	ACVDTTQYDYDY (SEQ ID NO: 339)	ACVDTTQYDYDY (SEQ ID NO: 339)	ATACVDTTQYDYDY (SEQ ID NO: 173)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
69	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYIAIGWFRQAPGKEREVSCISS PDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACVDTT QYEYDYWGQGTQVTVSS		
	CDR1	GFPLDYI (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYIA (SEQ ID NO: 211)
	CDR2	SSPDGS (SEQ ID NO: 340)	CISSPDGSTYYADSVKG (SEQ ID NO: 341)	ISSPDGST (SEQ ID NO: 235)
	CDR3	ACVDTTQYEYDY (SEQ ID NO: 339)	ACVDTTQYEYDY (SEQ ID NO: 339)	ATACVDTTQYEYDY (SEQ ID NO: 173)
70	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYIAIGWFRQAPGKEREVSCISS SDGSDGNTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATDCSL HGSDYPYDYWGQGTQVTVSS		
	CDR1	GFPLDYI (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYIA (SEQ ID NO: 211)
	CDR2	SSSDGSDGN (SEQ ID NO: 342)	CISSSDGSDGNTYYADSVKG (SEQ ID NO: 343)	ISSSDGSDGNT (SEQ ID NO: 251)
	CDR3	DCSLHGSDYPYDY (SEQ ID NO: 344)	DCSLHGSDYPYDY (SEQ ID NO: 344)	ATDCSLHGSDYPYDY (SEQ ID NO: 207)
71	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLDYIAIGWFRQAPGKEREVSCISS SDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTT QYEYDYWGQGTQVTVSS		
	CDR1	GFPLDYI (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYIA (SEQ ID NO: 211)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYDY (SEQ ID NO: 176)
72	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLEYYAIGWFRQAPGKEREVSCISS SDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACSDPRV YEYDYWGQGTQVTVSS		
	CDR1	GFPLEYY (SEQ ID NO: 345)	YYAIG (SEQ ID NO: 290)	GFPLEYYA (SEQ ID NO: 220)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	ACSDPRVYEYDY (SEQ ID NO: 332)	ACSDPRVYEYDY (SEQ ID NO: 332)	ATACSDPRVYEYDY (SEQ ID NO: 196)
73	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLGYAIGWFRQAPGKEREVSCISS SDDSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATDCAGGTS TPYDYWGQGTQVTVSS		
	CDR1	GFPLGYA (SEQ ID NO: 346)	YYAIG (SEQ ID NO: 290)	GFPLGYA (SEQ ID NO: 219)
	CDR2	SSSDDS (SEQ ID NO: 347)	CISSSDDSTYYADSVKG (SEQ ID NO: 348)	ISSSDDST (SEQ ID NO: 233)
	CDR3	DCAGGTSTPYDY (SEQ ID NO: 349)	DCAGGTSTPYDY (SEQ ID NO: 349)	ATDCAGGTSTPYDY (SEQ ID NO: 188)
74	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLHYAIGWFRQAPGKEREVSCISS GDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATSCVVVT KNEYDYWGQGTQVTVSS		
	CDR1	GFPLHYA (SEQ ID NO: 350)	YYAIG (SEQ ID NO: 290)	GFPLHYA (SEQ ID NO: 217)
	CDR2	SSGDGS (SEQ ID NO: 351)	CISSGDGSTYYADSVKG (SEQ ID NO: 352)	ISSGDGST (SEQ ID NO: 231)
	CDR3	SCVVVTKNEYDY (SEQ ID NO: 353)	SCVVVTKNEYDY (SEQ ID NO: 353)	ATSCVVVTKNEYDY (SEQ ID NO: 191)
75	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLHYAIGWFRQAPGKEREVSCISS SDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATACGGAT GPYDYWGQGTQVTVSS		
	CDR1	GFPLHYA (SEQ ID NO: 350)	YYAIG (SEQ ID NO: 290)	GFPLHYA (SEQ ID NO: 217)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
76	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLHYAIGWFRQAPGKEREVSCISS SDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATACVVAD RNEYDYWGQGTQVTVSS		
	CDR1	GFPLHYA (SEQ ID NO: 350)	YYAIG (SEQ ID NO: 290)	GFPLHYA (SEQ ID NO: 217)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	ACVVADRNEYDY (SEQ ID NO: 354)	ACVVADRNEYDY (SEQ ID NO: 354)	ATACVVADRNEYDY (SEQ ID NO: 190)
77	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLHYAIGWFRQAPGKEREVSCISSDGSTYYADSVKGRFTISRDNAKNTVYLMNSLRPEDTAVYYCATACVVADRNEYDYWGQGTQVTVSS		
	CDR1	GFPLHYA (SEQ ID NO: 350)	YYAIG (SEQ ID NO: 290)	GFPLHYA (SEQ ID NO: 217)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACVVADRNEYDY (SEQ ID NO: 354)	ACVVADRNEYDY (SEQ ID NO: 354)	ATACVVADRNEYDY (SEQ ID NO: 190)
78	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLNYAIGWFRQAPGKEREVSCISASDGNTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATTCASPEKYEYDYWGQGTQVTVSS		
	CDR1	GFPLNYA (SEQ ID NO: 355)	YYAIG (SEQ ID NO: 290)	GFPLNYA (SEQ ID NO: 216)
	CDR2	SASDGN (SEQ ID NO: 356)	CISASDGNTYYADSVKG (SEQ ID NO: 357)	ISASDGNT (SEQ ID NO: 248)
	CDR3	TCASPEKYEYDY (SEQ ID NO: 358)	TCASPEKYEYDY (SEQ ID NO: 358)	ATTCASPEKYEYDY (SEQ ID NO: 197)
79	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLNYAIGWFRQAPGKEREVSCISSDGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFPLNYA (SEQ ID NO: 355)	YYAIG (SEQ ID NO: 290)	GFPLNYA (SEQ ID NO: 216)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
80	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFPLNYAIGWFRQAPGKEREVSCISSDGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACGSAVHEYDYWGQGTQVTVSS		
	CDR1	GFPLNYA (SEQ ID NO: 355)	YYAIG (SEQ ID NO: 290)	GFPLNYA (SEQ ID NO: 216)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGSAVHEYDY (SEQ ID NO: 359)	ACGSAVHEYDY (SEQ ID NO: 359)	ATACGSAVHEYDY (SEQ ID NO: 203)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
81	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFLAYYAIGWFRQAPGKEREGVSCIAASVGSTYYADSVKGRFTISRDDAKNTVYLMNSLKPEDTAVYYCATDCAGGVGHEYDYWGQGTQVTVSS		
	CDR1	GFLAYY (SEQ ID NO: 360)	YYAIG (SEQ ID NO: 290)	GFLAYYA (SEQ ID NO: 223)
	CDR2	AASVGS (SEQ ID NO: 361)	CIAASVGSTYYADSVKG (SEQ ID NO: 362)	IAASVGST (SEQ ID NO: 363)
	CDR3	DCAGGVGHEYDY (SEQ ID NO: 364)	DCAGGVGHEYDY (SEQ ID NO: 364)	ATDCAGGVGHEYDY (SEQ ID NO: 206)
82	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFLDYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNNAKNAVYLMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFLDYA (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFLDYA (SEQ ID NO: 210)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
83	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFLDYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNNAKNAVYLMNSLKPEDTAVYYCATACVDTTQYDYWGQGTQVTVSS		
	CDR1	GFLDYA (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFLDYA (SEQ ID NO: 210)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACVDTTQYDY (SEQ ID NO: 339)	ACVDTTQYDY (SEQ ID NO: 339)	ATACVDTTQYDY (SEQ ID NO: 173)
84	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFLDYAIGWFRQAPGKEREGVSCISSDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATDCAGGTSPTYDYWGQGTQVTVSS		
	CDR1	GFLDYA (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFLDYA (SEQ ID NO: 210)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	DCAGGTSTPYDY (SEQ ID NO: 349)	DCAGGTSTPYDY (SEQ ID NO: 349)	ATDCAGGTSTPYDY (SEQ ID NO: 188)
85	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISS SDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTT QHEYDYWGQGTQVTVSS		
	CDR1	GFTLAYY (SEQ ID NO: 322)	YYAIG (SEQ ID NO: 290)	GFTLAYYA (SEQ ID NO: 214)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)
86	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISS SDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTT QYDYWGQGTQVTVSS		
	CDR1	GFTLAYY (SEQ ID NO: 322)	YYAIG (SEQ ID NO: 290)	GFTLAYYA (SEQ ID NO: 214)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYDY (SEQ ID NO: 324)	ACADTTQYDY (SEQ ID NO: 324)	ATACADTTQYDY (SEQ ID NO: 176)
87	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISS SDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGAT GPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
88	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISS SDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPQDTAVYYCATACGSLV GMYDYWGQGTQVTVSP		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGSLVGYDY (SEQ ID NO: 365)	ACGSLVGYDY (SEQ ID NO: 365)	ATACGSLVGYDY (SEQ ID NO: 202)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
89	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREVSCISA SDGNTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATTCASPEK YEYDYWGQGTQVTSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SASDGN (SEQ ID NO: 356)	CISASDGNTYYADSVK G (SEQ ID NO: 357)	ISASDGNT (SEQ ID NO: 248)
	CDR3	TCASPEKYEYDY (SEQ ID NO: 358)	TCASPEKYEYDY (SEQ ID NO: 358)	ATTCASPEKYEYDY (SEQ ID NO: 197)
90	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREVSCISA SNGNTYYADSVKGRFTISRDSAKNTVYLMNSLKPEDTAVYYCATTCSGLTH EYDYWGQGTQVTSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SASNGN (SEQ ID NO: 366)	CISASNGNTYYADSVK G (SEQ ID NO: 367)	ISASNGNT (SEQ ID NO: 246)
	CDR3	TCSGLTHEYDY (SEQ ID NO: 368)	TCSGLTHEYDY (SEQ ID NO: 368)	ATTCSGLTHEYDY (SEQ ID NO: 193)
91	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREVSCISS GDGNTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACGGAT GPYDYWGQGTQVTSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSGDGN (SEQ ID NO: 369)	CISSGDGNTYYADSVK G (SEQ ID NO: 370)	ISSGDGNT (SEQ ID NO: 239)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
92	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREVSCISS GDGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATHCGGSS WSNEYDYWGQGTQVTSS		

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSGDGS (SEQ ID NO: 351)	CISSGDGSTYYADSVKG (SEQ ID NO: 352)	ISSGDGST (SEQ ID NO: 231)
	CDR3	HCGGSSWSNEYDY (SEQ ID NO: 371)	HCGGSSWSNEYDY (SEQ ID NO: 371)	ATHCGGSSWSNEYDY (SEQ ID NO: 199)
93	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSNDGSTYYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSNDGS (SEQ ID NO: 372)	CISSNDGSTYYADSVKG (SEQ ID NO: 373)	ISSNDGST (SEQ ID NO: 234)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)
94	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSDGGTTYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGG (SEQ ID NO: 374)	CISSSDGGTTYADSVKG (SEQ ID NO: 375)	ISSSDGGT (SEQ ID NO: 241)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
95	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSDGSSSDGNTYYADSVKGRFTISRDNAKNTVYLMNNLKPEDTAVYYCATA CVVTTLYEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGSSSDGN (SEQ ID NO: 376)	CISSSDGSSSDGNTYYA DSVKG (SEQ ID NO: 377)	ISSSDGSSSDGNT (SEQ ID NO: 238)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	ACVVTTLYEYDY (SEQ ID NO: 378)	ACVVTTLYEYDY (SEQ ID NO: 378)	ATACVVTTLYEYD Y (SEQ ID NO: 183)
96	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKER EGVSCISSSDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATACADTTQYEYDYWGQGTQVTVSP		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYD Y (SEQ ID NO: 176)
97	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKER EGVSCISSSDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
98	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKER EGVSCISSSGGSTYYADSVKGRFTISRDNAKNTVYLQMNMMLKPEDT AVYYCATACADTTQYEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSGGS (SEQ ID NO: 379)	CISSSGGSTYYADSV KG (SEQ ID NO: 380)	ISSSGGST (SEQ ID NO: 230)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYD Y (SEQ ID NO: 176)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
99	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKER EGVSCISSSGGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATACASPVIYEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSGGS (SEQ ID NO: 379)	CISSSGGSTYYADSV KG (SEQ ID NO: 380)	ISSSGGST (SEQ ID NO: 230)
	CDR3	ACASPVIYEYDY (SEQ ID NO: 381)	ACASPVIYEYDY (SEQ ID NO: 381)	ATACASPVIYEYDY (SEQ ID NO: 205)
100	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKER EGVSCISSSGGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATDCAGGTSTPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSGGS (SEQ ID NO: 379)	CISSSGGSTYYADSV KG (SEQ ID NO: 380)	ISSSGGST (SEQ ID NO: 230)
	CDR3	DCAGGTSTPYDY (SEQ ID NO: 349)	DCAGGTSTPYDY (SEQ ID NO: 349)	ATDCAGGTSTPYD Y (SEQ ID NO: 188)
101	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKER EGVSCISSSDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATACADTTQYEYDYWGQGTQVTVSS		
	CDR1	GFTLGYY (SEQ ID NO: 382)	YYAIG (SEQ ID NO: 290)	GFTLGYYA (SEQ ID NO: 215)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYEYDY (SEQ ID NO: 324)	ACADTTQYEYDY (SEQ ID NO: 324)	ATACADTTQYEYD Y (SEQ ID NO: 176)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
102	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKER EGVSCISSSDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATACANWSSLGPYDYWGQGTQVTVSS		
	CDR1	GFTLGYY (SEQ ID NO: 382)	YYAIG (SEQ ID NO: 290)	GFTLGYYA (SEQ ID NO: 215)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACANWSSLGPYDY (SEQ ID NO: 383)	ACANWSSLGPYDY (SEQ ID NO: 383)	ATACANWSSLGPY DY (SEQ ID NO: 194)
103	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKER EGVSCISSSDGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT GVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFTLGYY (SEQ ID NO: 382)	YYAIG (SEQ ID NO: 290)	GFTLGYYA (SEQ ID NO: 215)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
104	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCEGSGFSLDYAIGWFRQAPGKER EGVSCISSGDGNTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDT AVYYCATDCVGFGSNWFDYWGQGTQVTVSS		
	CDR1	GFSLDY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYA (SEQ ID NO: 210)
	CDR2	SSGDGN (SEQ ID NO: 369)	CISSGDGNTYYADS VKG (SEQ ID NO: 370)	ISSGDGNT (SEQ ID NO: 239)
	CDR3	DCVGFGSNWFDY (SEQ ID NO: 384)	DCVGFGSNWFDY (SEQ ID NO: 384)	ATDCVGFGSNWFD Y (SEQ ID NO: 204)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
105	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYIAIGWFRQAPGKEREGVACISSRTGSTYYADSVKGRFTISRDNANKNTVALQMNSLKPEDTAVYYCATACVVVGDDQNDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVGDDQNDY (SEQ ID NO: 315)	ACVVVGDDQNDY (SEQ ID NO: 315)	ATACVVVGDDQNDY (SEQ ID NO: 186)
106	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYIAIGWFRQAPGKEREGVSCISSRTGGTYYADSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDRNDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGG (SEQ ID NO: 385)	CISSRTGGTYYADSVKG (SEQ ID NO: 386)	ISSRTGGT (SEQ ID NO: 236)
	CDR3	ACVVVGDRNDY (SEQ ID NO: 387)	ACVVVGDRNDY (SEQ ID NO: 387)	ATACVVVGDRNDY (SEQ ID NO: 187)
107	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYIAIGWFRQAPGKEREGVSCISSRTGGTYYADSVKGRFTISRDNANKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGG (SEQ ID NO: 385)	CISSRTGGTYYADSVKG (SEQ ID NO: 386)	ISSRTGGT (SEQ ID NO: 236)
	CDR3	ACVDTTQYEYDY (SEQ ID NO: 339)	ACVDTTQYEYDY (SEQ ID NO: 339)	ATACVDTTQYEYDY (SEQ ID NO: 173)
108	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYIAIGWFRQAPGKEREGVSCISSRTGGTYYADSVKGRFTISRDNANKNTVYLQMNSLKPEDTAVYYCATACVVVGDDQNDYWGQGTQVTVSS		

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGG (SEQ ID NO: 385)	CISSRTGGTTYADSVK G (SEQ ID NO: 386)	ISSRTGGT (SEQ ID NO: 236)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
109	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSC ISSRTGNTYYADSVKGRFTISRDDAKNMVYLQMNSLKPEDTAVYYCATA CVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGN (SEQ ID NO: 388)	CISSRTGNTYYADSVK G (SEQ ID NO: 389)	ISSRTGNT (SEQ ID NO: 243)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
110	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSC ISSRTGSTYYADSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATAC VVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVK G (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
111	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQALGKEREGVSC ISSRTGSTYYADSVKGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATA CVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVK G (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
112	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREVSCISS RTGSTYYADSVKGRFAISRDDAKNTVYLMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
113	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREVSCISS RTGSTYYADSVKGRFTISRDDAKNTVYLMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
114	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREVSCISS RTGSTYYADSVKGRFTVSRDDAKNTVYLMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
115	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFPLDYAIGWFRQAPGKEREVSCISS SDGSTYYADSVKGRFTISRDNNAKNTVYLMNSLKPEDTAVYYCATACGGAT GPYDYWGQGTQVTVSS		
	CDR1	GFPLDYA (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
116	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFSLDYYAIGWFRQAPGKEREGVSCISNSDGSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTTQYAYDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SNSDGS (SEQ ID NO: 390)	CISNSDGSTYYADSV KG (SEQ ID NO: 391)	ISNSDGST (SEQ ID NO: 225)
	CDR3	ACADTTQYAYDY (SEQ ID NO: 392)	ACADTTQYAYDY (SEQ ID NO: 392)	ATACADTTQYAYDY (SEQ ID NO: 171)
117	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSGSDGNTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACSGLTHEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSGSDGN (SEQ ID NO: 393)	CISSGSDGNTYYADSVKG (SEQ ID NO: 394)	ISSGSDGNT (SEQ ID NO: 247)
	CDR3	ACSGLTHEYDY (SEQ ID NO: 395)	ACSGLTHEYDY (SEQ ID NO: 395)	ATACSGLTHEYDY (SEQ ID NO: 192)
118	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSDDSTYYADSVKGRFTISRDNANKNTVYLMNSLKPEDTAVYYCATACADTTQYAYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDDS (SEQ ID NO: 347)	CISSDDSTYYADSV KG (SEQ ID NO: 348)	ISSDDST (SEQ ID NO: 233)
	CDR3	ACADTTQYAYDY (SEQ ID NO: 324)	ACADTTQYAYDY (SEQ ID NO: 324)	ATACADTTQYAYDY (SEQ ID NO: 176)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
119	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSC ISSSSDGNTYYADSVKGRFTISRDNAKNTVYQLQMNSLKPEDTAVYYCATT CSGLTHEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSSDGN (SEQ ID NO: 396)	CISSSSDGNTYYADSVKG (SEQ ID NO: 397)	ISSSSDGNT (SEQ ID NO: 245)
	CDR3	TCSGLTHEYDY (SEQ ID NO: 368)	TCSGLTHEYDY (SEQ ID NO: 368)	ATTCSGLTHEYDY (SEQ ID NO: 193)
120	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVASGFTLGYYAIGWFRQAPGKEREGVSC ISSSDGSTYYADSVKGRFTISRDNAKNTVYQLQMNSLKPEDTAVYYCATAC ADTTQYDYDYWGQGTQVTVSS		
	CDR1	GFTLGYY (SEQ ID NO: 382)	YYAIG (SEQ ID NO: 290)	GFTLGYYA (SEQ ID NO: 215)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSVKG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACADTTQYDYDY (SEQ ID NO: 297)	ACADTTQYDYDY (SEQ ID NO: 297)	ATACADTTQYDYDY (SEQ ID NO: 175)
121	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQPGGSLRLSCVSGFTLDYYAIGWFRQAPGKEREGVSC ISSNDGSTYYADSVKGRFTISRDNAKNTVYQLQMNSLKPEDTAVYYCATAC GGATGPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSNDGS (SEQ ID NO: 372)	CISSNDGSTYYADSVKG (SEQ ID NO: 373)	ISSNDGST (SEQ ID NO: 234)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
122	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSC ISASDGSTYYADSVKGRFTISRDNAKNTVYQLQMNSLKPEDTAVYYCATAC AETTLYEYDYWGQGTQVTVSS		

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SASDGS (SEQ ID NO: 316)	CISASDGSTYYADSV KG (SEQ ID NO: 317)	ISASDGST (SEQ ID NO: 226)
	CDR3	ACAETTLYEYDY (SEQ ID NO: 318)	ACAETTLYEYDY (SEQ ID NO: 318)	ATACAETTLYEYDY (SEQ ID NO: 179)
123	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGLVQGTGGSRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSVKGRFTISRDNKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSSDGS (SEQ ID NO: 319)	CISSSDGSTYYADSV KG (SEQ ID NO: 320)	ISSSDGST (SEQ ID NO: 227)
	CDR3	ACGGATGPYDY (SEQ ID NO: 335)	ACGGATGPYDY (SEQ ID NO: 335)	ATACGGATGPYDY (SEQ ID NO: 184)
124	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGMVQAGESRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADSVKGRFTISRDNKNTVYLQMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADSV KG (SEQ ID NO: 323)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADATQHEYDY (SEQ ID NO: 334)	ACADATQHEYDY (SEQ ID NO: 334)	ATACADATQHEYDY (SEQ ID NO: 174)
125	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGSVQPGESRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISASDGSTYYADSVKGRFTISRDNKNTVYLQMNSLKPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYYA (SEQ ID NO: 211)
	CDR2	SASDGS (SEQ ID NO: 316)	CISASDGSTYYADSV KG (SEQ ID NO: 317)	ISASDGST (SEQ ID NO: 226)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR3	ACADTTLYEYDY (SEQ ID NO: 331)	ACADTTLYEYDY (SEQ ID NO: 331)	ATACADTTLYEYDY (SEQ ID NO: 172)
126	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGSVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREVSC ISSGDGSTYYADSVKGRFTISRDNAKNTVYQLQMNSLKPEDTAVYYCATAC ADTTHYEYDYWGQGTQVTVSS		
	CDR1	GFTLDYY (SEQ ID NO: 298)	YYAIG (SEQ ID NO: 290)	GFTLDYYA (SEQ ID NO: 212)
	CDR2	SSGDGS (SEQ ID NO: 351)	CISSGDGSTYYADSVK G (SEQ ID NO: 352)	ISSGDGST (SEQ ID NO: 231)
	CDR3	ACADTTHYEYDY (SEQ ID NO: 398)	ACADTTHYEYDY (SEQ ID NO: 398)	ATACADTTHYEYDY (SEQ ID NO: 177)
127	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGSVQSGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREVSC ISSRTGSTYYADSVKGRFTVSRDDAKNTVYQLQMNSLKPEDTAVYYCATA CVVVGDQNDYWGQGTQVTVSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVK G (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVGQNDY (SEQ ID NO: 315)	ACVVVGQNDY (SEQ ID NO: 315)	ATACVVVGQNDY (SEQ ID NO: 186)
128	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGSVRPGGSLRLSCAASGFPLAYYYAIGWFRQAPGKEREVSC ISSSDGNTYYADAVKGRFTISRDNAKNAVYQLQMNSLKPEDTAVYYCATA CADTTQHEYDYWGQGTQVTVSS		
	CDR1	GFPLAYYY (SEQ ID NO: 289)	YYAIG (SEQ ID NO: 290)	GFPLAYYA (SEQ ID NO: 209)
	CDR2	SSSDGN (SEQ ID NO: 291)	CISSSDGNTYYADAVK G (SEQ ID NO: 292)	ISSSDGNT (SEQ ID NO: 228)
	CDR3	ACADTTQHEYDY (SEQ ID NO: 293)	ACADTTQHEYDY (SEQ ID NO: 293)	ATACADTTQHEYDY (SEQ ID NO: 180)

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
129	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVAQPGGSLRLSCAASGFPLDYAIGWFRQAPGKEREVSV CISASDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATA CADTTLYEYDYWGQGTQVTVSS		
	CDR1	GFPLDYY (SEQ ID NO: 294)	YYAIG (SEQ ID NO: 290)	GFPLDYA (SEQ ID NO: 211)
	CDR2	SASDGS (SEQ ID NO: 316)	CISASDGSTYYADSVK G (SEQ ID NO: 317)	ISASDGST (SEQ ID NO: 226)
	CDR3	ACADTTLYEYDY (SEQ ID NO: 331)	ACADTTLYEYDY (SEQ ID NO: 331)	ATACADTTLYEYDY (SEQ ID NO: 172)
130	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVVQAGGSLKLSCAASGSDFRADAMGWYRQAPGKEREPV AIDSITSIYYVDSVEGRFTISRDNKNTVYLMNTSLKPEDTAVYYCYARYS GRTYWGRGTQVTVSS		
	CDR1	GSDFRAD (SEQ ID NO: 325)	ADAMG (SEQ ID NO: 326)	GSDFRADA (SEQ ID NO: 221)
	CDR2	SITS (SEQ ID NO: 327)	IDSITSIYYVDSVEG (SEQ ID NO: 328)	DSITSI (SEQ ID NO: 329)
	CDR3	RYSGRTY (SEQ ID NO: 330)	RYSGRTY (SEQ ID NO: 330)	YARYSGRTY (SEQ ID NO: 200)
131	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVVQPGGSLRLSCAASGFSLDYAIGWFRQAPGKEREVSV CISSGDGSTYYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCATH CGGTSWGTSYDYWGQGTQVTVSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSGDGS (SEQ ID NO: 351)	CISSGDGSTYYADSVK G (SEQ ID NO: 352)	ISSGDGST (SEQ ID NO: 231)
	CDR3	HCGGTSWGTSYDY (SEQ ID NO: 399)	HCGGTSWGTSYDY (SEQ ID NO: 399)	ATHCGGTSWGTSYD Y (SEQ ID NO: 198)
132	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVVQPGGSLRLSCAASGLTFRSVGMGWFRRAPGKEREFVA TASPSGVITYYADSVKGRFTISRDNKNTVYLEMNSLKPEDTAVYYCAVR IYSGSFDNTLAYDYWGQGTQVTVSS		

SEQ ID NO	Name	CDR sequences as per Chothia	CDR sequences as per Kabat	CDR sequences as per IMGT
	CDR1	GLTFRSV (SEQ ID NO: 400)	SVGMG (SEQ ID NO: 401)	GLTFRSVG (SEQ ID NO: 224)
	CDR2	SPSGVI (SEQ ID NO: 402)	TASPSGVITYYADSVKG (SEQ ID NO: 403)	ASPSGVIT (SEQ ID NO: 252)
	CDR3	RIYSGSFDNTLAYDY (SEQ ID NO: 404)	RIYSGSFDNTLAYDY (SEQ ID NO: 404)	AVRIYSGSFDNTLAYDY (SEQ ID NO: 208)
133	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREVSCISS RTGSTYYADSVKGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTSS		
	CDR1	GFSLGYY (SEQ ID NO: 302)	YYAIG (SEQ ID NO: 290)	GFSLGYYA (SEQ ID NO: 218)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)
134	Anti-GPC3 binder heavy chain sequence	QVQLQESGGGVVQSGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREVSCISS RTGSTYYADSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVG DQNDYWGQGTQVTSS		
	CDR1	GFSLDYY (SEQ ID NO: 312)	YYAIG (SEQ ID NO: 290)	GFSLDYYA (SEQ ID NO: 210)
	CDR2	SSRTGS (SEQ ID NO: 313)	CISSRTGSTYYADSVKG (SEQ ID NO: 314)	ISSRTGST (SEQ ID NO: 242)
	CDR3	ACVVVG DQNDY (SEQ ID NO: 315)	ACVVVG DQNDY (SEQ ID NO: 315)	ATACVVVG DQNDY (SEQ ID NO: 186)

[0168] Provided herein is a composition comprising a recombinant nucleic acid sequence encoding a CFP comprising a phagocytic or tethering receptor (PR) subunit (e.g., a phagocytic receptor fusion protein (PFP)) comprising: an extracellular domain comprising an antigen binding domain specific to an antigen of a target cell; a transmembrane domain; and an intracellular domain comprising an intracellular signaling domain; and wherein the transmembrane domain and the extracellular domain are operatively linked; and wherein upon binding of the CFP to the antigen on the target cell, the killing or phagocytosis activity of the myeloid cell, such as a neutrophil, monocyte, myeloid dendritic cell (mDC), mast cell or macrophage cell expressing the CFP is increased by at least 1.1-fold, 1.5-fold, 2-fold, 2.5-fold, 3-fold, 3.5-fold, 4-fold, 4.5-fold, 5-fold, 5.5-fold, 6-fold, 6.5-fold, 7-fold, 7.5-

[0176] In some embodiments, an exemplary anti-TROP2-binding CFP described herein comprises an extracellular antigen binding domain having a sequence of any one of SEQ ID NOs: 1-3, or a heavy chain variable domain comprising a CDR3 sequence of GGFGSSYWYFDV (SEQ ID NO: 153), and/or a light chain variable domain comprising a CDR3 sequence of QQHYITPLT (SEQ ID NO: 281) and further comprises an intracellular domain of any one of the sequences in Table 2 or Table 3. In some embodiments, an exemplary anti-TROP2-binding CFP described herein comprises a sequence with at least 80-100% sequence identity to any one of SEQ ID NOs: 26-33.

IRF inducible proteins and IRF activation pathways

[0177] Type I IFNs are key cytokines mediating innate antiviral immunity and therefore drive a pro-inflammatory response. Type I IFNs are readily induced by cGMP-AMP synthase, retinoic acid-inducible protein 1 (RIG-I)-like receptors, and Toll-like receptors that recognize microbial double-stranded (ds)DNA, dsRNA, and LPS. These signaling pathways converge at the recruitment and activation of the transcription factor IRF-3 (IFN regulatory factor 3). The adaptor proteins STING (stimulator of IFN genes), MAVS (mitochondrial antiviral signaling), and TRIF (TIR domain-containing adaptor inducing IFN- β) mediate the recruitment of IRF-3 through a conserved *pLxIS* motif. The *pLxIS* motif of phosphorylated STING, MAVS, and TRIF generally binds to IRF-3 in a similar manner, whereas residues upstream of the motif confer specificity. Type I IFNs, such as IFN- α and - β , are a major family of cytokines mediating antiviral immunity. Microbial dsDNA in the cytosol binds to and activates the enzyme cGAS (cGMP-AMP synthase), which catalyzes the synthesis of a cyclic dinucleotide, cGAMP (cyclic [G(2',5')pA(3',5')p]). As a second messenger, cGAMP binds to the adaptor protein STING (stimulator of IFN genes) located on the endoplasmic reticulum (ER) membrane and directs the activation of transcription factor IRF-3 (IFN regulatory factor 3) through the protein kinase TBK1 (TANK-binding kinase 1). Phosphorylated IRF-3 dimerizes and translocates to the nucleus to initiate the transcription of the IFN- β gene. In contrast, viral dsRNA in the cytosol is sensed by the RLRs [retinoic acid-inducible protein 1 (RIG-I)-like receptors] to activate IRF-3 via the adaptor protein MAVS (mitochondrial antiviral signaling). Moreover, the TLRs (Toll-like receptors) TLR3 and TLR4, which recognize viral dsRNA in the endosome and bacterial cell wall component LPS, respectively, also mediate the induction of type I IFNs and inflammatory cytokines (1). These two TLRs use the adaptor protein TRIF (TIR domain-containing adaptor inducing IFN- β) to mediate the recruitment and activation of IRF-3. Strikingly, the signaling pathways of these three families of innate immune sensors converge at the activation of TBK1 and IRF-3. Mechanistically, the adaptor proteins STING, MAVS, and TRIF contain a conserved motif, *pLxIS* (in which *p* represents the hydrophilic residue, *x* represents any residue, and *S* represents the phosphorylation site), that is phosphorylated by TBK1 or IKK ϵ and mediates the recruitment of IRF-3 to the signaling complexes. The induced proximity between TBK1 and IRF-3 results in IRF-3 phosphorylation and activation. Moreover, IRF-3 itself also contains a *pLxIS* motif

HYITPLTFGAGTKVEIKRSGGGGAAADYKDDDDKGSDSIHQDYTTQNLIRMAVAGLVLVALLAILVRLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQGSGSIRTLQSNLGCLPSSALPSGTRSLRPIDGVSDWSQGCSLRSTGSPASLASNLEISQSPTMPFLSLHRSPHGPSKLCDDPQASLVPEVPVGGGCQEPEEMSWPPSGEIASPPELPSSPPPGLPEVAPDATSTGLPDTPAAPETSTNYPVECTEGSAGPQSLPLPILEPVKNPCSVKDQTPLQLSVEDTTSPNTKPCPPTPTTPETSPPPPPPPSSSTPCSAHLTPSSLPSSLE (SEQ ID NO: 150). (Respective CDRs 1, 2, and 3 of VH and VL are sequentially underlined, Kabat numbering system). Table 6A shows the individual domains.

[0280] Table 6A – Exemplary TROP2 binder first and second generation sequences

Structure	Domain	Sequence
Anti-TROP2-CD89 (SEQ ID NO: 143)	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-TROP2 antigen binding domain (VH of scFv, structure VH-linker-VL) (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSC KASGYTFTN <u>YGMN</u> WVKQAPGQGLKWMG <u>WINTYTGEPTYTDDFKGR</u> FAFSLDTSVSTAYLQISSLKADDTAVYFCARG <u>GFGSSYWF</u> FDVWGQGS LVTVSS (SEQ ID NO: 1)
	linker	GGGGSGGGGSGGGGS (SEQ ID NO: 405)
	VL domain of scFv (CDR 1, 2, and 3 underlined as per Kabat)	DIQLTQSPSSLSASVGDRVSITC <u>KASQDV</u> SI <u>AV</u> AWYQQKPGKAPKLLIY <u>SASYRYTG</u> VPDRFSGSGSGTDFTLTIS SLQPEDFAVYYC <u>QQHYITPLTF</u> GAGTKVEIKR (SEQ ID NO: 2)
	linker	GSGGS (SEQ ID NO: 406)
	CD89 TMD and intracellular domain	DSIHQDYTTQNLIRMAVAGLVLVALLAILVENWHSHTALNKEASADVAEPSWSQQMCQPGLTFARTPSVCK (SEQ ID NO: 407)
Anti-TROP2-CD89 (SEQ ID NO: 144)	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-TROP2 antigen binding domain (VH of scFv, structure VH-linker-VL) (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSC KASGYTFTN <u>YGMN</u> WVKQAPGQGLKWMG <u>WINTYTGEPTYTDDFKGR</u> FAFSLDTSVSTAYLQISSLKADDTAVYFCARG <u>GFGSSYWF</u> FDVWGQGS LVTVSS (SEQ ID NO: 1)
	linker	GGGGSGGGGSGGGGS (SEQ ID NO: 405)

	VL domain of scFv (CDR 1, 2, and 3 underlined as per Kabat)	DIQLTQSPSSLSASVGDRVSITCK <u>KASQDVSIAVA</u> WYQQKPGK APKLLIY <u>SASYRYT</u> GVPDRFSGSGSGTDFTLTISSLQPEDFAV YYC <u>QQHYITPLTF</u> GAGTKVEIKR (SEQ ID NO: 2)
	linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD and intracellular domain	DSIHQDYTTQNLIRMAVAGLVLVALLAILVENWHSHTALNK EASADVAEPSWSQQMCQPGLTFARTPSVCK (SEQ ID NO: 407)
Anti- TROP2- CD89- FcR (SEQ ID NO: 145)	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-TROP2 domain (VH-linker-VL) (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSC KASGYTFTN <u>YGMN</u> WVKQAP GQGLKWMG <u>WINTYTGEPTYTDDFKGRFA</u> SLDTSVSTAYLQIS SLKADDTAVYFCAR <u>GGFGSSYWYFDV</u> WGQGS LTVSSGGGGG GGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCK <u>KASQDVSIAVA</u> WYQQKPGKAPKLLIY <u>SASYRYT</u> GVPDRFSGSGSGTDFTLTISSL QPEDFAVYYC <u>QQHYITPLTF</u> GAGTKVEIKR (SEQ ID NO: 3)
	linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLVALLAILV (SEQ ID NO: 408)
	FcR intracellular domain (ICD)	RLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 15)
Anti- TROP2- CD89- FcR-PI3K (SEQ ID NO: 146)	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-TROP2 domain (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSC KASGYTFTN <u>YGMN</u> WVKQAP GQGLKWMG <u>WINTYTGEPTYTDDFKGRFA</u> SLDTSVSTAYLQIS SLKADDTAVYFCAR <u>GGFGSSYWYFDV</u> WGQGS LTVSSGGGGG GGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCK <u>KASQDVSIAVA</u> WYQQKPGKAPKLLIY <u>SASYRYT</u> GVPDRFSGSGSGTDFTLTISSL QPEDFAVYYC <u>QQHYITPLTF</u> GAGTKVEIKR (SEQ ID NO: 3)
	Linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLVALLAILV (SEQ ID NO: 408)
	FcR intracellular domain (ICD)	RLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 15)
	Linker	GS
	PI3K recruitment domain (PI3K) ICD	YEDMRGILYAAPQLRSIRGQPGPNHEEDADSYENM (SEQ ID NO: 17)
Anti- TROP2- CD89- CD40	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-TROP2 domain (CDR 1, 2,	QVQLQQSGSELKKPGASVKVSC KASGYTFTN <u>YGMN</u> WVKQAPGQGL KWMG <u>WINTYTGEPTYTDDFKGRFA</u> SLDTSVSTAYLQISSLKADDTA VYFCAR <u>GGFGSSYWYFDV</u> WGQGS LTV

(SEQ ID NO: 147)	and 3 underlined as per Kabat)	SSGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKASQDVSI VAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISLQ EDFAVYYCQQHYITPLTFGAGTKVEIKR (SEQ ID NO: 3)
	Linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLLVALLAILV (SEQ ID NO: 408)
	CD40 ICD	KKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQETLHGCQPV TQEDGKESRISVQERQ (SEQ ID NO: 18)
Anti-TROP2-CD89-CD40-FcR (SEQ ID NO: 148)	Signal peptide	MWLQSLLLLGTVACIS (SEQ ID NO: 7)
	Anti-TROP2 domain (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSCASGYTFTNYGMNWVKQAP GQGLKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVSTAYLQIS SLKADDTAVYFCARGGFGSSYWFYDVGQGS�TVSSGGGGS GGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKASQDVSI VAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISL QPEDFAVYYCQQHYITPLTFGAGTKVEIKR (SEQ ID NO: 3)
	Linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLLVALLAILV (SEQ ID NO: 408)
	CD40 ICD	KKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQETLHGC QPVTTQEDGKESRISVQERQ (SEQ ID NO: 18)
	Linker	GS
Anti-TROP2-CD89-TRIF (SEQ ID NO: 149)	FcR ICD	RLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 15)
	Signal peptide	MWLQSLLLLGTVACIS (SEQ ID NO: 7)
	Anti-TROP2 domain (CDR 1, 2, and 3 underlined as per Kabat)	QVQLQQSGSELKKPGASVKVSCASGYTFTNYGMNWVKQAP GQGLKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVSTAYLQIS SLKADDTAVYFCARGGFGSSYWFYDVGQGS�TVSSGGGGS GGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKASQDVSI VAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISL QPEDFAVYYCQQHYITPLTFGAGTKVEIKR (SEQ ID NO: 3)
	Linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLLVALLAILV (SEQ ID NO: 408)
	TRIF-ICD	RGSIRTLQSNLGLPSSALPSGTRSLRPIDGVSDWSQGCSLRS TGSPASLASNLEISQSPTMPFLSLHRSPHGPSKLCDDPQASLVPE PVPGGCQEPEEMSWPPSGEIASPPELPSSPPPGLPEVAPDATSTG LPDTPAAPETSTNYPVECTEGSAGPQSLPLPILEPVKNPCSVKDQ TPLQLSVEDTTSPNTKPCPPTPTTPETSPPPPPPPSSTPCSAHLTP SSLFPSSLE (SEQ ID NO: 21)
	Signal peptide	MWLQSLLLLGTVACIS (SEQ ID NO: 7)

Anti-TROP2-CD89-FcR-TRIF (SEQ ID NO: 150)	Anti-TROP2 scFv	QVQLQQSGSELKKPGASVKVSCKASGYTFT <u>NYGMN</u> WVKQ APGQGLKWMG <u>WINTYTGEPTYTDDFKGRFA</u> SLDTSVSTA YLQISLKAADDAVYFCARGGFGSSY <u>WYFDV</u> WGQGS�TV SSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKA <u>SQDVSI</u> AVA <u>WYQQKPGKAPKLLIYS</u> <u>SASYRYT</u> GVDPDRFSGSG SGTDFTLTISLQPEDFAVYYC <u>QQHYITPL</u> TFGAGTKVEIKR (SEQ ID NO: 3)
	Linker	SGGGGAAADYKDDDDKGS (SEQ ID NO: 9)
	CD89 TMD	DSIHQDYTTQNLIRMAVAGLVLLAILV (SEQ ID NO: 408)
	FcR ICD	RLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 15)
	Linker	GS
	TRIF-ICD	GSIRTLQSNLGCLPPSSALPSGTRSLRPIDGVSDWSQGCSLR STGSPASLASNLEISQSPTMPFLSLHRSPHGPSKLCDDPQASL VPEPVPGGCQEPEEMSWPPSGEIASPPPELSSPPPGLPEVAPD ATSTGLPDTPAAPETSTNYPVECTEGSAGPQSLPLPILEPVKN PCSVKDQTPQLQSVEDTTSPNTKPCPPTPTTPETSPPPPPPPS STPCSAHLTPSSLPSSLE (SEQ ID NO: 20)

[0281] Exemplary anti-GPC3-CD89 CFP sequences are shown below:

[0282] An exemplary anti-GPC3-CD89 has the amino acid sequence:

MWLQSLLLLGTVACISQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGL
EWMGALDPKTGDTAYSQKFKGKATLTADKSTSTAYMELSSLTSEDVAVYYCTRFYSYTYWGQ
GTLVTVSSGGGGSGGGGSGGGGSDVVMQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWY
LQKPGQSPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQNTHVPPTFGQG
TKLEIKSGGSDSIHQDYTTQNLIRMAVAGLVLLAILVENWHSHTALNKEASADVAEPSWSQQ
MCQPGLTFARTPSVCK (SEQ ID NO: 151). (Respective CDRs 1, 2, and 3 of VH and VL are
sequentially underlined, Kabat numbering system). Table 6B shows the individual domains.

[0283] An exemplary anti-GPC3-CD89 has the amino acid sequence:

MWLQSLLLLGTVACISQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGL
EWMGALDPKTGDTAYSQKFKGRVTLTADKSTSTAYMELSSLTSEDVAVYYCTRFYSYTYWGQ
GTLVTVSSGGGGSGGGGSGGGGSDVVMQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWY
LQKPGQSPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQNTHVPPTFGQGTK
LEIKSGGSDSIHQDYTTQNLIRMAVAGLVLLAILVENWHSHTALNKEASADVAEPSWSQQMC
QPGLTFARTPSVCK (SEQ ID NO: 152). (Respective CDRs 1, 2, and 3 of VH and VL are sequentially
underlined, Kabat numbering system). Table 6B shows the individual domains.

[0284] Table 6B – Exemplary GPC3 binder first and second generation sequences

Structure	Domain	Sequence
Anti-GPC3 - CD89 (SEQ ID NO: 151)	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-GPC3 VH domain (of ScFv, structure: VH-linker-VL) CDRs 1, 2, and 3 underlined (Kabat)	QVQLVQSGAEVKKPGASVKV SCKASGYTFTD <u>YEMH</u> WVRQA PGQGLEWMGALDPKTGDTAYSQKFKGKATLTADKSTSTAY MELSSLTSED TAVYYCTRF <u>YSYTY</u> WGQGTLVTVSS (SEQ ID NO: 4)
	linker	GGGGSGGGGSGGGGS (SEQ ID NO: 405)
	Anti-GPC3 VL domain of ScFv, CDRs 1, 2, and 3 underlined (Kabat)	DVVM TQSPLSLPVT PGEPASISCRSSQSLVHSNRNTYLHWYL QKPGQSPQLLIYKVS NRFS GVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQNT HVPPTFGQG TKLEIK (SEQ ID NO: 5)
	Linker	GSGGS (SEQ ID NO: 406)
	CD89 hinge	DSIHQDYTTQN (SEQ ID NO: 8)
	CD89 TMD	<i>LIRMAVAGLV L VALLAILV (SEQ ID NO: 11)</i>
Anti-GPC3 - CD89 (SEQ ID NO: 152)	CD89 ICD	ENWHSHTALNKEASADVAEPSWSQQMCQPGLTFARTPSVCK (SEQ ID NO: 12)
	Signal peptide	MWLQSLLLLGTVAC SIS (SEQ ID NO: 7)
	Anti-GPC3 VH domain (of ScFv: structure: VH-linker-VL) CDRs 1, 2, and 3 underlined (Kabat)	QVQLVQSGAEVKKPGASVKV SCKASGYTFTD <u>YEMH</u> WVRQA PGQGLEWMGALDPKTGDTAYSQKFKGRVTLTADKSTSTAY MELSSLTSED TAVYYCTRF <u>YSYTY</u> WGQGTLVTVSS (SEQ ID NO: 409)
	linker	GGGGSGGGGSGGGGS (SEQ ID NO: 405)
	Anti-GPC3 VL domain of ScFv CDRs 1, 2, and 3 underlined (Kabat)	DVVM TQSPLSLPVT PGEPASISCRSSQSLVHSNRNTYLHWYL QKPGQSPQLLIYKVS NRFS GVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQNT HVPPTFGQG TKLEIK (SEQ ID NO: 5)
	linker	GSGGS (SEQ ID NO: 406)
	CD89 hinge	DSIHQDYTTQN (SEQ ID NO: 8)
	CD89 TMD	<i>LIRMAVAGLV L VALLAILVE (SEQ ID NO: 410)</i>
	CD89 intracellular domain	NWHSHTALNKEASADVAEPSWSQQMCQPGLTFARTPSVCK (SEQ ID NO: 411)

Primary assessment of efficacy will be at 12 weeks. Subjects may enroll in a long-term extension study at 48 weeks if they have stable disease (SD), partial response (PR), or complete response (CR).

[0308] In Part B the maximum acceptable dose (MAD) from Part A will be assessed for safety, tolerability, and efficacy in patients with CRLM. Primary assessment of efficacy will be objective response rate (ORR) at 12 weeks.

[0309] In the event of treatment termination due to unacceptable toxicity the patient will continue in the study until the occurrence of progression of disease, at which time an end-of-study evaluation will be performed, with additional follow-up required until resolution or stabilization of any treatment-related toxicity. All patients will be followed for survival.

[0310] To ensure the safety of study subjects, the first two subjects in each dose cohort will be staggered by an interval of 14 days. If there are no safety concerns, then the remaining subjects may enroll at that dose level simultaneously.

[0311] An exemplary anti-TROP2 second generation chimeric fusion protein (e.g., a drug product) comprising an anti-TROP2 scFv has the sequence:

MWLQSLLLLGTVAC**SI**QVQLQQSGSELKKPGASVKV**SCKASGYTFTNYGMN****WVKQAP**
GQGLKWMGWINTYTGEPT**Y**TDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFC**ARGGF**
GSSYWYFDVWGQGSLVT**VSSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKAS**
QDVSI**AVAWYQQKPGKAPKLLI**YSAS**YRYTGVPDRFSGSGSGTDFTLT**ISSLQPEDFAVYYC
QQHYITPLTFGAGTKVEIKR**GSGGSDSIHQDYTTQNLIRMAVAGLV****L**VALLAIL**VENWHSHTAL**
NKEASADVAEPSWSQQMCQPGLTFARTPSVCK (SEQ ID NO: 143). The bold letters represent the signal peptide sequence. A mature protein lacks this signal sequence, and one of skill in the art can interpret the protein sequence as expressed without the signal peptide sequence, as disclosed below:
QVQLQQSGSELKKPGASVKV**SCKASGYTFTNYGMN****WVKQAPGQGLKWMGWINTYTGEPT**
Y**TDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFC****ARGGF****GSSYWYFDVWGQGSLVT**
VSSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKAS**QDVSI****AVAWYQQKPGKA**
PKLLI**YSAS****YRYTGVPDRFSGSGSGTDFTLT****ISSLQPEDFAVYYC****QQHYITPLTFGAGTKVEIK**
R**GSGGSDSIHQDYTTQNLIRMAVAGLV****L****VALLAIL****VENWHSHTALNKEASADVAEPSWSQQM**
CQPGLTFARTPSVCK (SEQ ID NO: 26). The underlined regions are the CDR sequence of the scFv that binds to TROP2 in sequence, CDR1, CDR2, CDR3 for the heavy and light chains. The italicized alphabets represent the amino acid sequence of the CD89 TMD.

[0312] The anti-TROP2 binder has been designed for systemic intravenous delivery as an mRNA-lipid nanoparticle (LNP) formulation. This approach takes advantage of the natural propensity for intravenous (i.v) administered LNP to accumulate in the liver. The lipid components of the anti-TROP2 binder also protect the mRNA encoding for the CAR from degradation by plasma and tissue nucleases. The proprietary mRNA construct encodes for a receptor consisting of a TROP2-targeted scFv (derived from the complementarity-determining regions (CDR) of sacituzumab), as well as the