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(54) **ANTI-DLL3 ANTIBODIES AND USES
THEREOF**

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30, 2019, now Pat. No. 12,037,391.

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(2013.01); **C07K 16/30** (2013.01); **G01N**

33/57492 (2013.01); **C07K 2317/24** (2013.01);

C07K 2317/31 (2013.01); **C07K 2317/56**

(2013.01); **C07K 2317/565** (2013.01); **C07K**

2317/92 (2013.01)

(57)

ABSTRACT

Anti-DLL3 antibodies and antigen-binding fragments thereof, anti-CD47 antibodies and antigen-binding fragments thereof, and anti-CD47/DLL3 bispecific antibodies and antigen-binding fragments thereof are described. Also described are nucleic acids encoding the antibodies, compositions comprising the antibodies, and methods of producing the antibodies and using the antibodies for treating or preventing diseases, such as cancer and/or associated complications.

Specification includes a Sequence Listing.

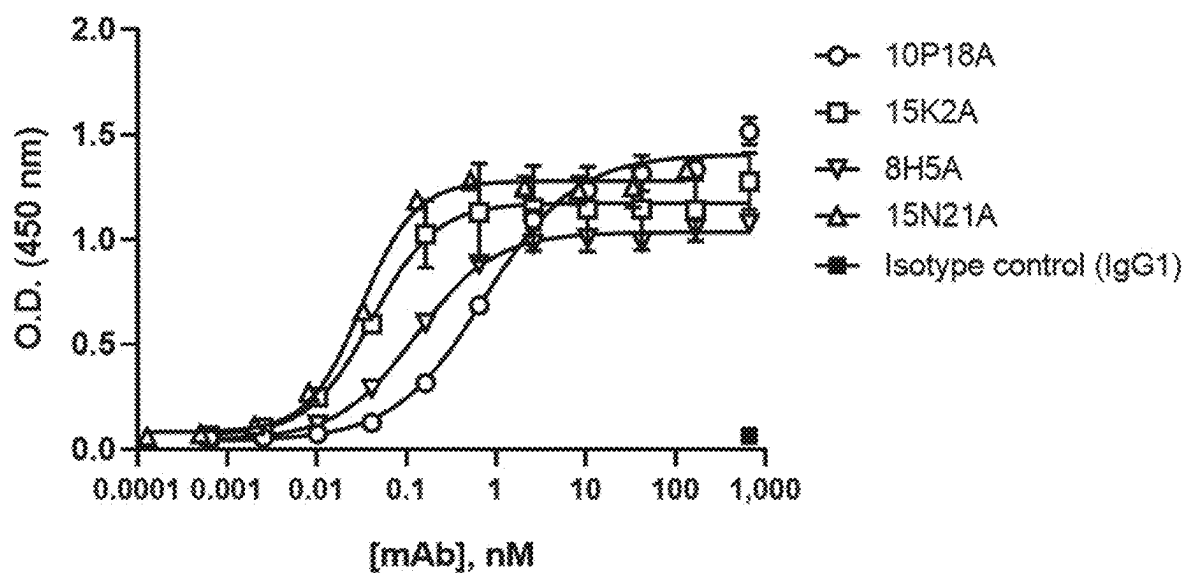


FIG. 1A

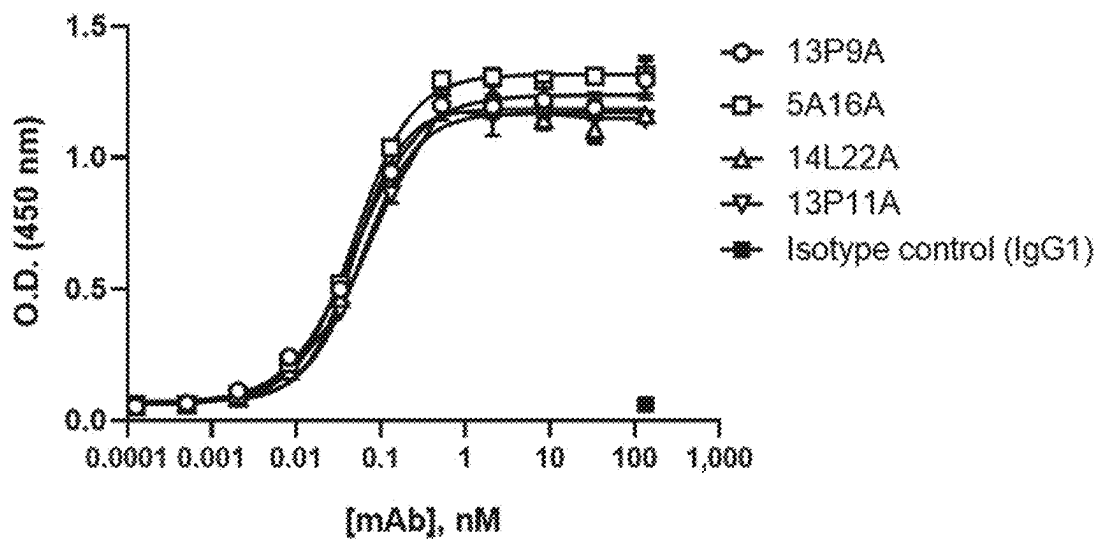


FIG. 1B

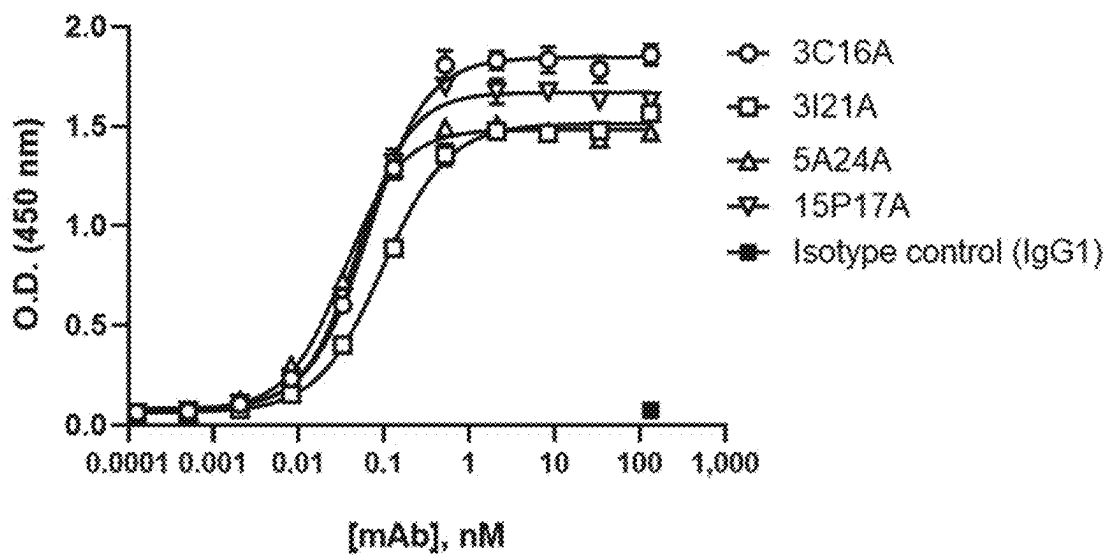


FIG. 1C

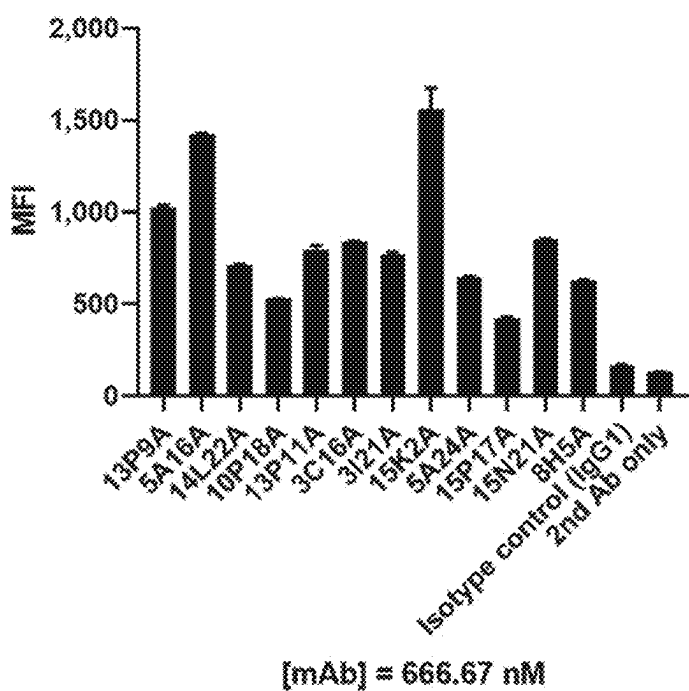


FIG. 2A

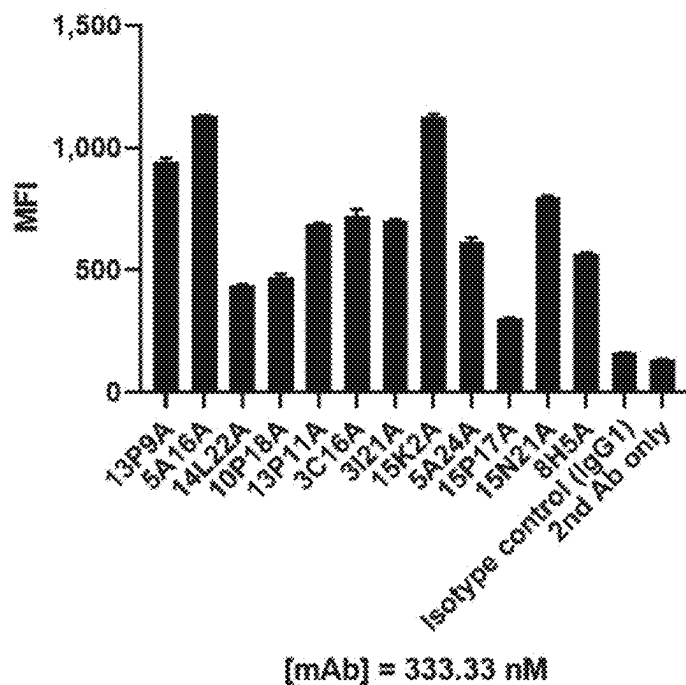


FIG. 2B

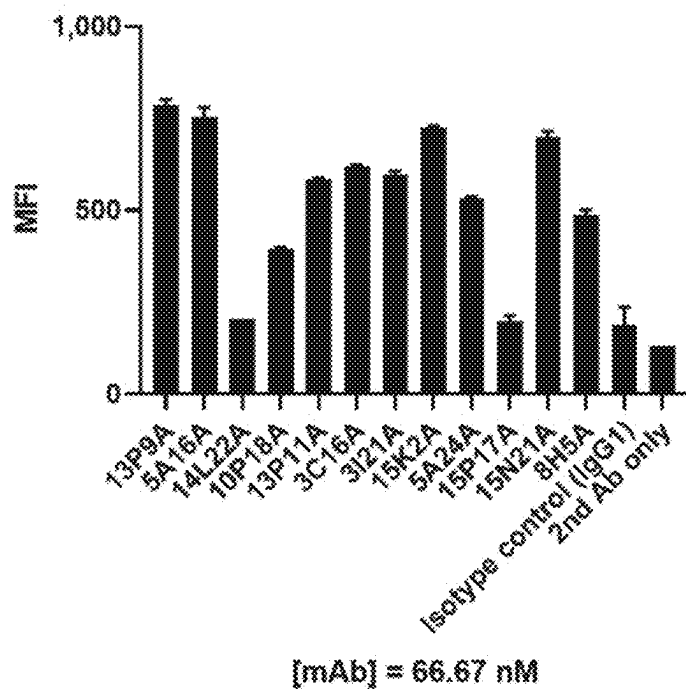


FIG. 2C

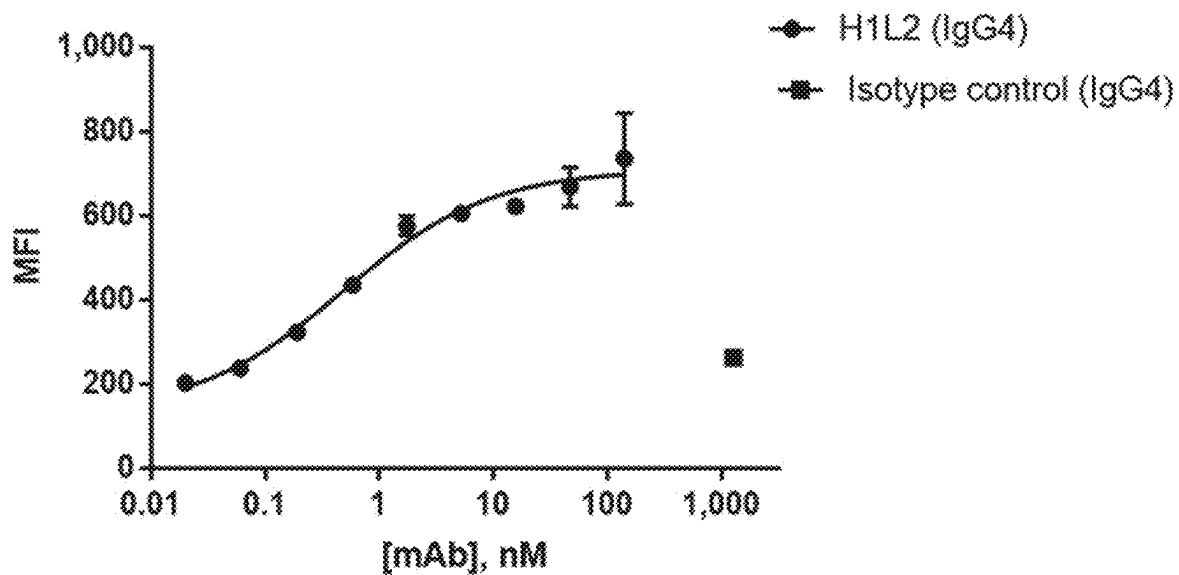


FIG. 3

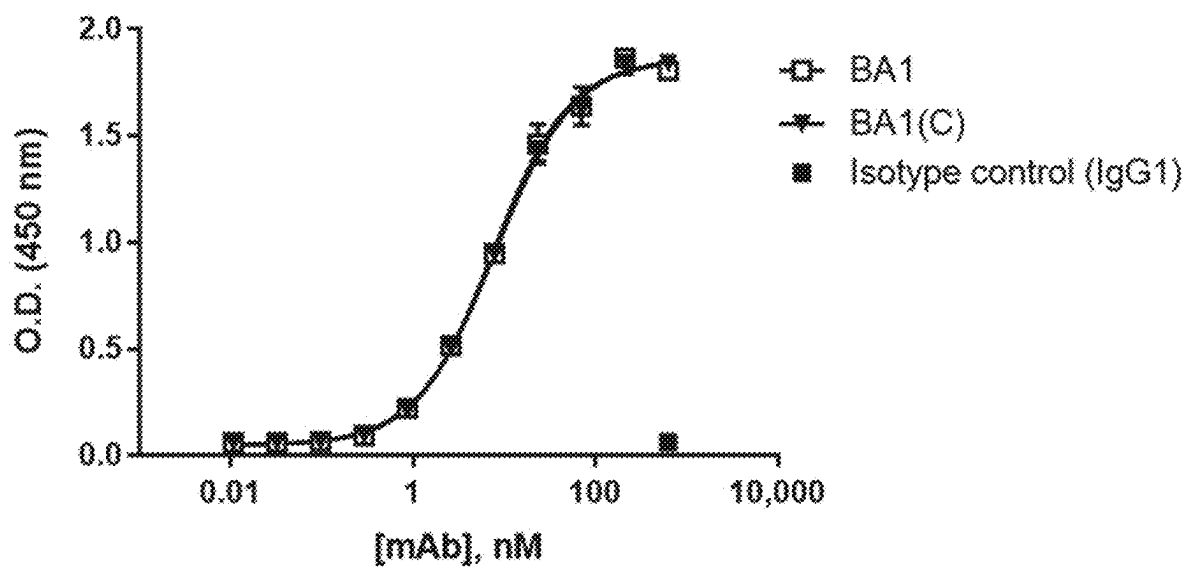


FIG. 4A

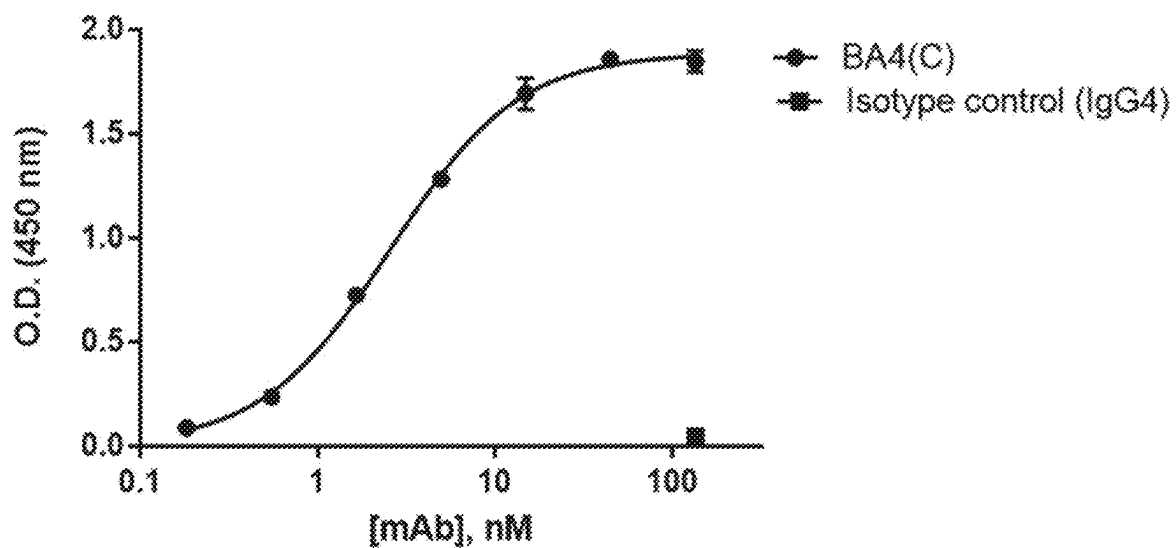


FIG. 4B

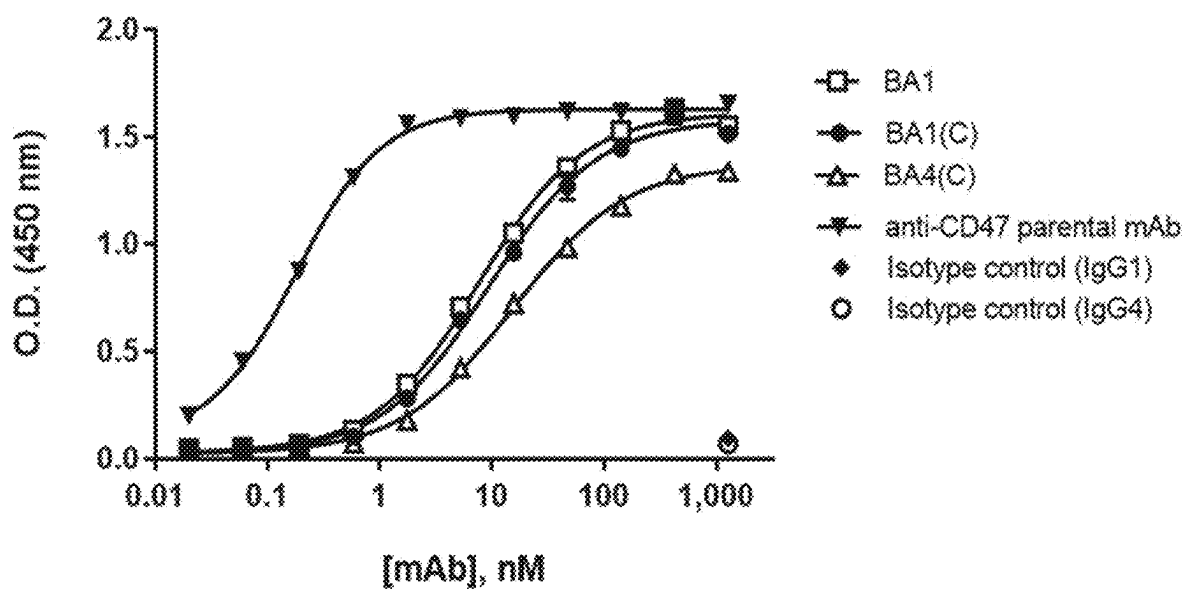


FIG. 5

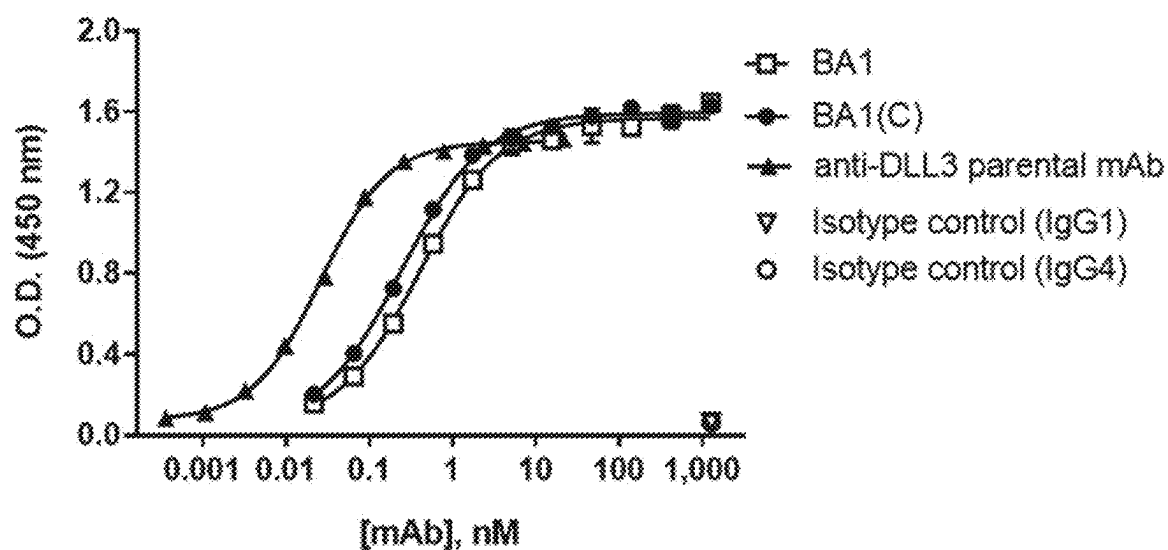


FIG. 6A

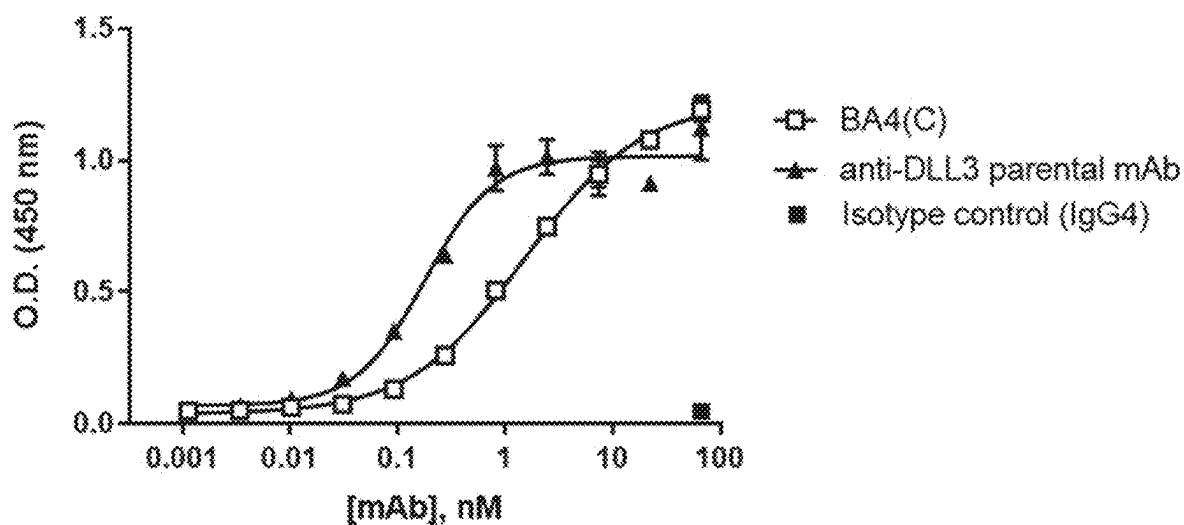


FIG. 6B

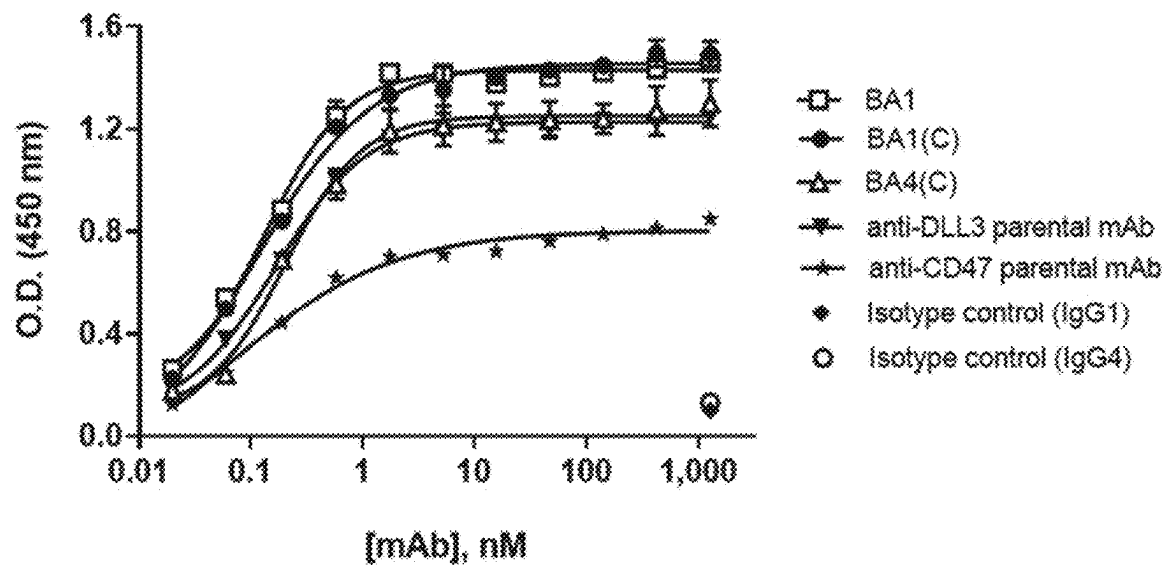


FIG. 7

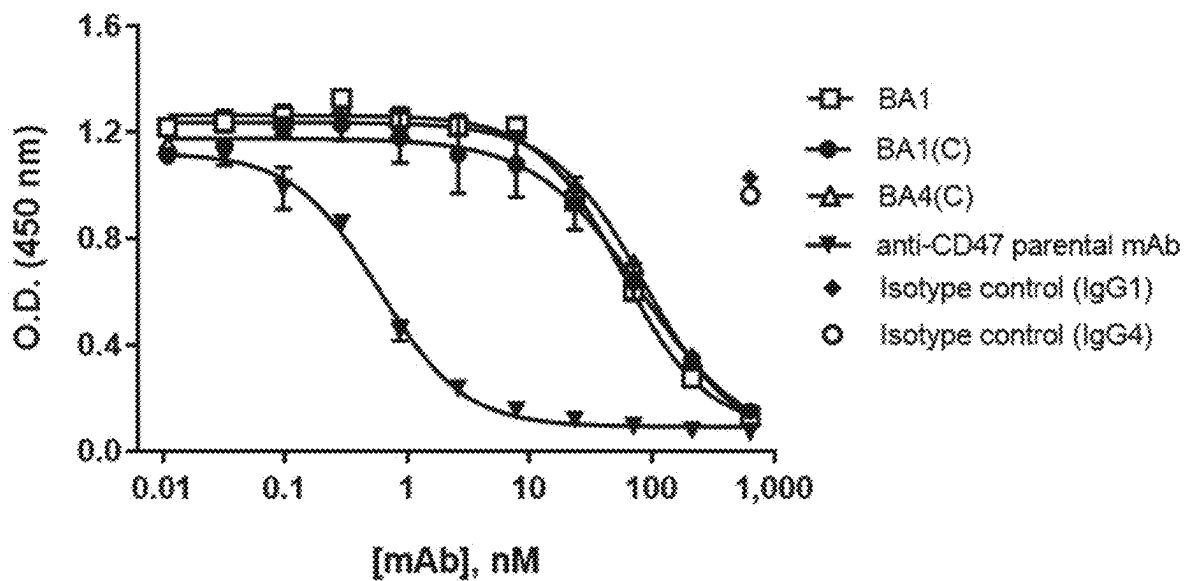


FIG. 8A

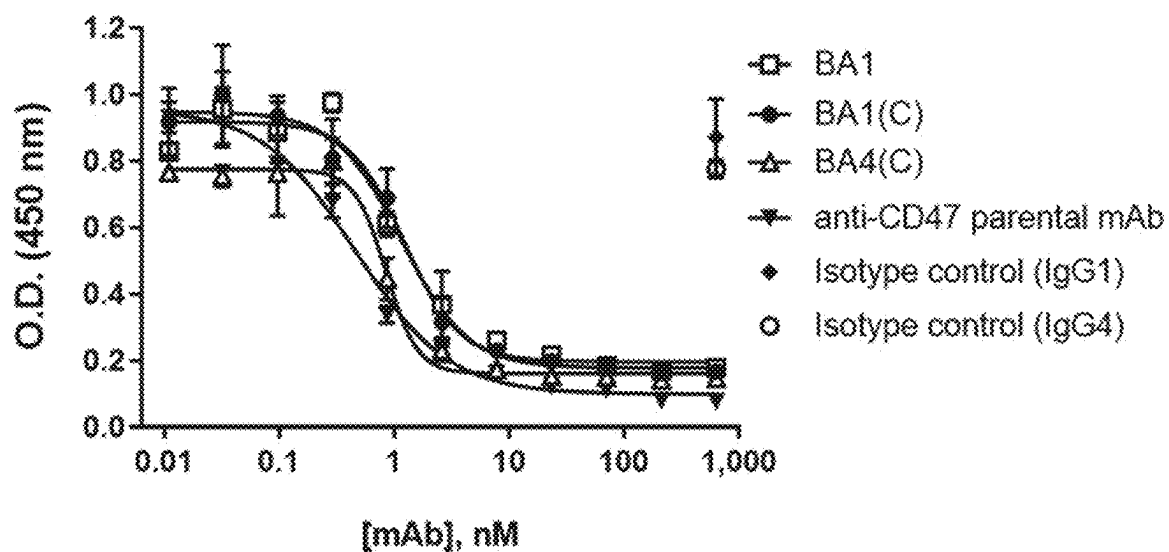


FIG. 8B

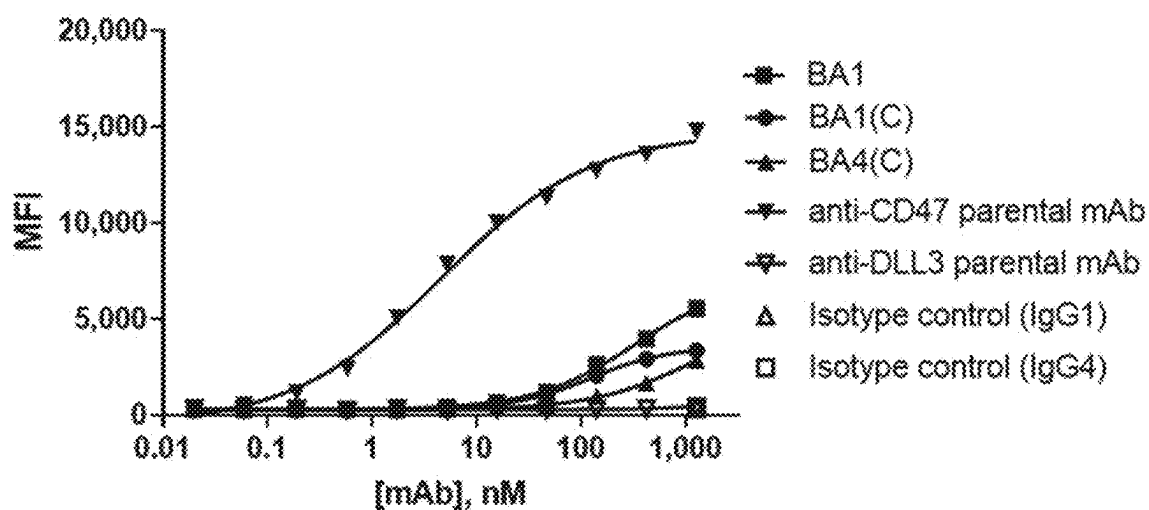


FIG. 9

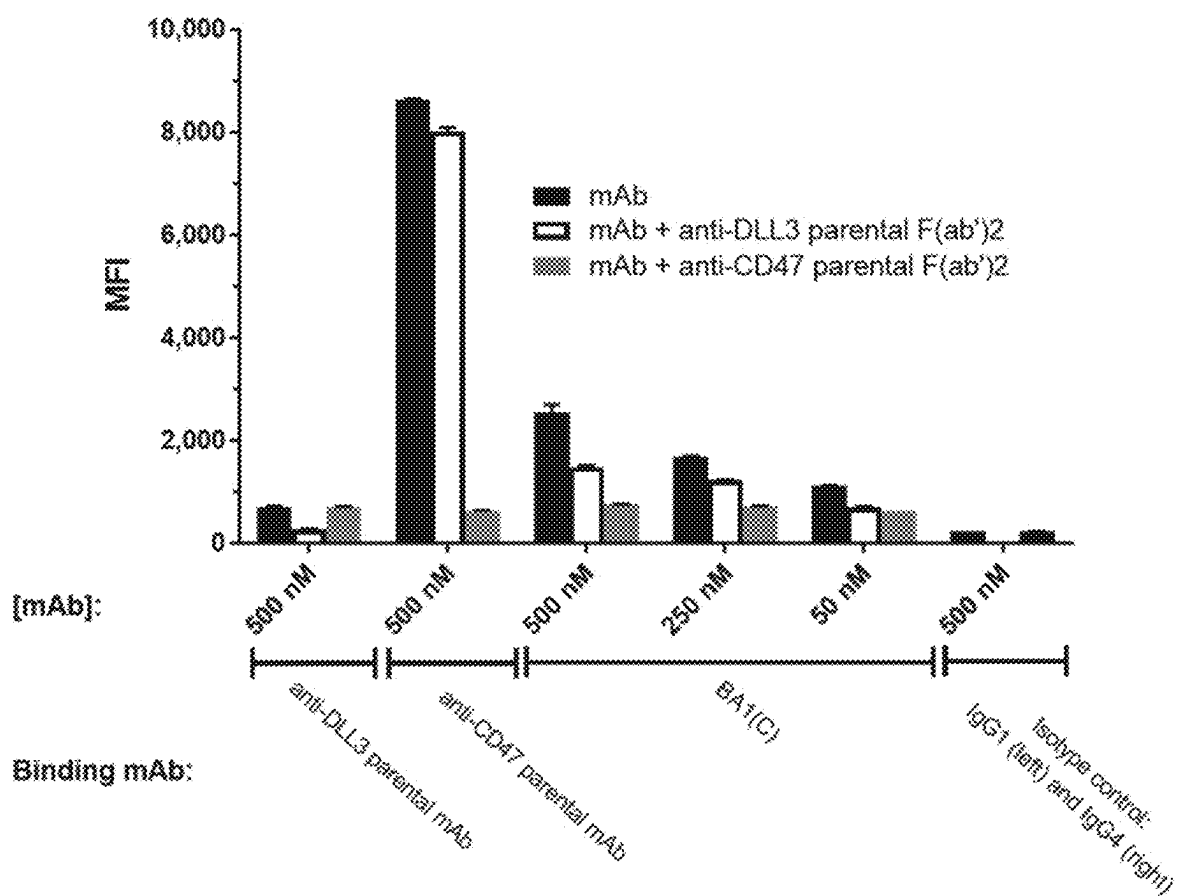


FIG. 10

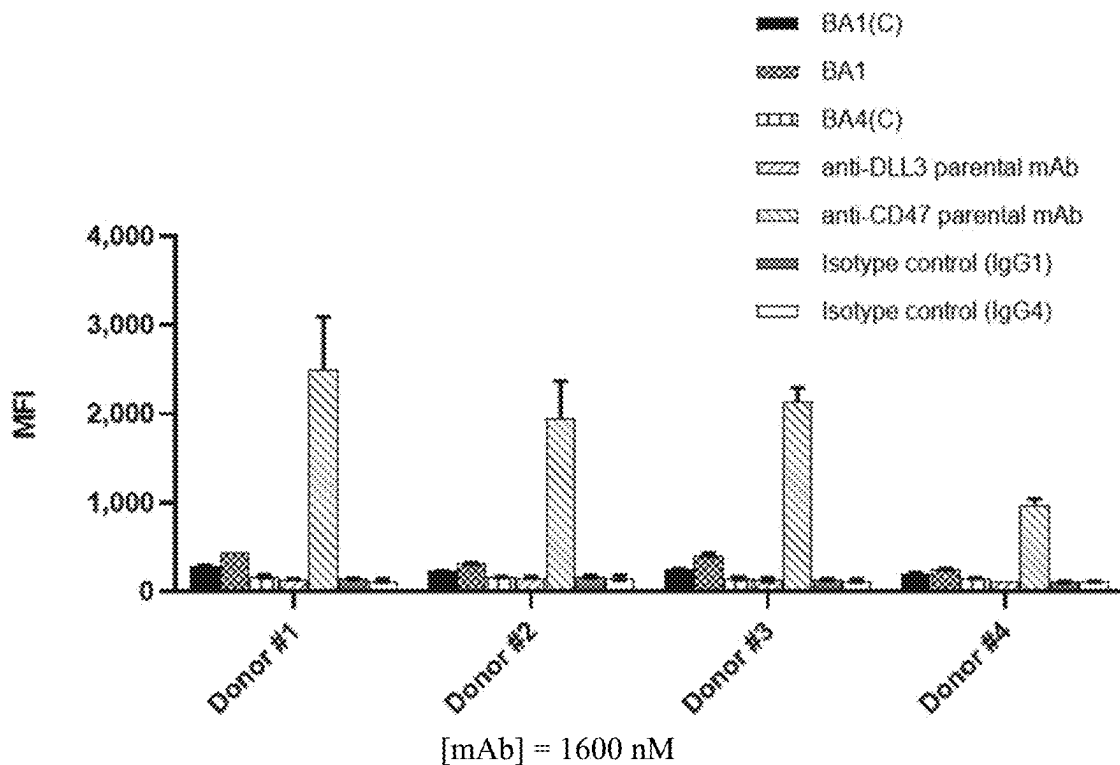


FIG. 11A

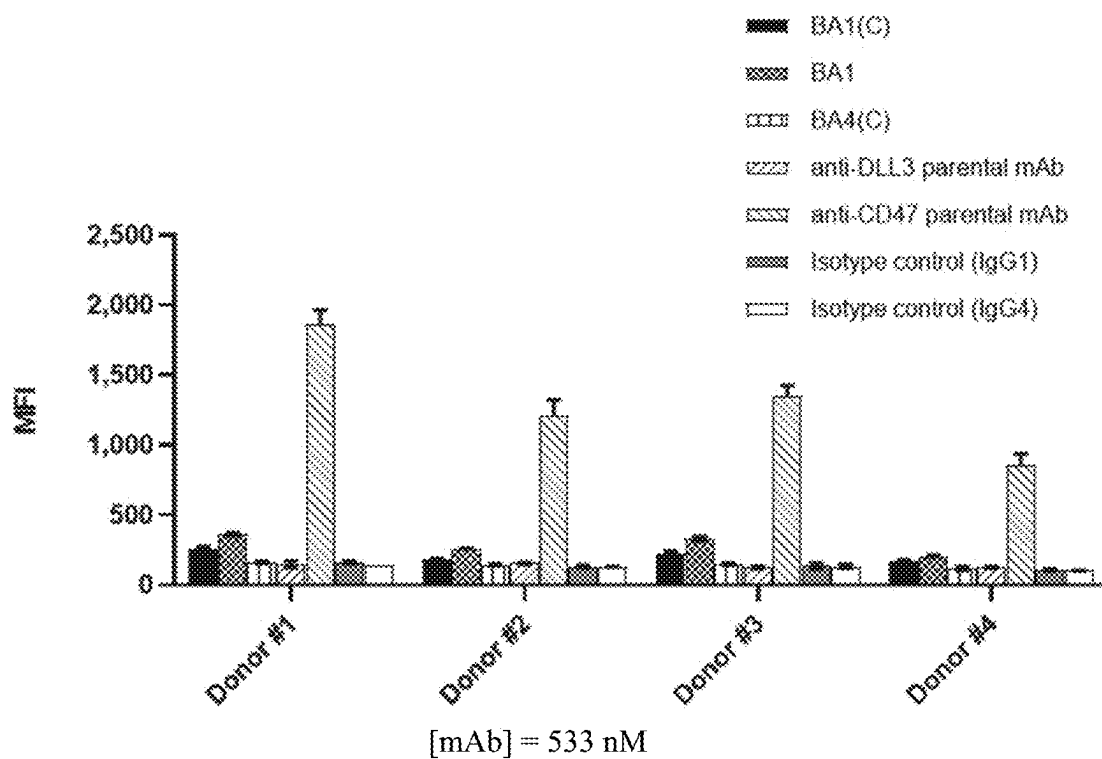


FIG. 11B

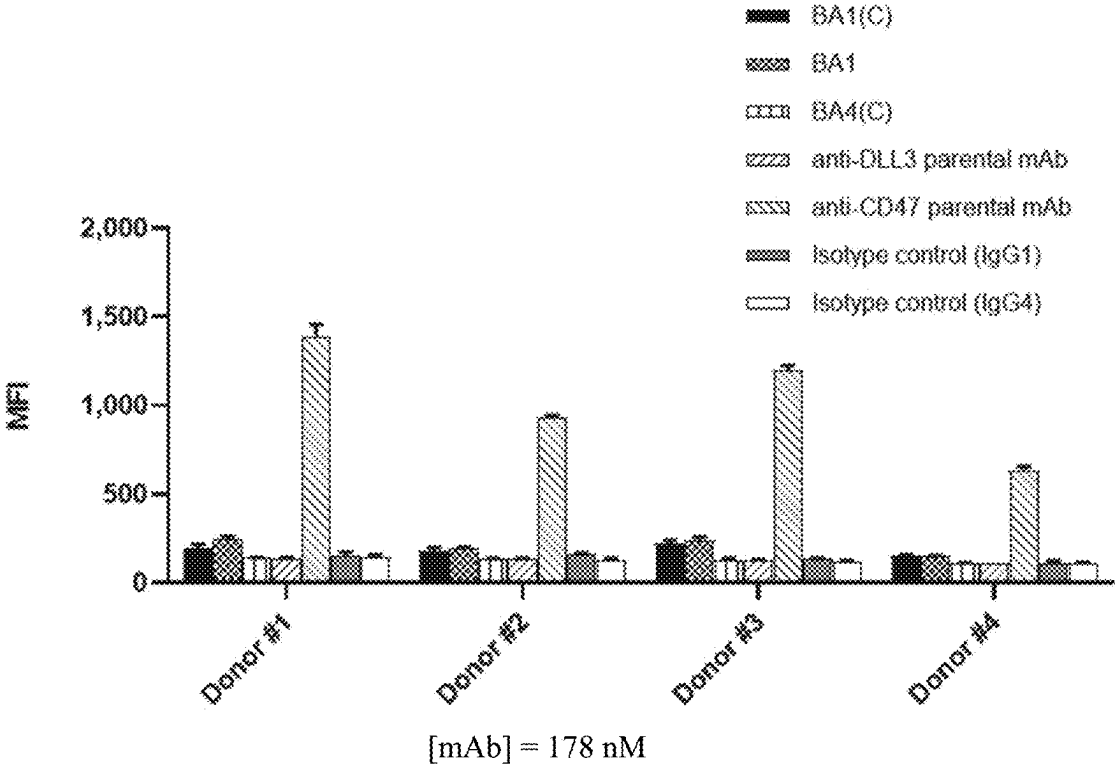


FIG. 11C

ANTI-DLL3 ANTIBODIES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a divisional of U.S. patent application Ser. No. 18/733,287, filed Jun. 4, 2024, which is a divisional of U.S. patent application Ser. No. 15/733,747, filed Oct. 14, 2020 and issued as U.S. Pat. No. 12,037,391 on Jul. 16, 2024, which is a section 371 of International Application No. PCT/US2019/029888 filed Apr. 30, 2019, which published in the English language on Nov. 14, 2019 under International Publication No. WO 2019/217145, which claims priority to U.S. Provisional Application No. 62/668,427, filed on May 8, 2018; U.S. Provisional Application No. 62/754,207, filed on Nov. 1, 2018; and U.S. Provisional Application 62/787,815, filed on Jan. 3, 2019. Each disclosure is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] This invention relates to monoclonal anti-DLL3 antibodies, anti-CD47 antibodies, and anti-CD47/DLL3 bispecific antibodies, nucleic acids and expression vectors encoding the antibodies, recombinant cells containing the vectors, and compositions comprising the antibodies. Methods of making the antibodies, and methods of using the antibodies to treat diseases including cancer and/or associated complications are also provided.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0003] This application contains a sequence listing, which is submitted electronically. The contents of the electronic sequence listing (065799.15US4 Sequence Listing.xml; Size: 233,156 bytes; and Date of Creation: Apr. 28, 2025) is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0004] Delta like canonical Notch ligand 3 (DLL3), also known as delta like 3 or delta like protein 3, is required for somite segmentation during early development (Dunwoodie et al., Development 129:1795-806 (2002)). Unlike the mammalian Notch family ligands DLL1, DLL4, JAG1, and JAG2 which all activate Notch receptor signaling in trans (Ntziachristos et al., Cancer Cell 25(3):318-34 (2014)), DLL3 is predominantly localized in the Golgi apparatus and is unable to activate Notch signaling (Chapman et al., Hum Mol Genet 20(5):905-16 (2011) and Geffers et al., J Cell Biol 178(3):465-76 (2007)). During normal development, DLL3 inhibits both cis- and trans-acting Notch pathway activation by interacting with Notch and DLL1 (Chapman et al., Hum Mol Genet 20(5):905-16 (2011)). DLL3 is normally either absent or present at very low levels in adult normal tissues except brain, but is overexpressed in lung cancer, testicular cancer, glioma and melanoma samples (Uhlen et al., Science 357(6352): ean2507 (2017)). Furthermore, DLL3 is detectable on the surface of small cell lung cancer (SCLC) and large cell neuroendocrine carcinoma (LCNEC) tumor cells (Saunders et al., Sci Transl Med 7(302):302ra136 (2015) and Sharma et al., Cancer Res 77(14):3931-41 (2017)), making it a potential target of monoclonal antibodies for cancer therapy. Therefore, an

anti-DLL3 monoclonal antibody could be used to specifically target DLL3-expressing tumor cells and serve as a potential anti-cancer therapeutic.

BRIEF SUMMARY OF THE INVENTION

[0005] In one general aspect, the invention relates to isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof that bind DLL3.

[0006] Provided are isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof comprising a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of:

[0007] (1) SEQ ID NOs: 25, 26, 27, 61, 62 and 63, respectively;

[0008] (2) SEQ ID NOs: 28, 29, 30, 64, 65 and 66, respectively;

[0009] (3) SEQ ID NOs: 31, 32, 33, 67, 68 and 69, respectively;

[0010] (4) SEQ ID NOs: 34, 35, 36, 70, 71 and 72, respectively;

[0011] (5) SEQ ID NOs: 37, 38, 39, 73, 74 and 75, respectively;

[0012] (6) SEQ ID NOs: 40, 41, 42, 76, 77 and 78, respectively;

[0013] (7) SEQ ID NOs: 43, 44, 45, 79, 80 and 81, respectively;

[0014] (8) SEQ ID NOs: 46, 47, 48, 82, 83 and 84, respectively;

[0015] (9) SEQ ID NOs: 49, 50, 51, 85, 86 and 87, respectively;

[0016] (10) SEQ ID NOs: 52, 53, 54, 88, 89 and 90, respectively;

[0017] (11) SEQ ID NOs: 55, 56, 57, 91, 92 and 93, respectively; or

[0018] (12) SEQ ID NOs: 58, 59, 60, 94, 95 and 96, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably human DLL3.

[0019] Provided are isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof comprising a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of:

[0020] (1) SEQ ID NOs: 97, 98, 99, 133, 134 and 135, respectively;

[0021] (2) SEQ ID NOs: 100, 101, 102, 136, 137 and 138, respectively;

[0022] (3) SEQ ID NOs: 103, 104, 105, 139, 140 and 141, respectively;

[0023] (4) SEQ ID NOs: 106, 107, 108, 142, 143 and 144, respectively;

[0024] (5) SEQ ID NOs: 109, 110, 111, 145, 146 and 147, respectively;

[0025] (6) SEQ ID NOs: 112, 113, 114, 148, 149 and 150, respectively;

[0026] (7) SEQ ID NOs: 115, 116, 117, 151, 152 and 153, respectively;

[0027] (8) SEQ ID NOs: 118, 119, 120, 154, 155 and 156, respectively;

[0028] (9) SEQ ID NOs: 121, 122, 123, 157, 158 and 159, respectively;

[0029] (10) SEQ ID NOs: 124, 125, 126, 160, 161 and 162, respectively;

[0030] (11) SEQ ID NOs: 127, 128, 129, 163, 164 and 165, respectively; or

[0031] (12) SEQ ID NOs: 130, 131, 132, 166, 167 and 168, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably human DLL3.

[0032] In certain embodiments, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 or 23, or a light chain variable region having a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 or 24.

[0033] In certain embodiments, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises:

[0034] (a) a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 1, and a light chain variable region having the polypeptide sequence of SEQ ID NO:2;

[0035] (b) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:3, and a light chain variable region having the polypeptide sequence of SEQ ID NO:4;

[0036] (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:5, and a light chain variable region having the polypeptide sequence of SEQ ID NO:6;

[0037] (d) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:7, and a light chain variable region having the polypeptide sequence of SEQ ID NO:8;

[0038] (e) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:9, and a light chain variable region having the polypeptide sequence of SEQ ID NO:10;

[0039] (f) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:11, and a light chain variable region having the polypeptide sequence of SEQ ID NO:12;

[0040] (g) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:13, and a light chain variable region having the polypeptide sequence of SEQ ID NO:14;

[0041] (h) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:15, and a light chain variable region having the polypeptide sequence of SEQ ID NO:16;

[0042] (i) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:17, and a light chain variable region having the polypeptide sequence of SEQ ID NO:18;

[0043] (j) a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 19, and a light chain variable region having the polypeptide sequence of SEQ ID NO:20;

[0044] (k) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:21, and a light chain variable region having the polypeptide sequence of SEQ ID NO:22; or

[0045] (l) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:23, and a light chain variable region having the polypeptide sequence of SEQ ID NO:24.

[0046] In certain embodiments, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof is chimeric.

[0047] In certain embodiments, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof is human or humanized. In certain embodiments, the humanized monoclonal antibody or antigen-binding fragment thereof comprises:

[0048] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0049] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172; or

[0050] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173.

[0051] In certain embodiments, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof is capable of inducing effector-mediated tumor cell lysis through antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent phagocytosis (ADPC) and complement-dependent cytotoxicity (CDC), and/or mediating the recruitment of conjugated drugs, and/or forming a bispecific antibody with another mAb or antigen-binding fragment with cancer-killing effect.

[0052] Also provided are isolated anti-CD47 monoclonal antibodies or antigen-binding fragments thereof comprising the humanized heavy chain variable region of an anti-CD47 monoclonal antibody and the humanized light chain variable region of an anti-DLL3 monoclonal antibody, wherein the anti-CD47 monoclonal antibody or antigen-binding fragment thereof comprises:

[0053] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0054] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;

[0055] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;

[0056] d. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0057] e. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;

[0058] f. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;

- [0059] g. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- [0060] h. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- [0061] i. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173; or
- [0062] j. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:174.
- [0063] In certain embodiments, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to signal regulatory protein alpha (SIRP α).
- [0064] In certain embodiments, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells.
- [0065] Provided are isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 178, 179 and 180; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 181, 182 and 183; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOs: 184, 185 and 186.
- [0066] Provided are isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 187, 188 and 189; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 190, 191 and 192; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOs: 193, 194 and 195.
- [0067] In certain embodiments, the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof comprise a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain variable region having a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:176, and a light chain variable region having a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:172; and wherein the second antigen-binding domain comprises a heavy chain variable region having a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:170, and a light chain variable region having the a polypeptide sequence at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:172.
- [0068] In certain embodiments, the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to signal regulatory protein alpha (SIRP α) on cancer cells that express both DLL3 and CD47.
- [0069] In certain embodiments, the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47.
- [0070] In certain embodiments, the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of binding cancer cells that express both DLL3 and CD47 with minimal to undetectable binding to human red blood cells (RBCs).
- [0071] Also provided are isolated nucleic acids encoding the anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof, the anti-CD47 monoclonal antibodies or antigen-binding fragments thereof, or the humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention disclosed herein.
- [0072] Also provided are vectors comprising the isolated nucleic acids encoding the anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof, the anti-CD47 monoclonal antibodies or antigen-binding fragments thereof, or the humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.
- [0073] Also provided are host cells comprising the vectors comprising the isolated nucleic acids encoding the anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof, the anti-CD47 monoclonal antibodies or antigen-binding fragments thereof, or the humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.
- [0074] In certain embodiments, provided is a pharmaceutical composition comprising the isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof, the isolated anti-CD47 monoclonal antibodies or antigen-binding fragments thereof, or the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention and a pharmaceutically acceptable carrier.
- [0075] Also provided are methods of targeting DLL3 on a cancer cell surface in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof of the invention.
- [0076] Also provided are methods of blocking binding of CD47 to signal regulatory protein alpha (SIRP α) in a subject

in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated anti-CD47 monoclonal antibodies or antigen-binding fragments thereof of the invention.

[0077] Also provided are methods of inducing macrophage-mediated phagocytosis of cancer cells in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated anti-CD47 monoclonal antibodies or antigen-binding fragments thereof of the invention.

[0078] Also provided are methods of targeting DLL3 and CD47 that are both expressed on a cancer cell surface in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.

[0079] Also provided are methods of blocking binding of CD47 to SIRP α on cancer cells that express both DLL3 and CD47 in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.

[0080] Also provided are methods of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47 in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.

[0081] Also provided are methods of binding cancer cells that express both DLL3 and CD47 by a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment with minimal to undetectable binding to human red blood cells (RBCs) in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions comprising the isolated humanized anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof of the invention.

[0082] Also provided are methods of treating cancer in a subject in need thereof, comprising administering to the subject the pharmaceutical compositions of the invention. The cancer can be any liquid or solid cancer, for example, it can be selected from, but not limited to, a lung cancer, such as small cell lung cancer (SCLC), large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, and other solid tumors, and a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), an acute myeloid leukemia (AML), and other liquid tumors.

[0083] Also provided are methods of producing the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention, comprising culturing a cell comprising a nucleic acid encoding the antibody or antigen-binding fragment thereof under conditions to produce the antibody or antigen-binding fragment thereof,

and recovering the antibody or antigen-binding fragment thereof from the cell or culture.

[0084] Also provided are methods of producing a pharmaceutical composition comprising the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention, comprising combining the antibody or antigen-binding fragment thereof with a pharmaceutically acceptable carrier to obtain the pharmaceutical composition.

[0085] Also provided are methods of determining a level of DLL3 in a subject. The methods comprise (a) obtaining a sample from the subject; (b) contacting the sample with an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of the invention; and (c) determining the level of DLL3 in the subject. In certain embodiments, the sample is a tissue sample. The tissue sample can, for example, be a cancer tissue sample. In certain embodiments, the sample is a blood sample.

BRIEF DESCRIPTION OF THE DRAWINGS

[0086] The foregoing summary, as well as the following detailed description of preferred embodiments of the present application, will be better understood when read in conjunction with the appended drawings. It should be understood, however, that the application is not limited to the precise embodiments shown in the drawings.

[0087] FIGS. 1A-1C show the binding of purified anti-DLL3 chimeric mAbs to coated recombinant DLL3 protein by ELISA.

[0088] FIGS. 2A-2C show the binding of chimeric anti-DLL3 mAbs to HEK293-huDLL3 cells by FACS. Three different mAb concentrations were used in the assay (666.67 nM (FIG. 2A); 333.33 nM (FIG. 2B); and 66.67 nM (FIG. 2C)).

[0089] FIG. 3 shows the binding of humanized anti-DLL3 mAb H1L2 to SHP-77 cells by FACS.

[0090] FIGS. 4A-4B show the bridging ELISA data of the bispecific antibodies BA1 and BA1(C) (FIG. 4A) and BA4(C) (FIG. 4B).

[0091] FIG. 5 shows the binding of the bispecific antibodies BA1, BA1(C) and BA4(C) to immobilized CD47 by ELISA assay.

[0092] FIGS. 6A-6B show the binding of the bispecific antibodies BA1 and BA1(C) (FIG. 6A) and BA4(C) (FIG. 6B) to immobilized DLL3 by ELISA assay.

[0093] FIG. 7 shows the binding of the bispecific antibodies BA1, BA1(C) and BA4(C) to simultaneously immobilized CD47 and DLL3 in a 1:1 concentration ratio by ELISA assay.

[0094] FIGS. 8A-8B show the activity of the bispecific antibodies BA1, BA1(C) and BA4(C) in blocking the CD47/SIRP α interaction in an ELISA assay. Only CD47 was immobilized in the assay in FIG. 8A and both CD47 and DLL3 were immobilized in a 2:1 concentration ratio in the assay in FIG. 8B.

[0095] FIG. 9 shows the binding of the bispecific antibodies BA1, BA1(C) and BA4(C) to Raji cells.

[0096] FIG. 10 shows the inhibitory effect of the anti-CD47 or anti-DLL3 F(ab')₂ on the binding of the bispecific antibody BA1(C) to SHP-77 cells.

[0097] FIGS. 11A-11C show the binding of the bispecific antibodies to human red blood cells (RBCs) at different mAb concentrations (1,600 nM (FIG. 11A), 533 nM (FIG. 11B), and 178 nM (FIG. 11C)).

DETAILED DESCRIPTION OF THE INVENTION

[0098] Various publications, articles and patents are cited or described in the background and throughout the specification; each of these references is herein incorporated by reference in its entirety. Discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is for the purpose of providing context for the invention. Such discussion is not an admission that any or all of these matters form part of the prior art with respect to any inventions disclosed or claimed.

[0099] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention pertains. Otherwise, certain terms used herein have the meanings as set forth in the specification.

[0100] It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise.

[0101] Unless otherwise stated, any numerical values, such as a concentration or a concentration range described herein, are to be understood as being modified in all instances by the term “about.” Thus, a numerical value typically includes $\pm 10\%$ of the recited value. For example, a concentration of 1 mg/mL includes 0.9 mg/mL to 1.1 mg/mL. Likewise, a concentration range of 1% to 10% (w/v) includes 0.9% (w/v) to 11% (w/v). As used herein, the use of a numerical range expressly includes all possible sub-ranges, all individual numerical values within that range, including integers within such ranges and fractions of the values unless the context clearly indicates otherwise.

[0102] Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the invention.

[0103] As used herein, the terms “comprises,” “comprising,” “includes,” “including,” “has,” “having,” “contains” or “containing,” or any other variation thereof, will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers and are intended to be non-exclusive or open-ended. For example, a composition, a mixture, a process, a method, an article, or an apparatus that comprises a list of elements is not necessarily limited to only those elements but can include other elements not expressly listed or inherent to such composition, mixture, process, method, article, or apparatus. Further, unless expressly stated to the contrary, “or” refers to an inclusive or and not to an exclusive or. For example, a condition A or B is satisfied by any one of the following: A is true (or present) and B is false (or not present), A is false (or not present) and B is true (or present), and both A and B are true (or present).

[0104] As used herein, the conjunctive term “and/or” between multiple recited elements is understood as encompassing both individual and combined options. For instance,

where two elements are conjoined by “and/or,” a first option refers to the applicability of the first element without the second. A second option refers to the applicability of the second element without the first. A third option refers to the applicability of the first and second elements together. Any one of these options is understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or” as used herein. Concurrent applicability of more than one of the options is also understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or.”

[0105] As used herein, the term “consists of,” or variations such as “consist of” or “consisting of,” as used throughout the specification and claims, indicate the inclusion of any recited integer or group of integers, but that no additional integer or group of integers can be added to the specified method, structure, or composition.

[0106] As used herein, the term “consists essentially of,” or variations such as “consist essentially of” or “consisting essentially of,” as used throughout the specification and claims, indicate the inclusion of any recited integer or group of integers, and the optional inclusion of any recited integer or group of integers that do not materially change the basic or novel properties of the specified method, structure or composition. See M.P.E.P. § 2111.03.

[0107] As used herein, “subject” means any animal, preferably a mammal, most preferably a human. The term “mammal” as used herein, encompasses any mammal. Examples of mammals include, but are not limited to, cows, horses, sheep, pigs, cats, dogs, mice, rats, rabbits, guinea pigs, monkeys, humans, etc., more preferably a human.

[0108] The words “right,” “left,” “lower,” and “upper” designate directions in the drawings to which reference is made.

[0109] It should also be understood that the terms “about,” “approximately,” “generally,” “substantially” and like terms, used herein when referring to a dimension or characteristic of a component of the preferred invention, indicate that the described dimension/characteristic is not a strict boundary or parameter and does not exclude minor variations therefrom that are functionally the same or similar, as would be understood by one having ordinary skill in the art. At a minimum, such references that include a numerical parameter would include variations that, using mathematical and industrial principles accepted in the art (e.g., rounding, measurement or other systematic errors, manufacturing tolerances, etc.), would not vary the least significant digit.

[0110] The terms “identical” or percent “identity,” in the context of two or more nucleic acids or polypeptide sequences (e.g., anti-DLL3 antibodies, anti-CD47 antibodies, anti-CD47/DLL3 bi-specific antibodies, DLL3 polypeptides, and polynucleotides that encode them), refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection.

[0111] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent

sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0112] Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (see generally, *Current Protocols in Molecular Biology*, F. M. Ausubel et al., eds., *Current Protocols*, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)).

[0113] Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1990) *J. Mol. Biol.* 215:403-410 and Altschul et al. (1997) *Nucleic Acids Res.* 25:3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

[0114] Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

[0115] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum prob-

ability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

[0116] A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions.

Antibodies

[0117] The invention generally relates to isolated anti-DLL3 antibodies, anti-CD47 antibodies, anti-CD47/DLL3 bispecific antibodies, nucleic acids and expression vectors encoding the antibodies, recombinant cells containing the vectors, and compositions comprising the antibodies. Methods of making the antibodies, and methods of using the antibodies to treat diseases, including cancer, are also provided. The antibodies of the invention possess one or more desirable functional properties, including but not limited to high-affinity binding to DLL3 and/or CD47, high specificity to DLL3 and/or CD47, the ability to induce effector-mediated tumor cell lysis, the ability to stimulate complement-dependent cytotoxicity (CDC), antibody-dependent phagocytosis (ADPC), and/or antibody-dependent cellular-mediated cytotoxicity (ADCC) against cells expressing DLL3 and/or CD47, the ability to mediate the recruitment of conjugated drugs, the ability to form a bispecific antibody with another mAb or antigen-binding fragment with cancer-killing effect, and the ability to inhibit tumor growth in subjects and animal models when administered alone or in combination with other anti-cancer therapies.

[0118] In a general aspect, the invention relates to isolated anti-DLL3 monoclonal antibodies or antigen-binding fragments thereof that bind DLL3.

[0119] As used herein, the term "antibody" is used in a broad sense and includes immunoglobulin or antibody molecules including human, humanized, composite and chimeric antibodies and antibody fragments that are monoclonal or polyclonal. In general, antibodies are proteins or peptide chains that exhibit binding specificity to a specific antigen. Antibody structures are well known. Immunoglobulins can be assigned to five major classes (i.e., IgA, IgD, IgE, IgG and IgM), depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA1, IgA2, IgG1, IgG2, IgG3 and IgG4. Accordingly, the antibodies of the invention can be of any of the five major classes or corresponding sub-classes. Preferably, the antibodies of the invention are IgG1, IgG2, IgG3 or IgG4. Antibody light chains of vertebrate species can be assigned to one of two clearly distinct types, namely kappa and lambda, based on the amino acid sequences of their constant domains. Accordingly, the antibodies of the invention can contain a kappa or lambda light chain constant domain. According to particular embodiments, the antibodies of the invention include heavy and/or light chain constant regions from rat or human antibodies. In addition to the heavy and light constant domains, antibodies contain an antigen-binding region that is made up of a light chain

variable region and a heavy chain variable region, each of which contains three domains (i.e., complementarity determining regions 1-3; CDR1, CDR2, and CDR3). The light chain variable region domains are alternatively referred to as LCDR1, LCDR2, and LCDR3, and the heavy chain variable region domains are alternatively referred to as HCDR1, HCDR2, and HCDR3.

[0120] As used herein, the term an “isolated antibody” refers to an antibody which is substantially free of other antibodies having different antigenic specificities (e.g., an isolated antibody that specifically binds to DLL3 is substantially free of antibodies that do not bind to DLL3, an isolated antibody that specifically binds to CD47 is substantially free of antibodies that do not bind to CD47, a bispecific antibody that specifically binds to CD47 and DLL3 is substantially free of antibodies that do not bind to CD47 and DLL3). In addition, an isolated antibody is substantially free of other cellular material and/or chemicals.

[0121] As used herein, the term “monoclonal antibody” refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The monoclonal antibodies of the invention can be made by the hybridoma method, phage display technology, single lymphocyte gene cloning technology, or by recombinant DNA methods. For example, the monoclonal antibodies can be produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, such as a transgenic mouse or rat, having a genome comprising a human heavy chain transgene and a light chain transgene.

[0122] As used herein, the term “antigen-binding fragment” refers to an antibody fragment such as, for example, a diabody, a Fab, a Fab', a F(ab')₂, an Fv fragment, a disulfide stabilized Fv fragment (dsFv), a (dsFv)₂, a bispecific dsFv (dsFv-dsFv'), a disulfide stabilized diabody (ds diabody), a single-chain antibody molecule (scFv), a single domain antibody (sdab) an scFv dimer (bivalent diabody), a multispecific antibody formed from a portion of an antibody comprising one or more CDRs, a camelized single domain antibody, a nanobody, a domain antibody, a bivalent domain antibody, or any other antibody fragment that binds to an antigen but does not comprise a complete antibody structure. An antigen-binding fragment is capable of binding to the same antigen to which the parent antibody or a parent antibody fragment binds. According to particular embodiments, the antigen-binding fragment comprises a light chain variable region, a light chain constant region, and an Fd segment of the heavy chain. According to other particular embodiments, the antigen-binding fragment comprises Fab and F(ab').

[0123] As used herein, the term “single-chain antibody” refers to a conventional single-chain antibody in the field, which comprises a heavy chain variable region and a light chain variable region connected by a short peptide of about 15 to about 20 amino acids. As used herein, the term “single domain antibody” refers to a conventional single domain antibody in the field, which comprises a heavy chain variable region and a heavy chain constant region or which comprises only a heavy chain variable region.

[0124] As used herein, the term “human antibody” refers to an antibody produced by a human or an antibody having an amino acid sequence corresponding to an antibody pro-

duced by a human made using any technique known in the art. This definition of a human antibody includes intact or full-length antibodies, fragments thereof, and/or antibodies comprising at least one human heavy and/or light chain polypeptide.

[0125] As used herein, the term “humanized antibody” refers to a non-human antibody that is modified to increase the sequence homology to that of a human antibody, such that the antigen-binding properties of the antibody are retained, but its antigenicity in the human body is reduced.

[0126] As used herein, the term “chimeric antibody” refers to an antibody wherein the amino acid sequence of the immunoglobulin molecule is derived from two or more species. The variable region of both the light and heavy chains often corresponds to the variable region of an antibody derived from one species of mammal (e.g., mouse, rat, rabbit, etc.) having the desired specificity, affinity, and capability, while the constant regions correspond to the sequences of an antibody derived from another species of mammal (e.g., human) to avoid eliciting an immune response in that species.

[0127] As used herein, the term “multispecific antibody” refers to an antibody that comprises a plurality of immunoglobulin variable domain sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, the first and second epitopes are on the same antigen, e.g., the same protein (or subunit of a multimeric protein). In an embodiment, the first and second epitopes overlap or substantially overlap. In an embodiment, the first and second epitopes do not overlap or do not substantially overlap. In an embodiment, the first and second epitopes are on different antigens, e.g., the different proteins (or different subunits of a multimeric protein). In an embodiment, a multispecific antibody comprises a third, fourth, or fifth immunoglobulin variable domain. In an embodiment, a multispecific antibody is a bispecific antibody molecule, a trispecific antibody molecule, or a tetraspecific antibody molecule.

[0128] As used herein, the term “bispecific antibody” refers to a multispecific antibody that binds no more than two epitopes or two antigens. A bispecific antibody is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope. In an embodiment, the first and second epitopes are on the same antigen, e.g., the same protein (or subunit of a multimeric protein). In an embodiment, the first and second epitopes overlap or substantially overlap. In an embodiment, the first and second epitopes are on different antigens, e.g., the different proteins (or different subunits of a multimeric protein). In an embodiment, a bispecific antibody comprises a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a first epitope and a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a second epitope. In an embodiment, a bispecific antibody comprises a half antibody, or fragment thereof, having binding specificity for a first epitope and a half antibody, or fragment thereof, having binding specificity for a second epitope. In an embodiment, a bispecific antibody comprises a scFv, or fragment thereof, having binding

specificity for a first epitope, and a scFv, or fragment thereof, having binding specificity for a second epitope. In an embodiment, the first epitope is located on DLL3 and the second epitope is located on PD-1, PD-L1, TIM-3, LAG-3, CD73, apelin, CTLA-4, EGFR, HER-2, CD3, CD19, CD20, CD33, CD47, TIP-1, CLDN18.2, FOLR1, and/or other tumor associated immune suppressors or surface antigens.

[0129] As used herein, the term “DLL3” refers to Delta like canonical Notch ligand 3 (DLL3), also known as delta like 3 or delta like protein 3, is required for somite segmentation during early development (Dunwoodie et al., Development 129:1795-806 (2002)). Unlike the mammalian Notch family ligands DLL1, DLL4, JAG1, and JAG2, which all activate Notch receptor signaling in trans (Ntziachristos et al., Cancer Cell 25(3):318-34 (2014)), DLL3 is predominantly localized in the Golgi apparatus and is unable to activate Notch signaling (Chapman et al., Hum Mol Genet 2011; 20(5): 905-16 and Geffers et al., J Cell Biol 178(3): 465-76 (2007)). During normal development, DLL3 inhibits both cis- and trans-acting Notch pathway activation by interacting with Notch and DLL1 (Chapman et al., Hum Mol Genet 20(5):905-16 (2011)). DLL3 is normally either absent or present at very low levels in adult normal tissues except brain, but is overexpressed in lung cancer, testicular cancer, glioma and melanoma samples (Uhlen et al., Science 357 (6352):eaan2507 (2017)). Further, DLL3 is detectable on the surface of small cell lung cancer (SCLC) and large cell neuroendocrine carcinoma (LCNEC) tumor cells (Saunders et al., Sci Transl Med 7(302):302ra136 (2015) and Sharma et al., Cancer Res 77(14):3931-3941 (2017)), making it a potential target of monoclonal antibodies for cancer therapy. The term “human DLL3” refers to a DLL3 originated from a human. An exemplary amino acid sequence of a human DLL3 is represented in GenBank Accession No. NP_058637.1 (SEQ ID NO:169).

[0130] As used herein, the term “CD47” refers to a multi-spanning transmembrane receptor belonging to the immunoglobulin superfamily, which has been indicated to be involved in multiple cellular process, including cell migration, adhesion, and T cell function. CD47, also known as integrin-associated protein (IAP), ovarian cancer antigen (OA3), Rh-related antigen, and MER6, was originally identified as a tumor antigen on human ovarian cancer and was subsequently shown to be expressed on multiple human tumor types, including both hematologic and solid tumors. The interaction between CD47 and signal regulatory protein alpha (SIRPα), an inhibitory protein expressed on macrophages, prevents phagocytosis of CD47-expressing cells. CD47 is additionally expressed at low levels on virtually all non-malignant cells. The term “human CD47” refers to a CD47 originated from a human. An exemplary amino acid sequence of a human CD47 is represented in GenBank Accession No. NP_001768.1.

[0131] As used herein, an antibody that “specifically binds to DLL3,” “specifically binds to CD47,” or an antibody that “specifically binds to CD47 and DLL3” refers to an antibody that binds to a DLL3, preferably a human DLL3; binds to CD47, preferably a human CD47; or DLL3 and CD47, preferably human DLL3 and human CD47, with a KD of 1×10^{-7} M or less, preferably 1×10^{-8} M or less, more preferably 5×10^{-9} M or less, 1×10^{-9} M or less, 5×10^{-10} M or less, or 1×10^{-10} M or less. The term “KD” refers to the dissociation constant, which is obtained from the ratio of Kd to Ka (i.e., Kd/Ka) and is expressed as a molar concentration

(M). KD values for antibodies can be determined using methods in the art in view of the present disclosure. For example, the KD of an antibody can be determined by using surface plasmon resonance, such as by using a biosensor system, e.g., a Biacore® system, or by using bio-layer interferometry technology, such as an Octet RED96 system. **[0132]** The smaller the value of the KD of an antibody, the higher affinity that the antibody binds to a target antigen.

[0133] According to a particular aspect, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain complementarity determining region 1 (HCDR1), a HCDR2, a HCDR3, a light chain complementarity determining region 1 (LCDR1), a LCDR2, and a LCDR3, having the polypeptide sequences of:

- [0134]** (1) SEQ ID NOs: 25, 26, 27, 61, 62 and 63, respectively;
- [0135]** (2) SEQ ID NOs: 28, 29, 30, 64, 65 and 66, respectively;
- [0136]** (3) SEQ ID NOs: 31, 32, 33, 67, 68 and 69, respectively;
- [0137]** (4) SEQ ID NOs: 34, 35, 36, 70, 71 and 72, respectively;
- [0138]** (5) SEQ ID NOs: 37, 38, 39, 73, 74 and 75, respectively;
- [0139]** (6) SEQ ID NOs: 40, 41, 42, 76, 77 and 78, respectively;
- [0140]** (7) SEQ ID NOs: 43, 44, 45, 79, 80 and 81, respectively;
- [0141]** (8) SEQ ID NOs: 46, 47, 48, 82, 83 and 84, respectively;
- [0142]** (9) SEQ ID NOs: 49, 50, 51, 85, 86 and 87, respectively;
- [0143]** (10) SEQ ID NOs: 52, 53, 54, 88, 89 and 90, respectively;
- [0144]** (11) SEQ ID NOs: 55, 56, 57, 91, 92 and 93, respectively; or
- [0145]** (12) SEQ ID NOs: 58, 59, 60, 94, 95 and 96, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably human DLL3.

[0146] According to a particular aspect, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain complementarity determining region 1 (HCDR1), a HCDR2, a HCDR3, a light chain complementarity determining region 1 (LCDR1), a LCDR2, and a LCDR3, having the polypeptide sequences of:

- [0147]** (1) SEQ ID NOs: 97, 98, 99, 133, 134 and 135, respectively;
- [0148]** (2) SEQ ID NOs: 100, 101, 102, 136, 137 and 138, respectively;
- [0149]** (3) SEQ ID NOs: 103, 104, 105, 139, 140 and 141, respectively;
- [0150]** (4) SEQ ID NOs: 106, 107, 108, 142, 143 and 144, respectively;
- [0151]** (5) SEQ ID NOs: 109, 110, 111, 145, 146 and 147, respectively;
- [0152]** (6) SEQ ID NOs: 112, 113, 114, 148, 149 and 150, respectively;
- [0153]** (7) SEQ ID NOs: 115, 116, 117, 151, 152 and 153, respectively;
- [0154]** (8) SEQ ID NOs: 118, 119, 120, 154, 155 and 156, respectively;

[0155] (9) SEQ ID NOs: 121, 122, 123, 157, 158 and 159, respectively;

[0156] (10) SEQ ID NOs: 124, 125, 126, 160, 161 and 162, respectively;

[0157] (11) SEQ ID NOs: 127, 128, 129, 163, 164 and 165, respectively; or

[0158] (12) SEQ ID NOs: 130, 131, 132, 166, 167 and 168, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably human DLL3.

[0159] According to another particular aspect, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to one of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 or 23, or a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to one of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 or 24. According to one preferred embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of the invention comprises a heavy chain variable region having the polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 or 23, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 or 24, respectively.

[0160] According to another particular aspect, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of the invention, comprising:

[0161] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:1, and a light chain variable region having the polypeptide sequence of SEQ ID NO:2;

[0162] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:3, and a light chain variable region having the polypeptide sequence of SEQ ID NO:4;

[0163] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:5, and a light chain variable region having the polypeptide sequence of SEQ ID NO:6;

[0164] d. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:7, and a light chain variable region having the polypeptide sequence of SEQ ID NO:8;

[0165] e. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:9, and a light chain variable region having the polypeptide sequence of SEQ ID NO:10;

[0166] f. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 11, and a light chain variable region having the polypeptide sequence of SEQ ID NO:12;

[0167] g. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:13, and a light chain variable region having the polypeptide sequence of SEQ ID NO:14;

[0168] h. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 15, and a light chain variable region having the polypeptide sequence of SEQ ID NO: 16;

[0169] i. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:17, and a light chain variable region having the polypeptide sequence of SEQ ID NO:18;

[0170] j. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:19, and a light chain variable region having the polypeptide sequence of SEQ ID NO:20;

[0171] k. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:21, and a light chain variable region having the polypeptide sequence of SEQ ID NO:22; or

[0172] l. a heavy chain variable region having the polypeptide sequence of SEQ ID NO:23, and a light chain variable region having the polypeptide sequence of SEQ ID NO:24.

[0173] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 25, 26, 27, 61, 62 and 63, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:1, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:2. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 1; and a light chain variable region having the polypeptide sequence of SEQ ID NO:2.

[0174] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 28, 29, 30, 64, 65 and 66, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:3, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:4. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO:3; and a light chain variable region having the polypeptide sequence of SEQ ID NO:4.

[0175] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 31, 32, 33, 67, 68 and 69, respectively. In another embodiment, the isolated anti-DLL3

[0190] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 112, 113, 114, 148, 149 and 150, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:11, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:12. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO:11; and a light chain variable region having the polypeptide sequence of SEQ ID NO: 12.

[0192] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding

[0193] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 121, 122, 123, 157, 158 and 159, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:17, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:18. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO:17; and a light chain variable region having the polypeptide sequence of SEQ ID NO:18.

[0195] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOs: 127, 128, 129, 163, 164 and 165, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably

95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:21, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:22. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO:21; and a light chain variable region having the polypeptide sequence of SEQ ID NO:22.

[0196] In one embodiment, the invention relates to an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, comprising HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, having the polypeptide sequences of SEQ ID NOS: 130, 131, 132, 166, 167 and 168, respectively. In another embodiment, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:23, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:24. Preferably, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprises a heavy chain variable region having the polypeptide sequence of SEQ ID NO:23; and a light chain variable region having the polypeptide sequence of SEQ ID NO:24.

[0197] According to another particular aspect, the invention relates to an isolated monoclonal antibody or antigen-binding fragment thereof of the invention, wherein the antibody or antigen-binding fragment thereof is chimeric.

[0198] According to another particular aspect, the invention relates to an isolated monoclonal antibody or antigen-binding fragment thereof of the invention, wherein the antibody or antigen-binding fragment thereof is human or humanized.

[0199] According to another particular aspect, the invention relates to an isolated humanized anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, wherein the isolated humanized antibody or antigen-binding fragment thereof comprises:

[0200] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0201] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172; or

[0202] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173.

[0203] According to another particular aspect, the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof is capable of inducing effector-mediated tumor cell lysis through antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent phagocytosis (ADPC) and complement-dependent cytotoxicity (CDC), and/or mediating the recruitment of conjugated drugs, and/or forming a bispecific antibody with another mAb or antigen-binding fragment with cancer-killing effect.

[0204] According to another particular aspect, the invention relates to an isolated anti-CD47 monoclonal antibody or antigen-binding fragment comprising the humanized heavy chain variable region of an anti-CD47 monoclonal antibody and the humanized light chain variable region of an anti-DLL3 monoclonal antibody, wherein the anti-CD47 monoclonal antibody or antigen-binding fragment thereof comprises:

[0205] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0206] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;

[0207] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;

[0208] d. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0209] e. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;

[0210] f. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;

[0211] g. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;

[0212] h. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;

[0213] i. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173; or

[0214] j. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:174.

[0215] According to another particular aspect, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to signal regulatory protein alpha (SIRPα).

[0216] According to another particular aspect, the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells.

[0217] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1

(HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 178, 179 and 180; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 181, 182 and 183; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOs: 184, 185 and 186.

[0218] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 187, 188 and 189; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 190, 191 and 192; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOs: 193, 194 and 195.

[0219] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:176, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:172; and wherein the second antigen-binding domain comprises a heavy chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:170, and a light chain variable region having a polypeptide sequence at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 172.

[0220] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to SIRP α on cancer cells that express both DLL3 and CD47.

[0221] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-

binding domain that specifically binds DLL3, preferably human DLL3, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47.

[0222] According to another particular aspect, the invention relates to an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of binding cancer cells that express both DLL3 and CD47 with minimal to undetectable binding to human red blood cells (RBCs).

[0223] In another general aspect, the invention relates to an isolated nucleic acid encoding an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention. It will be appreciated by those skilled in the art that the coding sequence of a protein can be changed (e.g., replaced, deleted, inserted, etc.) without changing the amino acid sequence of the protein. Accordingly, it will be understood by those skilled in the art that nucleic acid sequences encoding antibodies or antigen-binding fragments thereof of the invention can be altered without changing the amino acid sequences of the proteins.

[0224] In another general aspect, the invention relates to a vector comprising an isolated nucleic acid encoding an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention. Any vector known to those skilled in the art in view of the present disclosure can be used, such as a plasmid, a cosmid, a phage vector or a viral vector. In some embodiments, the vector is a recombinant expression vector such as a plasmid. The vector can include any element to establish a conventional function of an expression vector, for example, a promoter, ribosome binding element, terminator, enhancer, selection marker, and origin of replication. The promoter can be a constitutive, inducible or repressible promoter. A number of expression vectors capable of delivering nucleic acids to a cell are known in the art and can be used herein for production of an antibody or antigen-binding fragment thereof in the cell. Conventional cloning techniques or artificial gene synthesis can be used to generate a recombinant expression vector according to embodiments of the invention. Such techniques are well known to those skilled in the art in view of the present disclosure.

[0225] In another general aspect, the invention relates to a host cell comprising an isolated nucleic acid encoding an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention. Any host cell known to those skilled in the art in view of the present disclosure can be used for recombinant expression of antibodies or antigen-binding fragments thereof of the invention. In some embodiments, the host cells are *E. coli* TG1 or BL21 cells (for expression of, e.g.,

an scFv or Fab antibody), CHO-DG44 or CHO-K1 cells or HEK293 cells (for expression of, e.g., a full-length IgG antibody). According to particular embodiments, the recombinant expression vector is transformed into host cells by conventional methods such as chemical transfection, heat shock, or electroporation, where it is stably integrated into the host cell genome such that the recombinant nucleic acid is effectively expressed.

[0226] In another general aspect, the invention relates to a method of producing an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention, comprising culturing a cell comprising a nucleic acid encoding the antibody or antigen-binding fragment thereof under conditions to produce an antibody or antigen-binding fragment thereof of the invention, and recovering the antibody or antigen-binding fragment thereof from the cell or cell culture (e.g., from the supernatant). Expressed antibodies or antigen-binding fragments thereof can be harvested from the cells and purified according to conventional techniques known in the art and as described herein.

Pharmaceutical Compositions

[0227] In another general aspect, the invention relates to a pharmaceutical composition, comprising an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention and a pharmaceutically acceptable carrier. The term “pharmaceutical composition” as used herein means a product comprising an antibody of the invention together with a pharmaceutically acceptable carrier. Antibodies of the invention and compositions comprising them are also useful in the manufacture of a medicament for therapeutic applications mentioned herein.

[0228] As used herein, the term “carrier” refers to any excipient, diluent, filler, salt, buffer, stabilizer, solubilizer, oil, lipid, lipid containing vesicle, microsphere, liposomal encapsulation, or other material well known in the art for use in pharmaceutical formulations. It will be understood that the characteristics of the carrier, excipient or diluent will depend on the route of administration for a particular application. As used herein, the term “pharmaceutically acceptable carrier” refers to a non-toxic material that does not interfere with the effectiveness of a composition according to the invention or the biological activity of a composition according to the invention. According to particular embodiments, in view of the present disclosure, any pharmaceutically acceptable carrier suitable for use in an antibody pharmaceutical composition can be used in the invention.

[0229] The formulation of pharmaceutically active ingredients with pharmaceutically acceptable carriers is known in the art, e.g., Remington: The Science and Practice of Pharmacy (e.g. 21st edition (2005), and any later editions). Non-limiting examples of additional ingredients include: buffers, diluents, solvents, tonicity regulating agents, preservatives, stabilizers, and chelating agents. One or more pharmaceutically acceptable carrier can be used in formulating the pharmaceutical compositions of the invention.

[0230] In one embodiment of the invention, the pharmaceutical composition is a liquid formulation. A preferred example of a liquid formulation is an aqueous formulation, i.e., a formulation comprising water. The liquid formulation can comprise a solution, a suspension, an emulsion, a microemulsion, a gel, and the like. An aqueous formulation typically comprises at least 50% w/w water, or at least 60%, 70%, 75%, 80%, 85%, 90%, or at least 95% w/w of water.

[0231] In one embodiment, the pharmaceutical composition can be formulated as an injectable which can be injected, for example, via an injection device (e.g., a syringe or an infusion pump). The injection can be delivered subcutaneously, intramuscularly, intraperitoneally, intravitreally, or intravenously, for example.

[0232] In another embodiment, the pharmaceutical composition is a solid formulation, e.g., a freeze-dried or spray-dried composition, which can be used as is, or where the physician or the patient adds solvents, and/or diluents prior to use. Solid dosage forms can include tablets, such as compressed tablets, and/or coated tablets, and capsules (e.g., hard or soft gelatin capsules). The pharmaceutical composition can also be in the form of sachets, dragees, powders, granules, lozenges, or powders for reconstitution, for example.

[0233] The dosage forms can be immediate release, in which case they can comprise a water-soluble or dispersible carrier, or they can be delayed release, sustained release, or modified release, in which case they can comprise water-insoluble polymers that regulate the rate of dissolution of the dosage form in the gastrointestinal tract or under the skin.

[0234] In other embodiments, the pharmaceutical composition can be delivered intranasally, intrabuccally, or sublingually.

[0235] The pH in an aqueous formulation can be between pH 3 and pH 10. In one embodiment of the invention, the pH of the formulation is from about 7.0 to about 9.5. In another embodiment of the invention, the pH of the formulation is from about 3.0 to about 7.0.

[0236] In another embodiment of the invention, the pharmaceutical composition comprises a buffer. Non-limiting examples of buffers include: arginine, aspartic acid, bicine, citrate, disodium hydrogen phosphate, fumaric acid, glycine, glycyglycine, histidine, lysine, maleic acid, malic acid, sodium acetate, sodium carbonate, sodium dihydrogen phosphate, sodium phosphate, succinate, tartaric acid, tricine, and tris(hydroxymethyl)-aminomethane, and mixtures thereof. The buffer can be present individually or in the aggregate, in a concentration from about 0.01 mg/ml to about 50 mg/ml, for example from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific buffers constitute alternative embodiments of the invention.

[0237] In another embodiment of the invention, the pharmaceutical composition comprises a preservative. Non-limiting examples of preservatives include: benzethonium chloride, benzoic acid, benzyl alcohol, bronopol, butyl 4-hydroxybenzoate, chlorobutanol, chlorocresol, chlorohexidine, chlorphenesin, o-cresol, m-cresol, p-cresol, ethyl 4-hydroxybenzoate, imidurea, methyl 4-hydroxybenzoate, phenol, 2-phenoxyethanol, 2-phenylethanol, propyl 4-hydroxybenzoate, sodium dehydroacetate, thiomerosal, and mixtures thereof. The preservative can be present individually or in the aggregate, in a concentration from about 0.01 mg/ml to about 50 mg/ml, for example from about 0.1

mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific preservatives constitute alternative embodiments of the invention.

[0238] In another embodiment of the invention, the pharmaceutical composition comprises an isotonic agent. Non-limiting examples of the isotonic agents include a salt (such as sodium chloride), an amino acid (such as glycine, histidine, arginine, lysine, isoleucine, aspartic acid, tryptophan, and threonine), an alditol (such as glycerol, 1,2-propanediol propyleneglycol), 1,3-propanediol, and 1,3-butanediol), polyethyleneglycol (e.g. PEG400), and mixtures thereof. Another example of an isotonic agent includes a sugar. Non-limiting examples of sugars may be mono-, di-, or polysaccharides, or water-soluble glucans, including for example fructose, glucose, mannose, sorbose, xylose, maltose, lactose, sucrose, trehalose, dextran, pullulan, dextrin, cyclodextrin, alpha and beta-HPCD, soluble starch, hydroxyethyl starch, and sodium carboxymethylcellulose. Another example of an isotonic agent is a sugar alcohol, wherein the term “sugar alcohol” is defined as a C(4-8) hydrocarbon having at least one-OH group. Non-limiting examples of sugar alcohols include mannitol, sorbitol, inositol, galactitol, dulcitol, xylitol, and arabitol. Pharmaceutical compositions comprising each isotonic agent listed in this paragraph constitute alternative embodiments of the invention. The isotonic agent can be present individually or in the aggregate, in a concentration from about 0.01 mg/ml to about 50 mg/ml, for example from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific isotonic agents constitute alternative embodiments of the invention.

[0239] In another embodiment of the invention, the pharmaceutical composition comprises a chelating agent. Non-limiting examples of chelating agents include citric acid, aspartic acid, salts of ethylenediaminetetraacetic acid (EDTA), and mixtures thereof. The chelating agent can be present individually or in the aggregate, in a concentration from about 0.01 mg/ml to about 50 mg/ml, for example from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific chelating agents constitute alternative embodiments of the invention.

[0240] In another embodiment of the invention, the pharmaceutical composition comprises a stabilizer. Non-limiting examples of stabilizers include one or more aggregation inhibitors, one or more oxidation inhibitors, one or more surfactants, and/or one or more protease inhibitors.

[0241] In another embodiment of the invention, the pharmaceutical composition comprises a stabilizer, wherein said stabilizer is carboxy-/hydroxycellulose and derivatives thereof (such as HPC, HPC-SL, HPC-L and HPMC), cyclodextrins, 2-methylthioethanol, polyethylene glycol (such as PEG 3350), polyvinyl alcohol (PVA), polyvinyl pyrrolidone, salts (such as sodium chloride), sulphur-containing substances such as monothioglycerol), or thioglycolic acid. The stabilizer can be present individually or in the aggregate, in a concentration from about 0.01 mg/ml to about 50 mg/ml, for example from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific stabilizers constitute alternative embodiments of the invention.

[0242] In further embodiments of the invention, the pharmaceutical composition comprises one or more surfactants, preferably a surfactant, at least one surfactant, or two different surfactants. The term “surfactant” refers to any

molecules or ions that are comprised of a water-soluble (hydrophilic) part, and a fat-soluble (lipophilic) part. The surfactant can, for example, be selected from the group consisting of anionic surfactants, cationic surfactants, non-ionic surfactants, and/or zwitterionic surfactants. The surfactant can be present individually or in the aggregate, in a concentration from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific surfactants constitute alternative embodiments of the invention.

[0243] In a further embodiment of the invention, the pharmaceutical composition comprises one or more protease inhibitors, such as, e.g., EDTA, and/or benzamidine hydrochloric acid (HCl). The protease inhibitor can be present individually or in the aggregate, in a concentration from about 0.1 mg/ml to about 20 mg/ml. Pharmaceutical compositions comprising each one of these specific protease inhibitors constitute alternative embodiments of the invention.

[0244] In another general aspect, the invention relates to a method of producing a pharmaceutical composition comprising an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention, comprising combining an antibody or antigen-binding fragment thereof with a pharmaceutically acceptable carrier to obtain the pharmaceutical composition.

Methods of Use

[0245] In another general aspect, the invention relates to a method of targeting DLL3 on a cancer cell surface in a subject in need thereof, the method comprises administering to the subject in need thereof an isolated anti-DLL3 monoclonal antibody or antigen binding fragment thereof that specifically binds DLL3 or a pharmaceutical composition of the invention. Binding of the monoclonal antibody or antigen-binding fragment thereof to DLL3 can mediate complement-dependent cytotoxicity (CDC), antibody-dependent phagocytosis (ADPC), and/or antibody-dependent cellular cytotoxicity (ADCC) or other effects that result in the death of the targeted cancer cell. The monoclonal antibody or antigen-binding fragment thereof can, for example, serve to recruit conjugated drugs, and/or can form a bispecific antibody with another monoclonal antibody or antigen-binding fragment thereof to mediate the death of the targeted cancer cell.

[0246] In another general aspect, the invention relates to a method of blocking binding of CD47 to signal regulatory protein alpha (SIRPα) in a subject in need thereof, the method comprises administering to the subject in need thereof an anti-CD47 monoclonal antibody or antigen-binding fragment thereof or a pharmaceutical composition of the invention.

[0247] In another general aspect, the invention relates to a method of inducing macrophage-mediated phagocytosis of cancer cells in a subject in need thereof, the method comprises administering to the subject in need thereof an anti-CD47 monoclonal antibody or antigen-binding fragment thereof or a pharmaceutical composition of the invention.

[0248] In another general aspect, the invention relates to a method of targeting DLL3 and CD47 on a cancer cell surface in a subject in need thereof, the method comprises

administering to the subject in need thereof a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, or a pharmaceutical composition of the invention.

[0249] In another general aspect, the invention relates to a method of blocking binding of CD47 to signal regulatory protein alpha (SIRP α) on cancer cells that express both DLL3 and CD47 in a subject in need thereof, the method comprises administering to the subject in need thereof an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, or a pharmaceutical composition of the invention. Binding of the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof to the cancer cells can mediate blocking the binding of CD47 to SIRP α .

[0250] In another general aspect, the invention relates to a method of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47 in a subject in need thereof, the method comprises administering to the subject in need thereof an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, or a pharmaceutical composition of the invention. Binding of the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment to the cancer cells can induce macrophage-mediated phagocytosis of the cancer cells.

[0251] In another general aspect, the invention relates to a method of binding cancer cells that express both DLL3 and CD47 with minimal to undetectable binding to human red blood cells (RBCs) in a subject in need thereof, the method comprises administering to the subject in need thereof an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, or a pharmaceutical composition of the invention. The humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention has high selectivity for cancer cells with minimal to undetectable binding to human red blood cells (RBCs).

[0252] The functional activity of antibodies and antigen-binding fragments thereof that bind DLL3 or CD47, or bispecific antibodies and antigen binding fragments thereof that bind DLL3 and CD47 can be characterized by methods known in the art and as described herein. Methods for characterizing antibodies and antigen-binding fragments thereof that bind DLL3 or CD47, or bispecific antibodies and antigen binding fragments thereof that bind DLL3 and CD47 include, but are not limited to, affinity and specificity assays including Biacore, ELISA, FACS and OctetRed analysis. According to particular embodiments, the methods for characterizing antibodies and antigen-binding fragments thereof that bind DLL3 or CD47, or bispecific antibodies

and antigen binding fragments thereof that bind DLL3 and CD47 include those described below.

[0253] In another general aspect, the invention relates to a method of treating a cancer in a subject in need thereof, comprising administering to the subject in need thereof an isolated anti-DLL3 monoclonal antibody or antigen binding fragment thereof, an isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof or a pharmaceutical composition of the invention. The cancer can, for example, be selected from but not limited to, a lung cancer, such as small cell lung cancer (SCLC), large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, and other solid tumors, and a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), an acute myeloid leukemia (AML), and other liquid tumors.

[0254] According to embodiments of the invention, the pharmaceutical composition comprises a therapeutically effective amount of an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, an anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or a humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of the invention. As used herein, the term "therapeutically effective amount" refers to an amount of an active ingredient or component that elicits the desired biological or medicinal response in a subject. A therapeutically effective amount can be determined empirically and in a routine manner, in relation to the stated purpose.

[0255] As used herein with reference to anti-DLL3 antibodies or antigen-binding fragments thereof, anti-CD47 antibodies or antigen-binding fragments thereof, or anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof, a therapeutically effective amount means an amount of the anti-DLL3 antibody or antigen-binding fragment thereof, anti-CD47 antibody or antigen-binding fragment thereof, or anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof that modulates an immune response in a subject in need thereof. Also as used herein with reference to anti-DLL3 antibodies or antigen-binding fragments thereof, anti-CD47 antibody or antigen-binding fragment thereof, or anti-CD47/DLL3 bispecific antibodies or antigen-binding fragments thereof, a therapeutically effective amount means an amount of the anti-DLL3 antibody or antigen-binding fragment thereof, anti-CD47 antibody or antigen-binding fragment thereof, or anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof that results in treatment of a disease, disorder, or condition; prevents or slows the progression of the disease, disorder, or condition; or reduces or completely alleviates symptoms associated with the disease, disorder, or condition.

[0256] According to particular embodiments, the disease, disorder or condition to be treated is cancer, preferably a cancer selected from the group consisting of a lung cancer, such as small cell lung cancer (SCLC), large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a

bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, and other solid tumors, and a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), an acute myeloid leukemia (AML), and other liquid tumors.

[0257] According to particular embodiments, a therapeutically effective amount refers to the amount of therapy which is sufficient to achieve one, two, three, four, or more of the following effects: (i) reduce or ameliorate the severity of the disease, disorder or condition to be treated or a symptom associated therewith; (ii) reduce the duration of the disease, disorder or condition to be treated, or a symptom associated therewith; (iii) prevent the progression of the disease, disorder or condition to be treated, or a symptom associated therewith; (iv) cause regression of the disease, disorder or condition to be treated, or a symptom associated therewith; (v) prevent the development or onset of the disease, disorder or condition to be treated, or a symptom associated therewith; (vi) prevent the recurrence of the disease, disorder or condition to be treated, or a symptom associated therewith; (vii) reduce hospitalization of a subject having the disease, disorder or condition to be treated, or a symptom associated therewith; (viii) reduce hospitalization length of a subject having the disease, disorder or condition to be treated, or a symptom associated therewith; (ix) increase the survival of a subject with the disease, disorder or condition to be treated, or a symptom associated therewith; (xi) inhibit or reduce the disease, disorder or condition to be treated, or a symptom associated therewith in a subject; and/or (xii) enhance or improve the prophylactic or therapeutic effect(s) of another therapy.

[0258] The therapeutically effective amount or dosage can vary according to various factors, such as the disease, disorder or condition to be treated, the means of administration, the target site, the physiological state of the subject (including, e.g., age, body weight, health), whether the subject is a human or an animal, other medications administered, and whether the treatment is prophylactic or therapeutic. Treatment dosages are optimally titrated to optimize safety and efficacy.

[0259] According to particular embodiments, the compositions described herein are formulated to be suitable for the intended route of administration to a subject. For example, the compositions described herein can be formulated to be suitable for intravenous, subcutaneous, or intramuscular administration.

[0260] As used herein, the terms “treat,” “treating,” and “treatment” are all intended to refer to an amelioration or reversal of at least one measurable physical parameter related to a cancer, which is not necessarily discernible in the subject, but can be discernible in the subject. The terms “treat,” “treating,” and “treatment,” can also refer to causing regression, preventing the progression, or at least slowing down the progression of the disease, disorder, or condition. In a particular embodiment, “treat,” “treating,” and “treatment” refer to an alleviation, prevention of the development or onset, or reduction in the duration of one or more symptoms associated with the disease, disorder, or condition, such as a tumor or more preferably a cancer. In a particular embodiment, “treat,” “treating,” and “treatment” refer to prevention of the recurrence of the disease, disorder,

or condition. In a particular embodiment, “treat,” “treating,” and “treatment” refer to an increase in the survival of a subject having the disease, disorder, or condition. In a particular embodiment, “treat,” “treating,” and “treatment” refer to elimination of the disease, disorder, or condition in the subject.

[0261] According to particular embodiments, a composition used in the treatment of a cancer. For cancer therapy, it can be used in combination with another treatment including, but not limited to, a chemotherapy, an anti-TIM-3 mAb, an anti-LAG-3 mAb, an anti-CD73 mAb, an anti-apelin mAb, an anti-CTLA-4 antibody, an anti-EGFR mAb, an anti-HER-2 mAb, an anti-CD19 mAb, an anti-CD20 mAb, an anti-CD33 mAb, an anti-CD47 mAb, an anti-TIP-1 mAb, an anti-CLDN18.2 mAb, an anti-FOLR1 mAb, an anti-PD-L1 antibody, an anti-PD-1 antibody, a PD-1/PD-L1 therapy, other immuno-oncology drugs, an antiangiogenic agent, a radiation therapy, an antibody-drug conjugate (ADC), a targeted therapy, or other anticancer drugs.

[0262] As used herein, the term “in combination,” in the context of the administration of two or more therapies to a subject, refers to the use of more than one therapy. The use of the term “in combination” does not restrict the order in which therapies are administered to a subject. For example, a first therapy (e.g., a composition described herein) can be administered prior to (e.g., 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 16 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks before), concomitantly with, or subsequent to (e.g., 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 16 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks after) the administration of a second therapy to a subject.

[0263] In another general aspect, the invention relates to a method of determining a level of DLL3 in a subject. The methods comprise (a) obtaining a sample from the subject; (b) contacting the sample with an anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of the invention; and (c) determining a level of DLL3 in the subject.

[0264] As used herein, “sample” refers to a biological sample isolated from a subject and can include, but is not limited to, whole blood, serum, plasma, blood cells, endothelial cells, tissue biopsies (e.g., a cancer tissue), lymphatic fluid, ascites fluid, interstitial fluid, bone marrow, cerebrospinal fluid, saliva, mucous, sputum, sweat, urine, or any other secretion, excretion, or other bodily fluids. A “blood sample” refers to whole blood or any fraction thereof, including blood cells, serum, and plasma.

[0265] In certain embodiments, the level of DLL3 in the subject can be determined utilizing assays selected from, but not limited to, a Western blot assay, an ELISA assay, and/or an immunohistochemistry (IHC) assay. Relative protein levels can be determined by utilizing Western blot analysis and IHC, and absolute protein levels can be determined by utilizing an ELISA assay. When determining the relative levels of DLL3, the levels of DLL3 can be determined between at least two samples, e.g., between samples from the same subject at different time points, between samples from different tissues in the same subject, and/or between samples from different subjects. Alternatively, when determining absolute levels of DLL3, such as by an ELISA assay,

the absolute level of DLL3 in the sample can be determined by creating a standard for the ELISA assay prior to testing the sample. A person skilled in the art would understand which analytical techniques to utilize to determine the level of DLL3 in a sample from the subject utilizing the antibodies or antigen-binding fragments thereof of the invention.

[0266] Utilizing methods of determining a level of DLL3 in a sample from a subject can lead to the diagnosis of abnormal (elevated, reduced, or insufficient) DLL3 levels in a disease and making appropriate therapeutic decisions. Such a disease can be, but not limited to, a cancer. Additionally, by monitoring the levels of DLL3 in a subject, the risk of developing a disease as indicated above can be determined based on the knowledge of the level of DLL3 in a particular disease and/or during the progression of the particular disease.

EMBODIMENTS

[0267] The invention provides also the following non-limiting embodiments.

[0268] Embodiment 1 is an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of

- [0269]** (1) SEQ ID NOs: 25, 26, 27, 61, 62 and 63, respectively;
- [0270]** (2) SEQ ID NOs: 28, 29, 30, 64, 65 and 66, respectively;
- [0271]** (3) SEQ ID NOs: 31, 32, 33, 67, 68 and 69, respectively;
- [0272]** (4) SEQ ID NOs: 34, 35, 36, 70, 71 and 72, respectively;
- [0273]** (5) SEQ ID NOs: 37, 38, 39, 73, 74 and 75, respectively;
- [0274]** (6) SEQ ID NOs: 40, 41, 42, 76, 77 and 78, respectively;
- [0275]** (7) SEQ ID NOs: 43, 44, 45, 79, 80 and 81, respectively;
- [0276]** (8) SEQ ID NOs: 46, 47, 48, 82, 83 and 84, respectively;
- [0277]** (9) SEQ ID NOs: 49, 50, 51, 85, 86 and 87, respectively;
- [0278]** (10) SEQ ID NOs: 52, 53, 54, 88, 89 and 90, respectively;
- [0279]** (11) SEQ ID NOs: 55, 56, 57, 91, 92 and 93, respectively; or
- [0280]** (12) SEQ ID NOs: 58, 59, 60, 94, 95 and 96, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably specifically binds human DLL3.

[0281] Embodiment 2 is an isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of

- [0282]** (1) SEQ ID NOs: 97, 98, 99, 133, 134 and 135, respectively;
- [0283]** (2) SEQ ID NOs: 100, 101, 102, 136, 137 and 138, respectively;

- [0284]** (3) SEQ ID NOs: 103, 104, 105, 139, 140 and 141, respectively;
- [0285]** (4) SEQ ID NOs: 106, 107, 108, 142, 143 and 144, respectively;
- [0286]** (5) SEQ ID NOs: 109, 110, 111, 145, 146 and 147, respectively;
- [0287]** (6) SEQ ID NOs: 112, 113, 114, 148, 149 and 150, respectively;
- [0288]** (7) SEQ ID NOs: 115, 116, 117, 151, 152 and 153, respectively;
- [0289]** (8) SEQ ID NOs: 118, 119, 120, 154, 155 and 156, respectively;
- [0290]** (9) SEQ ID NOs: 121, 122, 123, 157, 158 and 159, respectively;
- [0291]** (10) SEQ ID NOs: 124, 125, 126, 160, 161 and 162, respectively;
- [0292]** (11) SEQ ID NOs: 127, 128, 129, 163, 164 and 165, respectively; or
- [0293]** (12) SEQ ID NOs: 130, 131, 132, 166, 167 and 168, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3, preferably specifically binds human DLL3.

[0294] Embodiment 3 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment of embodiment 1 or 2, comprising a heavy chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 or 23, or a light chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 or 24.

[0295] Embodiment 4 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment of any one of embodiments 1-3, comprising

- [0296]** (a) a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 1, and a light chain variable region having the polypeptide sequence of SEQ ID NO:2;
- [0297]** (b) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:3, and a light chain variable region having the polypeptide sequence of SEQ ID NO:4;
- [0298]** (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:5, and a light chain variable region having the polypeptide sequence of SEQ ID NO:6;
- [0299]** (d) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:7, and a light chain variable region having the polypeptide sequence of SEQ ID NO:8;
- [0300]** (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:9, and a light chain variable region having the polypeptide sequence of SEQ ID NO: 10;
- [0301]** (f) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:11, and a light chain variable region having the polypeptide sequence of SEQ ID NO:12;
- [0302]** (g) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:13, and a light chain variable region having the polypeptide sequence of SEQ ID NO:14;

- [0303] (h) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:15, and a light chain variable region having the polypeptide sequence of SEQ ID NO:16;
- [0304] (i) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:17, and a light chain variable region having the polypeptide sequence of SEQ ID NO:18;
- [0305] (j) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:19, and a light chain variable region having the polypeptide sequence of SEQ ID NO:20;
- [0306] (k) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:21, and a light chain variable region having the polypeptide sequence of SEQ ID NO:22; or
- [0307] (l) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:23, and a light chain variable region having the polypeptide sequence of SEQ ID NO:24.
- [0308] Embodiment 5 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment of any one of embodiments 1-4, wherein the antibody or antigen-binding fragment thereof is chimeric.
- [0309] Embodiment 6 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment of any one of embodiments 1-4, wherein the antibody or antigen-binding fragment thereof is human or humanized.
- [0310] Embodiment 7 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of embodiment 6, wherein the antibody or antigen-binding fragment thereof comprises:
- [0311] (a) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- [0312] (b) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172; or
- [0313] (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:170, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173.
- [0314] Embodiment 8 is the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of any one of embodiments 1-7, wherein the anti-DLL3 monoclonal antibody or antigen-binding fragment thereof is capable of inducing effector-mediated tumor cell lysis.
- [0315] Embodiment 9 is an isolated anti-CD47 monoclonal antibody or antigen-binding fragment comprising a humanized heavy chain variable region of an anti-CD47 monoclonal antibody and a humanized light chain variable region of an anti-DLL3 monoclonal antibody, wherein the anti-CD47 monoclonal antibody or antigen-binding fragment thereof comprises:
- [0316] a. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- [0317] b. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- [0318] c. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;
- [0319] d. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- [0320] e. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- [0321] f. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;
- [0322] g. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- [0323] h. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- [0324] i. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173; or
- [0325] j. a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:174.
- [0326] Embodiment 10 is the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof of embodiment 9, wherein the anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to signal regulatory protein alpha (SIRP α).
- [0327] Embodiment 11 is the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof of embodiment 9, wherein the anti-CD47 monoclonal antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells.
- [0328] Embodiment 12 is an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, preferably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOS: 178, 179 and 180; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOS: 181, 182 and 183; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOS: 184, 185 and 186.
- [0329] Embodiment 13 is an isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment comprising a first antigen-binding domain that specifically binds CD47, preferably human CD47, and a second antigen-binding domain that specifically binds DLL3, pref-

erably human DLL3, wherein the first antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 187, 188 and 189; the second antigen-binding domain comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, having the polypeptide sequences of SEQ ID NOs: 190, 191 and 192; and the first antigen-binding domain and the second antigen-binding domain each comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of SEQ ID NOs: 193, 194 and 195.

[0330] Embodiment 14 is the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of embodiment 12 or 13, wherein the first antigen-binding domain comprises a heavy chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO:176, and a light chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO:172; and wherein the second antigen-binding domain comprises a heavy chain variable region a polypeptide sequence at least 95% identical to SEQ ID NO: 170, and a light chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO:172.

[0331] Embodiment 15 is the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-14, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to SIRP α on cancer cells that express both DLL3 and CD47.

[0332] Embodiment 16 is the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-14, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47.

[0333] Embodiment 17 is the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-14, wherein the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof is capable of binding cancer cells that express both DLL3 and CD47 with minimal to undetectable binding to human red blood cells (RBCs).

[0334] Embodiment 18 is an isolated nucleic acid encoding the anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, the anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment of any one of embodiments 1-17.

[0335] Embodiment 19 is a vector comprising the isolated nucleic acid of embodiment 18.

[0336] Embodiment 20 is a host cell comprising the vector of embodiment 19.

[0337] Embodiment 21 is a pharmaceutical composition, comprising the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, the anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1-17 and a pharmaceutically acceptable carrier.

[0338] Embodiment 22 is a method of targeting DLL3 on a cancer cell surface in a subject in need thereof, comprising

administering to the subject in need thereof the pharmaceutical composition comprising the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of any one of embodiments 1-8.

[0339] Embodiment 23 is a method of blocking binding of CD47 to signal regulatory protein alpha (SIRP α) in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the anti-CD47 monoclonal antibody or antigen-binding fragment thereof of any one of embodiments 9-11.

[0340] Embodiment 24 is a method of inducing macrophage-mediated phagocytosis of cancer cells in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the anti-CD47 monoclonal antibody or antigen-binding fragment thereof of any one of embodiments 9-11.

[0341] Embodiment 25 is a method of targeting DLL3 and CD47 that are both expressed on a cancer cell surface in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the isolated humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-17.

[0342] Embodiment 26 is a method of blocking binding of CD47 to SIRP α on cancer cells that express both DLL3 and CD47 in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-17.

[0343] Embodiment 27 is a method of inducing macrophage-mediated phagocytosis of cancer cells that express both DLL3 and CD47 in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-17.

[0344] Embodiment 28 is a method of binding cancer cells that express both DLL3 and CD47 with minimal to undetectable binding to human red blood cells (RBCs) in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition comprising the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 12-17.

[0345] Embodiment 29 is a method of treating cancer in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition of embodiment 21.

[0346] Embodiment 30 is the method of embodiment 29, wherein the cancer is selected from the group consisting of a lung cancer, such as small cell lung cancer (SCLC), large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, and other solid tumors, and a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), an acute myeloid leukemia (AML), and other liquid tumors.

[0347] Embodiment 31 is a method of producing the anti-DLL3 monoclonal antibody or antigen-binding frag-

ment thereof, the anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1-17, comprising culturing a cell comprising a nucleic acid encoding the antibody or antigen-binding fragment thereof under conditions to produce the antibody or antigen-binding fragment thereof, and recovering the antibody or antigen-binding fragment thereof from the cell or culture.

[0348] Embodiment 32 is a method of producing a pharmaceutical composition comprising the anti-DLL3 monoclonal antibody or antigen-binding fragment thereof, the anti-CD47 monoclonal antibody or antigen-binding fragment thereof, or the humanized anti-CD47/DLL3 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1-17, comprising combining the antibody or antigen-binding fragment thereof with a pharmaceutically acceptable carrier to obtain the pharmaceutical composition.

[0349] Embodiment 33 is a method of determining a level of DLL3 in a subject, the method comprising:

- [0350]** a. obtaining a sample from the subject;
- [0351]** b. contacting the sample with the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of any one of embodiments 1-8; and
- [0352]** c. determining a level of DLL3 in the subject.

[0353] Embodiment 34 is the method of embodiment 33, wherein the sample is a tissue sample.

[0354] Embodiment 35 is the method of embodiment 34, wherein the tissue sample is a cancer tissue sample.

[0355] Embodiment 36 is the method of embodiment 33, wherein the sample is a blood sample.

EXAMPLES

Example 1: Identification of Anti-DLL3 Monoclonal Antibodies

[0356] Mice were immunized with recombinant FLAG-huDLL3 (Adipogen, Cat #: AG40B-0151), a fusion protein of human DLL3 extracellular domain (ECD) with FLAG tag at the N-terminus. Plasma titer was determined by ELISA. After euthanization, spleens and lymph nodes were collected to produce hybridomas. Hybridomas were grown in 384-well tissue culture plates and supernatants from individual wells were screened by ELISA using FLAG-huDLL3, FACS using stable pools of HEK293-huDLL3 and HEK293-cyDLL3, and Octet off-rate analysis using FLAG-huDLL3. Top positive clones were isolated and sequenced.

[0357] Sequences of heavy and light chain variable regions for anti-DLL3 monoclonal antibodies are provided in Tables 1 and 2, and the CDR regions for the anti-DLL3 monoclonal antibodies are provided in Tables 3-6.

TABLE 1

Sequences of heavy chain variable regions for anti-DLL3 mAbs		
mAb clones	VH	SEQ ID NO:
13P9A	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQPDWIGYI NPYNDATKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGYDY DGDYWGQGTTLTVSS	1
5A16A	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYILHWVKLKPQGLEWIGYIN PYNDGTYNEKFKGKATLTSDKSSSTAYMELSRLLTSYDSAVYYCARDSSGYG GAYAMDFWGQGTSTVTVSS	3
14L22A	EVQLVESGGGLVKGPGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVAAIN SNGGNTYYPDVTVDKRTISRDNKNTLYLQMSLSRSEDALYYCARHGGFFY YAVDYWGQGTSTVTVSS	5
10P18A	EVQLQQSGPELVKPGASVKISCKASGYSTGYIDWVKQSPGKSLEWIGYIYP SNGETSYNQKFKGKATLTVDKSSSTVNMQLNSLTSEDSAVYYCARESYAMD YWGQGTSTVTVSS	7
13P11A	DVQLQESGPGLVKPSQTVSLTCTVTGYSTINGNHWMSWIRQVSGSKLEWMMG YISSSGSTDSNPSLKSRIISITRDTSKNQFLHLNSVTTEDIATYYCATGTGWYF DYWGQGTTLTVSS	9
3C16A	EVQLQQSGPELVKPGTSVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYV IPYNDGTYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARPSNWDE FDYWGQGTTLTVSS	11
3I21A	QVQLQQPGAELVKPGASVKLSCKASGYTFTNYWMNWVKQRPGRGLEWIGRI HPSDSETHYNQKFKATLTVDKSSSTAYIQLSSLTSEDSAVYYCARYDGYFA YWGQGTTLTVSA	13
8H5A	QVTLKESGPGILQPSQTLSTCSFSGFSLSTFGMGVGVIRQPSGKLEWLAHIW WDDDKYYPALKSRLTISKDTSKNQVFLKIANVDIADTATYYCARTYDYDEY FDYWGQGTTLTVSS	15
15K2A	QVQLQQPGAELVQPGASVKLSCKASGYTFTSYWMNMWKQRPGRGLEWIGRI HPSDSETHYNQKFRKATLTVDKSSSTAYIQLSSLTSEDSAVYYCAREDDGYW YFDVWGAGTTTVTVSS	17
5A24A	EVQLQQSGAELVKPGASVKIPCKASGYKFTDFNMDWVKQSHGKSLEWIGDIN PNSGGTIYNQKFKGKATLTVDKSLSTAYMELGSLTSEDVAVYYCARWDYGNF AYWGQGTTLTVSA	19

TABLE 1-continued

Sequences of heavy chain variable regions for anti-DLL3 mAbs		
mAb clones	VH	SEQ ID NO:
15P17A	QVQLQQPGAELVKPGASVKLSCKASGYTFTNYWMNWVKQRPGRGLEWIGRI HPSDSETHYNQKFKSKATLTVDKSSSTAYIQLSSLTSEDSAVYYCAREGGYYW YFDVWGAGTTVTVSS	21
15N21A	EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPPEKRLWVAAIN SNGGRNYYPDVTVKDRFTISRDNAKNTLYLQMSSLRSEDTALYYCARHRGGYY YAMDYWGQGTSTVTSS	23

VH: heavy chain variable region

TABLE 2

Sequences of light chain variable regions for anti-DLL3 mAbs		
mAb clones	VL	SEQ ID NO:
13P9A	DIQMNQSPSSLSASLGDSITITCHASQININVLWSYQQKPGNIPKLLIYKASNLH TGVPSRFRSGSGSGTGFTLTISSLQPEDATYYCQQGQSYPTFGSGTKLEIK	2
5A16A	DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGRSPQLLVYNAKT LPYGVPSRFRSGSGSGTGYSLKINSLQPEDFGSYQCQHFWTTPWTFGGGKLEIK	4
14L22A	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLL IYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSRRTFGGGT KLEIK	6
10P18A	DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHYQQKPGQPPKLLIYL ASNLESGVPARFSGSGSGTDFTLTNIHPVEEDAATYYCQHSRELPTYTFGGGKLEIK	8
13P11A	NIVMTQSPKSMMSVGERVTLSCASENVGTIVSWYQQKPEQSPKLLIYGASN RFTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQSYSPFTFGSGTKLEIK	10
3C16A	DIVMTQSQKFMSTSVGDRVSITCKASQNVRTAVAWYQQKPGQSPKALIYLASN RHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNYPLTFGAGTKLELK	12
3I21A	DIQMTQSSSYLSVSLGGRVTITCKASDHINNWLAWYQQKPGNAPRLIISGATSL ETGDPFRFSGSGSGKDYLSTISLQIEDVATYYCQYWSIPFTFGAGTKLELK	14
8H5A	DIVMTQAAFSNPVTLTGTSASISCRSSKSLHNSNGITYFYWYLQKPGQSPQLLIYQ MSNLAGVDPDRFSSSGSGTDFTLRISRVEAEDVGYYCAQNLELPFTFGSGTKLEIK	16
15K2A	NIVLTQSPASLAVSLGQRATISCRASESVDIYGNFMHWYQQKPGQPPKLLIYL ASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQNNEDPWTFGGGTKLEIK	18
5A24A	DIVMTQAAFSNPVTLTGTSASISCRSSKSLHNSNGITYLYWYLQKPGQSPQLLIYQ MSNLAGVDPDRFSSSGSGTDFTLRISRVEAEDVGYYCAQNLELPFTFGAGTKLELK	20
15P17A	NIVLTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQQKPGQPPKLLIYL ASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQNNHEDPWTFGGGTKLEIK	22
15N21A	DIVMSQSPSSLAVSAGEKVTMSCKSSQLLYSSNQKNYLAWYQQKPGQSPKLLI YWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQYYTYLTFGAGTKLELK	24

VL: light chain variable region

TABLE 3

CDR regions 1-3 of heavy chain for anti-DLL3 mAbs					
mAb clones	HC CDR1	SEQ ID NO:	HC CDR2	SEQ ID NO:	HC CDR3
13P9A	GYTFTSYV	25	INPYNDAT	26	ARGGYDYDGDY
5A16A	GYTFTRYI	28	INPYNDGT	29	ARDSSGYGGAYAMDF
14L22A	GFTFSSYA	31	INSNGGNT	32	ARHRGGFYAVDY
10P18A	GYSFTGYY	34	IYPSNGET	35	ARESYAMDY
13P11A	GYSFINGNH	37	ISSSGST	38	ATTGTWGYFDY
3C16A	GYTFTSYV	40	VIPYNDGT	41	ARPSNWDEFDY
3I21A	GYTFTNYW	43	IHPSDSET	44	ARYDGYFAY
8H5A	GFSLSFTFGMG	46	IWWDDDK	47	ARTYDYDEYFDY
15K2A	GYTFTSYW	49	IHPSDSET	50	AREGGYWWYFDV
5A24A	GYKFTDFN	52	INPNSGGT	53	ARWDYGNPAY
15P17A	GYTFTNYW	55	IHPSDSET	56	AREGGYWWYFDV
15N21A	GFTFSSYA	58	INSNGGRN	59	ARHRGGYYYAMDY

HC: heavy chain; CDR: complementarity determining region

The HC CDRs for the anti-DLL3 mAbs were determined utilizing the IMGT method (Lefranc, M.-P. et al., Nucleic Acids Res. 1999; 27:209-212).

TABLE 4

CDR regions 1-3 of light chain for anti-DLL3 mAbs						
mAb clones	LC CDR1	SEQ ID NO:	LC CDR2	SEQ ID NO:	LC CDR3	SEQ ID NO:
13P9A	QNINW	61	KAS	62	QQGQSYPT	63
5A16A	GNIHNY	64	NAK	65	QHFWTPWT	66
14L22A	QSVLYSSNQKNY	67	WAS	68	HQYLSSRT	69
10P18A	KSVSTSGYSY	70	LAS	71	QHSRELPYT	72
13P11A	ENVGTY	73	GAS	74	GQSYSYPT	75
3C16A	QNVRTA	76	LAS	77	LQHWNYPLT	78
3I21A	DHINW	79	GAT	80	QQWSSIPPT	81
8H5A	KSLLSHNGITY	82	QMS	83	AQNLELPPT	84
15K2A	ESVDIYGNSF	85	LAS	86	QQNNEDPWT	87
5A24A	KSLLSHNGITY	88	QMS	89	AQNLELPPT	90
15P17A	ESVDSYGNSF	91	LAS	92	QQNHEDPWT	93
15N21A	QSLLYSSNQKNY	94	WAS	95	QQYYTYLT	96

LC: light chain; CDR: complementarity determining region

The LC CDRs for the anti-DLL3 mAbs were determined utilizing the IMGT method (Lefranc, M.-P. et al., Nucleic Acids Res. 1999; 27:209-212).

TABLE 5

CDR regions 1-3 of heavy chain for anti-DLL3 mAbs						
mAb clones	HC CDR1	SEQ ID NO:	HC CDR2	SEQ ID NO:	HC CDR3	SEQ ID NO:
13P9A	SYVMH	97	YINPYNDATKYNEKFKG	98	GGYDYDGDY	99
5A16A	RYILH	100	YINPYNDGTYNEKFKG	101	DSSGYGGAYAMDF	102
14L22A	SYAMS	103	AINSNNGNTYYPDTVKD	104	HRGGFYAVDY	105
10P18A	GYIID	106	YIYPSNGETSYNQKFKG	107	ESYAMDY	108
13P11A	NGNHWW	109	YISSSGSTDSNPSLKS	110	TGTWGYFDY	111
3C16A	SYVMH	112	YVIPYNDGTYNEKFKG	113	PSNWDEFDY	114
3I21A	NYWMN	115	RIHPSDSETHYNQKPKT	116	YDGYFAY	117
8H5A	TFGMGVG	118	HIWWDDDKYYPALKS	119	TYDYDEYFDY	120
15K2A	SYWMN	121	RIHPSDSETHYNQKFRT	122	EDGYYWYFDV	123
5A24A	DFNMD	124	DINPNSGGTIYNQKFKG	125	WDYGNFAY	126
15P17A	NYWMN	127	RIHPSDSETHYNQKFKS	128	EDGYYWYFDV	129
15N21A	SYAMS	130	AINSNNGRNYYPDTVKD	131	HRGGYYYAMDY	132

HC: heavy chain; CDR: complementarity determining region

The HC CDRs for the anti-DLL3 mAbs were determined utilizing the Kabat method (Elvin A. Kabat et al, Sequences of Proteins of Immunological Interest 5th ed. (1991)).

TABLE 6

CDR regions 1-3 of light chain for anti-DLL3 mAbs						
mAb clones	LC CDR1	SEQ ID NO:	LC CDR2	SEQ ID NO:	LC CDR3	SEQ ID NO:
13P9A	HASQININWLS	133	KASNLHT	134	QQGQSYPT	135
5A16A	RASGNIHNYLA	136	NAKTLPY	137	QHFWTTPWT	138
14L22A	KSSQSVLYSSNQKNYLA	139	WASTRES	140	HQYLSSRT	141
10P18A	RASKSVSTSGYSYMH	142	LASNLES	143	QHSRELPTY	144
13P11A	KASENVGTYS	145	GASNRFT	146	QGSYSYPT	147
3C16A	KASQNVRTAVA	148	LASNRHT	149	LQHWNYPLT	150
3I21A	KASDHINNWL	151	GATSLET	152	QQYWSIPT	153
8H5A	RSSKSLLSHNGITYFY	154	QMSNLAS	155	AQNLELPFT	156
15K2A	RASESVDIYGNFSMH	157	LASNLES	158	QQNNEDPWT	159
5A24A	RSSKSLLSHNGITYLY	160	QMSNLAS	161	AQNLELPPLT	162
15P17A	RASESVDSYGNFSMH	163	LASNLES	164	QQNHEDPWT	165
15N21A	KSSQSLLYSSNQKNYLA	166	WASTRES	167	QQYYTYLT	168

LC: light chain; CDR: complementarity determining region

The LC CDRs for the anti-DLL3 mAbs were determined utilizing the Kabat method (Elvin A. Kabat et al, Sequences of Proteins of Immunological Interest 5th ed. (1991)).

Example 2: Production and Purification of Chimeric mAbs from the Culture Media of Transfected Cells

[0358] To obtain the recombinant anti-DLL3 chimeric mAbs, the expression vectors containing the mouse variable regions (VH and VL) fused to the constant regions of human IgG1 heavy chain and kappa light chain, respectively, were transiently transfected into 293E, ExpiCHO-S, or Expi293F cells. The recombinant antibodies produced in the suspension of the cells were purified using Protein A affinity chromatography.

Example 3: ELISA Binding Analysis of Purified Chimeric Antibodies

[0359] FLAG-huDLL3 in carbonate coating buffer (50 µL/well at 0.25 µg/mL) was coated on an ELISA plate for 1 hour at room temperature. After washing, the ELISA plate was blocked in 5% BSA in TBST for 1 hour at room temperature and washed again. An anti-DLL3 mAb was added, mixed, and incubated for 1 hour at room temperature. The plate was washed and the binding of anti-DLL3 mAb to the immobilized FLAG-huDLL3 was detected by adding a secondary antibody, an anti-human IgG conjugated to horseradish peroxidase (hIgG-HRP) (ThermoFisher Scientific, Cat #: H10007) in 5% BSA in TBST, incubating for 1 hour, and then washing the plate. The ELISA was developed using One-step Detection Solution (ThermoFisher Scientific, Cat #: 34028) and measured as the absorbance at 450 nm. An isotype control IgG1 mAb that does not cross-react with DLL3 was used as negative control to ensure assay specificity. Binding results of the chimeric anti-DLL3 mAbs are provided in FIGS. 1A-1C.

Example 4: FACS Analysis of Chimeric Anti-DLL3 mAbs

[0360] A HEK293 cell line stably expressing human DLL3 (HEK-huDLL3) was used in a FACS assay. The cells (100,000 cells per well on a 96-well plate) were incubated with either a solution of the purified mAbs at various concentrations (e.g., 666.67 nM, 333.33 nM, or 66.67 nM) or an isotype control in Hanks' Balanced Salt Solution

(HBSS) containing 0.05% sodium azide and 0.1% BSA. Using an Alexa Fluor 488-conjugated anti-human IgG secondary antibody (ThermoFisher, Cat #: H10120), the presence of the mAb on HEK293-huDLL3 cells was measured by FACS (Attune NxT; ThermoFisher, Carlsbad, CA). The result of the FACS binding analysis is provided in FIGS. 2A-2C.

Example 5: Humanization of an Anti-DLL3 mAb

[0361] The mouse anti-DLL3 13P9A was humanized to reduce the potential of immunogenicity when used in human patients. The sequences of the variable regions of the heavy and light chains (VH and VL) were compared with the human antibody sequences in the Protein Data Bank (PDB) database and homology models were built. The CDRs in both the heavy and light chains of the mouse mAbs were grafted into human frameworks that have the highest possibility of maintaining the proper structure likely required for antigen binding. Backmutations from human residues to mouse residues or other mutations were designed when necessary. The sequences of the humanized VH and VL regions are shown in Tables 7 and 8. The humanized VH and VL regions were fused to the constant regions of human IgG4 heavy chain and kappa light chain, respectively. Antibodies were purified from transiently transfected 293E cells and analyzed for their ability to bind recombinant human FLAG-huDLL3 on a plate using ELISA. The EC₅₀ values for DLL3 binding by the humanized mAbs are provided in Table 9.

TABLE 7

Sequence of the humanized heavy chain variable region of anti-DLL3 mAb 13P9A		
Design	VH	SEQ ID NO:
H1	EVRLSQSGGQMKKPGESMRLSCRASGYTFTSYVMH WVRQAPGRRPWIGYINPYNDATKYARKFQGRATL TSDKYSDTAFLELRSLTSDDTAVYYCARGGYDYDG DYWGRGAPVTVSS	170

TABLE 8

Sequences of humanized light chain variable regions of anti-DLL3 mAb 13P9A		
Design	VL	SEQ ID NO:
L1	EIVMTQSPGTLTSLSPGERATLSCHASQNINVWLSWYQQKPGQAPRLLIYKA SNLHTGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQGSYPFTFGQGTK VEIK	171
L2	EIVLTQSPGTLTSLSPGERATLSCHASQNINVWLSWYQQKPGQAPRLLIYKA SNLHTGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQGSYPFTFGQGTK VEIK	172
L3	EIVMTQSPATLSLSPGETAIISCHASQNINVWLSWYQQRPQAPRLLIYKAS NLHTGIPDRFSGSGWGTDFNLSISNLESGLFGVYYCQQGSYPFTFGQGTK VEIK	173
L4	EIVMTQSPATLSLSPGETAIISCHASQNINVWLSWYQQRPQAPRLLIYKAS NLHTGIPDRFSGSGWGTDFNLSISNLESGLFGVYYCQQGSYPFTFGQGT KVEIK	174

TABLE 9

EC ₅₀ values for DLL3 binding by humanized anti-DLL3 mAbs in an ELISA assay	
mAb ID	EC50 (nM)
H1L1	0.13
H1L2	0.12
H1L3	0.15

H1L1 refers to the mAb with the H1 heavy chain variable region and the L1 light chain variable region; all the other humanized mAbs in the table adopt the same naming rule.

[0362] The humanized anti-DLL3 mAb H1L2 was analyzed by flow cytometry for its ability to bind cell surface DLL3. SHP-77 cells have been reported to express DLL3 (Barretina et al., Nature 483 (7391): 603-7 (2012)) and therefore were used in the assay. SHP-77 (ATCC #CRL-2195) cells (14,000 cells per well on a 96-well plate) were incubated with either a solution of the purified mAb at various concentrations or an isotype control in Hanks' Balanced Salt Solution (HBSS) containing 0.05% sodium

[0364] The purified mAbs were analyzed for their ability to bind to the extracellular domain of CD47 (CD47 (ECD)) in an ELISA assay as follows: human CD47 (ECD) (Acro-Bio, Cat #: CD7-HA2E9-50 µg) in carbonate coating buffer (50 µL/well at 1 µg/mL) was coated on a 96-well ELISA plate for 1 hour at room temperature. After washing, the plate was blocked in 5% BSA in TBST for 1 hour at room temperature and washed again. In each well of the plate, an antibody at 50 µL/well at various concentrations was added and incubated for 1 hour at room temperature. The plate was washed and the binding of the antibody to the immobilized CD47 was detected by incubating with anti-human IgG conjugated to horseradish peroxidase (hIgG-HRP) (ThermoFisher Scientific, Cat #: H10007) for 60 minutes at room temperature. Then after washing, the ELISA was developed using One-step Detection Solution (ThermoFisher Scientific, Cat #: 34028) and measured as the absorbance at 450 nm. The binding EC₅₀ values are shown in Table 11. These data indicate that the humanized anti-DLL3 light chains can pair with the humanized heavy chains of 17C6A to form mAbs with strong affinity for CD47.

TABLE 10

Sequences of humanized heavy chain variable regions of an anti-CD47 mAb		
Design	VH	SEQ ID NO:
KH1	QVQLVQSGAEVKKPGSSVKVCKASGYTFTSYWMHWVRQAPGQGLEWI GNIDPSDSETHYAQKFQGRATLTVDKSTSTAYMELSSLRSEDTAVYYCAG TDLAYWGQGLVTVSS	175
KH2	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQGLEWI GNIDPSDSETHYAQKFQGRVTLTVDKSTSTVYMELSSLRSEDTAVYYCAG TDLAYWGQGLVTVSS	176
KH3	EVRLSQSGGQMKKPGESMRLSCRASGYTFTSYWMHWVRQAPGRRLIEWIG NIDPSDSETHYARKFQGRATLTVDKYSDTAPLELRSLTSDDTAVYYCAGTD LAYWGRGAPVTVSS	177

azide and 0.1% BSA. Using a PE-Cy7-conjugated anti-human IgG secondary antibody, the presence of the mAb on SHP-77 cells was measured by FACS (Attune NXT; ThermoFisher, Carlsbad, CA). The result of the FACS binding analysis is provided in FIG. 3.

Example 6: Assembly of Anti-CD47 mAbs Using the Humanized Heavy Chain Variable Region of an Anti-CD47 mAb and the Humanized Light Chain Variable Region of an Anti-DLL3 mAb

[0363] To assess whether the humanized light chain variable (VL) regions of the anti-DLL3 mAb in Table 8 can form mAbs with the heavy chain variable (VH) region of anti-CD47 mAb 17C6A (described in International Patent Application No. PCT/US18/44384), humanized sequences of the VH region of 17C6A provided in Table 10 were used for antibody expression. The humanized VL regions of the anti-DLL3 mAb in Table 8 and the humanized VH regions of 17C6A in Table 10 were fused to the constant regions of human kappa light chain and IgG4 heavy chain, respectively, and the mAbs were expressed in 293E cells or ExpiCHO-S cells. The recombinant antibodies produced in the suspension of the 293E cell or ExpiCHO-S cultures were purified using Protein A affinity chromatography.

TABLE 11

EC ₅₀ values for CD47 binding by humanized anti-CD47 mAbs in an ELISA assay	
mAb ID	EC50 (nM)
KH1L1	1.17
KH1L2	0.64
KH1L3	0.76
KH2L1	0.19
KH2L2	0.18
KH2L3	0.09
KH3L1	0.09
KH3L2	0.08
KH3L3	0.18
KH3L4	0.08

KH1L1 refers to the mAb with the KH1 heavy chain variable region and the L1 light chain variable region; all the other humanized mAbs in the table adopt the same naming rule.

Example 7: Expression and Purification of Bispecific Antibodies Carrying a Common Light Chain

[0365] As mentioned above, DLL3 is detectable on the surface of small cell lung cancer (SCLC) and large cell neuroendocrine carcinoma (LCNEC) tumor cells (Saunders et al., Sci Transl Med 7(302):302ra136 (2015) and Sharma

et al., Cancer Res 77(14):3931-41 (2017)). Further, CD47 which mediates the “don’t eat me” signal is overexpressed in many tumors such as SCLC (Weiskopf et al., J Clin Invest 126 (7): 2610-2620 (2016)). A bispecific antibody with one arm binding to CD47 and the other arm binding to DLL3 (termed anti-CD47/DLL3 bispecific antibody) can be used to selectively target a cell that expresses both antigens. Binding of the bispecific antibody to both antigens on the same cell can result in increased affinity compared with either arm due to avidity. The bispecific antibody is expected to have weaker activity against cells that express only CD47 (but not DLL3) due to lack of avidity. This helps avoid targeting normal cells that express certain levels of CD47 by the bispecific antibody and increase its safety and/or tolerability. An anti-CD47/DLL3 bispecific antibody can selectively block the CD47/SIRPα interaction on a cell that express both CD47 and DLL3 and activate the innate immune system against the cell, such as a cancer cell. Thus,

homodimeric HCs (KH2/KH2 or H1/H1). The resulting bispecific antibody (KH2/H1/L2), termed BA1, was further modified by introducing a S354C cysteine mutation on the anti-CD47 HC (KH2) and a Y349C cysteine mutation on the anti-DLL3 HC (H1) to stabilize the heterodimeric pairing of the heavy chains KH2 and H1 (Merchant et al. Nat. Biotechnol. 16(7):677-81 (1998)). The resulting bispecific antibody was termed BA1(C). The variable regions of BA1 were also fused to the IgG4 frame work with the same cysteine mutations in BA1(C) to produce a bispecific antibody termed BA4(C). The simultaneous expression of the two heavy chains and the light chain in the same cell led to the expression and assembly of a desired bispecific antibody, which contains the anti-CD47 arm and the anti-DLL3 arm. Different ratios of the heavy chain DNAs were used to optimize the expression. The bispecific antibodies were produced in the suspension of ExpiCHO-S cells and purified using Protein A affinity and ion exchange chromatography.

TABLE 12

CDR regions 1-3 of the heavy chains and the common light chain for the bispecific antibodies			
	CDR1 (SEQ ID NO:)	CDR2 (SEQ ID NO:)	CDR3 (SEQ ID NO:)
KH2	GYTFTSYW (178)	IDPSDSET (179)	AGTDLAY (180)
H1	GYTFTSYV (181)	INPYNDAT (182)	ARGGYDYDGDY (183)
L2	QNINVW (184)	KAS (185)	QQGQSYPF (186)

The CDRs were determined utilizing the IMGT method.

TABLE 13

CDR regions 1-3 of the heavy chains and the common light chain for the bispecific antibodies			
	CDR1 (SEQ ID NO:)	CDR2 (SEQ ID NO:)	CDR3 (SEQ ID NO:)
KH2	SYWMH (187)	NIDPSDSETHYAQKFQG (188)	TDLAY (189)
H1	SYVMH (190)	YINPYNDATKYARKFQG (191)	GGYDYDGDY (192)
L2	HASQNINWLS (193)	KASNLHT (194)	QQGQSYPF (195)

The HC and LC CDRs were determined utilizing the Kabat method.

an anti-CD47/DLL3 bispecific antibody can be an effective therapy for SCLC, LCNEC and other tumors that express significant levels of both CD47 and DLL3 on the cell surface.

[0366] A bispecific antibody against CD47 and DLL3 was constructed with the humanized heavy chain variable region H1 in Table 7, the humanized heavy chain variable region KH2 in Table 10, and the humanized light chain variable region L2 in Table 8. The CDR regions for the bispecific mAb KH2/H1/L2 are provided in Table 12 and Table 13. The VH and VL regions of the bispecific antibody were fused to the constant regions of IgG1 heavy chain and kappa light chain, respectively. The HC containing KH2 has the T366W mutation to form a “knob” and the HC containing H1 has the mutations T366S, L368A, and Y407V to form a “hole”, so that the two heavy chains were favored to form a bispecific antibody with heterodimeric HCs (KH2/H1) rather than

Example 8: Characterization of Bispecific Antibodies

[0367] The purified bispecific antibodies were analyzed in a bridging ELISA assay to demonstrate that a bispecific antibody can bind both antigens at the same time. Human FLAG-huDLL3 in carbonate coating buffer (50 μL/well at 0.25 ug/mL) was coated on a 96-well ELISA plate for 1 hour at room temperature. The plate was blocked by 5% BSA in TBST for 1 hour at room temperature. In each well of the plate, a bispecific mAb (50 μL/well at various concentrations) was added and incubated for 1 hour at room temperature. After washing, biotinylated human CD47 extracellular domain (ECD) (AcroBio, Cat #: CD7-H82E9) was added to each well (50 μL/well at 0.05 ug/mL) and incubated at room temperature for 60 minutes. The plate was washed and the binding of biotinylated CD47 to the immobilized bispecific antibody was detected by adding horseradish peroxidase-

conjugated streptavidin (JIR, Cat #: 016-030-084) and incubating at room temperature for 60 minutes. Then, after washing, the ELISA was developed using One-step Detection Solution (ThermoFisher Scientific, Cat #: 34028) and measured as the absorbance at 450 nm. The results of the bridging ELISA assay for the bispecific antibodies BA1 and BA1(C) are provided in FIG. 4A; the result of the bridging ELISA assay for BA4(C) is provided in FIG. 4B.

[0368] The bispecific antibodies were analyzed for their ability to bind CD47 (ECD) or DLL3(ECD)-6His (R&D, Cat #: 9749-DL-050) immobilized on regular or nickel-coated plates in an ELISA assay. The results of the CD47 binding assay for the bispecific antibodies BA1, BA1(C), and BA4C are provided in FIG. 5 (CD47 (ECD) was coated on regular plates). The anti-CD47 parental mAb KH2L2 (labeled as anti-CD47 parental mAb in the FIG.) on the IgG4 framework was used as a control. The results of the DLL3 binding assay for the bispecific antibodies BA1 and BA1(C) are provided in FIG. 6A (DLL3(ECD)-6His was coated on a regular plate); the result of the DLL3 binding assay for BA4(C) is provided in FIG. 6B (DLL3(ECD)-6His was immobilized on a nickel-coated plate). The anti-DLL3 parental mAb HIL2 (labeled as anti-DLL3 parental mAb in the FIG.) on the IgG4 framework was used as a control. The results in FIG. 5 indicated that the bispecific antibodies, which have one anti-CD47 arm, were capable of binding CD47, but at a lower affinity than the parental mAb KH2L2 which has two anti-CD47 arms (FIG. 5). Similarly, the results in FIGS. 6A and 6B demonstrated that the bispecific antibodies, which have one anti-DLL3 arm, had weaker binding to DLL3 when compared with the parental anti-DLL3 mAb HIL2 which has two anti-DLL3 arms.

[0369] The bispecific antibodies were analyzed for their ability to bind both CD47 (ECD) and DLL3(ECD)-6His when they were simultaneously immobilized on the same plate (50 μ L/well at 20 nM for both antigens). The results of the CD47/DLL3 binding assay for the bispecific antibodies BA1, BA1(C) and BA4(C) are provided in FIG. 7.

[0370] The bispecific antibodies were also analyzed for their ability to block the CD47/SIRP α interaction in an ELISA assay. Human CD47 (ECD) (AcroBio, Cat #: CD7-HA2E9-50 ug) at 1 μ g/mL in carbonate coating buffer was coated on a 96-well plate (50 μ L/well) at 4° C. overnight. The plate was blocked by 5% BSA in TBST for 1 hour at room temperature. A bispecific and parental mAb at various concentrations were added to the plate and incubated at room temperature for 30 minutes. SIRP α extracellular domain (ECD) fused to mouse Fc (AcroBio, Cat #: SIA-H52A8-100 ug) was added to each well (50 μ L/well at 1 μ g/mL) and incubated at room temperature for 1 hour. The plate was washed and the binding of SIRP α to the immobilized CD47 was detected by anti-mouse IgG conjugated to horseradish peroxidase (mIgG-HRP) (ThermoFisher Scientific, Cat #: A16084) with incubation for 1 hour at room temperature. Then after washing, the ELISA was developed using One-step Detection Solution (ThermoFisher Scientific, Cat #: 34028) and measured as the absorbance at 450 nm. Consistent with the data from the CD47 binding assay on ELISA, the bispecific Abs have reduced ability to block the CD47/SIRP α interaction in this context (FIG. 8A). The assay was also carried out when both CD47 (ECD) and DLL3(ECD)-6His were simultaneously immobilized on the same plate at a CD47:DLL3 ratio of 2:1 (50 μ L/well with

CD47 at 40 nM and DLL3 at 20 nM) for 1 hour at room temperature and the plate was blocked by 5% BSA in DPBS. Under such a condition, the bispecific Abs have similar ability to block the CD47/SIRP α interaction when compared with the anti-CD47 parental mAb (FIG. 8B), suggesting that binding to the immobilized DLL3 on the plate by the anti-DLL3 arm of each of the bispecific Abs contributes to the blockade of the CD47/SIRP α interaction.

[0371] The bispecific antibodies were analyzed for their ability to bind Raji cells which have no detectable DLL3 expression. Raji cells (14,000 cells per well on a 96-well plate) were incubated with either a solution of a purified mAb at various concentrations or an isotype control in Hanks' Balanced Salt Solution (HBSS) containing 0.05% sodium azide and 0.1% BSA at room temperature for 30 minutes. After incubation, the plates were washed three times with the same buffer. Using a PE-Cy7-conjugated anti-human IgG secondary antibody, the presence of the mAb on Raji cells was measured by FACS (Attune NxT; ThermoFisher, Carlsbad, CA). The result of the FACS binding analysis is provided in FIG. 9.

[0372] The binding of the bispecific mAb BA1(C) and the two parental control mAbs to SHP-77 cells were tested in the presence or absence of one of the competing F(ab')₂'s: anti-DLL3 parental F(ab')₂ (final concentration in the assay was 25 μ M) and anti-CD47 parental F(ab')₂ (final concentration in the assay was 10 μ M). F(ab')₂'s were generated from mAbs using immobilized pepsin (Thermo Fisher Scientific, Cat: #20343) according to the instruction and purified. The result of the binding analysis is provided in FIG. 10. Inhibition of the binding of BA1(C) to SHP-77 cells by both F(ab')₂'s indicates that both the anti-CD47 and anti-DLL3 arms of the bispecific antibody contribute to its binding to SHP-77 cells.

[0373] The bispecific antibodies were tested for their ability to bind to human and cynomolgus red blood cells (RBCs). 14,000 RBCs were resuspended into 20 μ L FACS buffer (1 \times HBSS (Thermo Fisher Scientific, Cat #: 14175079) with 0.1% BSA and 0.05% sodium azide) containing diluted mAbs and incubated at room temperature for 30 minutes. After incubation, the plates were washed three times with FACS buffer and the cells were resuspended with PE-Cy7 conjugated anti-human IgG-Fc secondary antibody (BioLegend, Cat #: 409316) and incubated for 15 minutes at room temperature in dark. Plates were washed 2 \times with FACS buffer. Cells were resuspended and transferred to a 384-well plate for analysis with Attune NxT Flow Cytometer. FIGS. 11A-11C show the binding of the bispecific antibodies to human red blood cells (RBCs) at the following mAb concentrations: 1,600 nM (FIG. 11A), 533 nM (FIG. 11B), and 178 nM (FIG. 11C). Anti-CD47 and anti-DLL3 parental antibodies and IgG1 and IgG4 isotypes were used as controls.

[0374] It will be appreciated by those skilled in the art that changes could be made to the embodiments described above without departing from the broad inventive concept thereof. It is understood, therefore, that this invention is not limited to the particular embodiments disclosed, but it is intended to cover modifications within the spirit and scope of the present invention as defined by the present description.

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SEQ ID NO: 1      moltype = AA   length = 118
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                  organism = synthetic construct

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SEQ ID NO: 2          multype = AA  length = 107
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source               1..107
                    mol_type = protein
                    organism = synthetic construct

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SEQ ID NO: 3          multype = AA  length = 122
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source               1..122
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                     organism = synthetic construct

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SEQ ID NO: 4          moltype = AA  length = 107
FEATURE               Location/Qualifiers
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                     note = 5A16A Light Chain Variable Region
source               1..107
                     mol_type = protein
                     organism = synthetic construct

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SEQ ID NO: 5      multype = AA  length = 120
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source            1..120
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                  organism = synthetic construct

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SEQ ID NO: 6      multype = AA   length = 112
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                  note = 14L22A Light Chain Variable Region
source            1..112
                  mol_type = protein
                  organism = synthetic construct

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SEQ ID NO: 7      multype = AA  length = 116
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source            1..116
                  mol_type = protein
                  organism = synthetic construct
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SEQUENCE: 7
EVQLQQSGPE LVKPGASVKI SCKASGYSFT GYYIDWVKQS PGKSLEWIGY IYPSNGETSY 60
NQKFKGKATL TVDKSSSTVN MQLNSLTSED SAVYYCARES YAMDYWGQGT SVTVSS 116

SEQ ID NO: 8 moltype = AA length = 111
FEATURE Location/Qualifiers
REGION 1..111
 note = 10P18A Light Chain Variable Region
source 1..111
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 8
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYMHWY QQKPGQPPKL LIYLASNLES 60
GVPARFSGSG SGTDFTLNIH PVVEEDAATY YCQHSRELPY TFGGGTKLEI K 111

SEQ ID NO: 9 moltype = AA length = 119
FEATURE Location/Qualifiers
REGION 1..119
 note = 13P11A Heavy Chain Variable Region
source 1..119
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 9
DVQLQESGPG LVKPSQTVSL TCTVTGYSIT NGNHWWSWIR QVSGSKLEWM GYISSSGSTD 60
SNPSLKSRIS ITRDTSKNQL FLHLNSVTTE DIATYYCATT GTWGYFDYWG QGTTLTVSS 119

SEQ ID NO: 10 moltype = AA length = 107
FEATURE Location/Qualifiers
REGION 1..107
 note = 13P11A Light Chain Variable Region
source 1..107
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 10
NIVMTQSPKS MSMSVGERVT LSCKASENVG TYVSWYQQKP EQSPKLLIYG ASNRFTGVDP 60
RFTGSGSATD FTLTISSVQA EDLADYHCGQ SYSYPFTFGS GTKLEIK 107

SEQ ID NO: 11 moltype = AA length = 118
FEATURE Location/Qualifiers
REGION 1..118
 note = 3C16A Heavy Chain Variable Region
source 1..118
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 11
EVQLQQSGPE LVKPGTSVKM SCKASGYTFT SYVMHWVKQK PGQGLEWIGY VIPYNDGTKY 60
NEKFKGKATL TSDKSSSTAY MELSSLTSED SAVYYCARPS NWDEFDYGQ GTTLTVSS 118

SEQ ID NO: 12 moltype = AA length = 107
FEATURE Location/Qualifiers
REGION 1..107
 note = 3C16A Light Chain Variable Region
source 1..107
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 12
DIVMTQSQKF MSTSVGDRVS ITCKASQNVN TAVAWYQQKP GQSPKALIYL ASNRHTGVDP 60
RFTGSGSGTD FTLTISNVQS EDLADYFCLQ HWNYPLTFGA GTKLELK 107

SEQ ID NO: 13 moltype = AA length = 116
FEATURE Location/Qualifiers
REGION 1..116
 note = 3I21A Heavy Chain Variable Region
source 1..116
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 13
QVQLQQPGAE LVKPGASVKL SCKASGYTFT NYWMNVVKQR PGRGLEWIGR IHPSDSETHY 60
NQKFKTKATL TVDKSSSTAY IQLSSLTSED SAVYYCARYD GYFAYWGQGT LTVSA 116

SEQ ID NO: 14 moltype = AA length = 107
FEATURE Location/Qualifiers
REGION 1..107
 note = 3I21A Light Chain Variable Region
source 1..107
 mol_type = protein

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SEQUENCE: 14
DIQMTQSSSY LSVSLGGRVT ITCKASDHIN NWLAWYQQKP GNAPRLLISG ATSLETGDPS 60
RFSGSGSGKD YTLSITSLQI EDVATYYCQQ YWSIPFTFGA GTKLELK 107

SEQ ID NO: 15      moltype = AA length = 120
FEATURE           Location/Qualifiers
REGION            1..120
                  note = 8H5A Heavy Chain Variable Region
source            1..120
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 15
QVTLKESGPG ILQPSQTLSTL TCSFSGFSLT TFGMGVGWIR QPSGKGLEWL AHIWDDDKY 60
YNPALKSRLT ISKDTSKNQV FLKIANVDIA DTATYYCART YDYDEYFDYW GQGTTLTVSS 120

SEQ ID NO: 16      moltype = AA length = 112
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                  note = 8H5A Light Chain Variable Region
source            1..112
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 16
DIVMTQAAPS NPVTLGTSAS ISCRSSKSLT HSGNITYFYW YLQKPGQSPQ LLIYQMSNLA 60
SGVPRDRFSSS GSGTDFTLRI SRVEAEDVGV YYCAQNLELP FTFGSGTKLE IK 112

SEQ ID NO: 17      moltype = AA length = 119
FEATURE           Location/Qualifiers
REGION            1..119
                  note = 15K2A Heavy Chain Variable Region
source            1..119
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 17
QVQLQQPGAE LVQPGASVKL SCKASGYTFT SYWMNWMKQR PGRGLEWIGR IHPSDSETHY 60
NQKFRITKATL TVDKSSSTAY IQLSSLTSED SAVYYCARED GYYWYFDVWG AGTTVTVSS 119

SEQ ID NO: 18      moltype = AA length = 111
FEATURE           Location/Qualifiers
REGION            1..111
                  note = 15K2A Light Chain Variable Region
source            1..111
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 18
NIVLTQSPAS LAVSLGQRAT ISCRASESVD IYGNSFMHWY QKQPGQPPKL LIYLASNLES 60
GVPARFSGSG SRTDFTLTID PVEADDAATY YCQONNEDPW TFGGGTKLEI K 111

SEQ ID NO: 19      moltype = AA length = 117
FEATURE           Location/Qualifiers
REGION            1..117
                  note = 5A24A Heavy Chain Variable Region
source            1..117
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 19
EVQLQQSGAE LVKPGASVKI PCKASGYKFT DFNMDWVKQS HGKSLEWIGD INPNSGGTIY 60
NQKFKGKATL TVDKSLSTAY MELGSLTSED TAVYYCARWD YGNFAYWGQG TLVTVSA 117

SEQ ID NO: 20      moltype = AA length = 112
FEATURE           Location/Qualifiers
REGION            1..112
                  note = 5A24A Light Chain Variable Region
source            1..112
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 20
DIVMTQAAPS NPVTLGTSAS ISCRSSKSLT HSGNITYLYW YLQKPGQSPQ LLIYQMSNLA 60
SGVPRDRFSSS GSGTDFTLRI SRVEAEDVGV YYCAQNLELP LTFGAGTKLE LK 112

SEQ ID NO: 21      moltype = AA length = 119
FEATURE           Location/Qualifiers
REGION            1..119
                  note = 15P17A Heavy Chain Variable Region
source            1..119

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mol_type = protein
organism = synthetic construct

SEQUENCE: 21
QVQLQQPGAE LVKPGASVKL SCKASGYTFT NYWMNWVKQR PGRGLEWIGR IHPSDSETHY 60
NQFKSKATL TVDKSSSTAY IQLSSLTSED SAVYYCARED GYYWYFDVWG AGTTVTVSS 119

SEQ ID NO: 22      moltype = AA length = 111
FEATURE           Location/Qualifiers
REGION            1..111
                  note = 15P17A Light Chain Variable Region
source            1..111
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 22
NIVLTQSPAS LAVSLGQRAT ISCRASESVD SYGNSFMHWY QQKPGQPPKL LIYLASNLES 60
GVPARFSGSG SRTDFTLTID PVEADDAATY YCQNHEDPW TFGGGTKLEI K 111

SEQ ID NO: 23      moltype = AA length = 120
FEATURE           Location/Qualifiers
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                  note = 15N21A Heavy Chain Variable Region
source            1..120
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 23
EVQLVESGGG LVKPGGSLKL SCAASGFTFS SYAMSWVRQT PEKRLIEWVAA INSNGGRNYY 60
PDTVKDRFTI SRDPAKNTLY LQMSSLRSED TALYYCARHR GGYYYAMDYW GQGTSTVTVSS 120

SEQ ID NO: 24      moltype = AA length = 112
FEATURE           Location/Qualifiers
REGION            1..112
                  note = 15N21A Light Chain Variable Region
source            1..112
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 24
DIVMSQSPSS LAVSVGEKVT MSCKSSQSL L YSSNQKNYLA WYQQKPGQSP KLLIYWASTR 60
ESGVPDRFTG SGSGTDFTLT ISSVKAEDLA VYYCQQYYTY LTFGAGTKLE LK 112

SEQ ID NO: 25      moltype = AA length = 8
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REGION            1..8
                  note = 13P9A HC CDR1
source            1..8
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 25
GYTFTSYV 8

SEQ ID NO: 26      moltype = AA length = 8
FEATURE           Location/Qualifiers
REGION            1..8
                  note = 13P9A HC CDR2
source            1..8
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 26
INPYNDAT 8

SEQ ID NO: 27      moltype = AA length = 11
FEATURE           Location/Qualifiers
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                  note = 13P9A HC CDR3
source            1..11
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 27
ARGGYDYDGD Y 11

SEQ ID NO: 28      moltype = AA length = 8
FEATURE           Location/Qualifiers
REGION            1..8
                  note = 5A16A HC CDR1
source            1..8
                  mol_type = protein
                  organism = synthetic construct

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SEQUENCE: 28 GYTFTRYI		8
SEQ ID NO: 29 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 5A16A HC CDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 29 INPYNDGT		8
SEQ ID NO: 30 FEATURE REGION source	moltype = AA length = 15 Location/Qualifiers 1..15 note = 5A16A HC CDR3 1..15 mol_type = protein organism = synthetic construct	
SEQUENCE: 30 ARDSSGYGGA YAMDF		15
SEQ ID NO: 31 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 14L22A HC CDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 31 GFTFSSYA		8
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SEQUENCE: 32 INSNGGNT		8
SEQ ID NO: 33 FEATURE REGION source	moltype = AA length = 13 Location/Qualifiers 1..13 note = 14L22A HC CDR3 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 33 ARHRGGFYA VDY		13
SEQ ID NO: 34 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 10P18A HC CDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 34 GYSFTGYI		8
SEQ ID NO: 35 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 10P18A HC CDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 35 IYPSNGET		8
SEQ ID NO: 36 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9	

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source	note = 10P18A HC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 36 ARESYAMDY		9
SEQ ID NO: 37 FEATURE REGION	moltype = AA length = 10 Location/Qualifiers 1..10 note = 13P11A HC CDR1	
source	1..10 mol_type = protein organism = synthetic construct	
SEQUENCE: 37 GYSITNGNHW		10
SEQ ID NO: 38 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 13P11A HC CDR2	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 38 ISSSGST		7
SEQ ID NO: 39 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 13P11A HC CDR3	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 39 ATTGTWGYFD Y		11
SEQ ID NO: 40 FEATURE REGION	moltype = AA length = 8 Location/Qualifiers 1..8 note = 3C16A HC CDR1	
source	1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 40 GYTFTSYV		8
SEQ ID NO: 41 FEATURE REGION	moltype = AA length = 8 Location/Qualifiers 1..8 note = 3C16A HC CDR2	
source	1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 41 VIPYNDGT		8
SEQ ID NO: 42 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 3C16A HC CDR3	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 42 ARPSNWDEFD Y		11
SEQ ID NO: 43 FEATURE REGION	moltype = AA length = 8 Location/Qualifiers 1..8 note = 3I21A HC CDR1	
source	1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 43 GYTFTNYW		8

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	1..8	
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	organism = synthetic construct	
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IHPDSET		8
SEQ ID NO: 45	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
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source	note = 3I21A HC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 45		
ARYDGYFAY		9
SEQ ID NO: 46	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
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source	note = 8H5A HC CDR1	
	1..10	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 46		
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SEQ ID NO: 47	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
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source	note = 8H5A HC CDR2	
	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 47		
IWWDDDK		7
SEQ ID NO: 48	moltype = AA length = 12	
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source	note = 8H5A HC CDR3	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 48		
ARTYDYDEYF DY		12
SEQ ID NO: 49	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
source	note = 15K2A HC CDR1	
	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 49		
GYTFTSYW		8
SEQ ID NO: 50	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
source	note = 15K2A HC CDR2	
	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 50		
IHPDSET		8
SEQ ID NO: 51	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = 15K2A HC CDR3	
	1..12	

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SEQ ID NO: 52 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 5A24A HC CDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 52 GYKFTDFN		8
SEQ ID NO: 53 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 5A24A HC CDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 53 INPNSGGT		8
SEQ ID NO: 54 FEATURE REGION source	moltype = AA length = 10 Location/Qualifiers 1..10 note = 5A24A HC CDR3 1..10 mol_type = protein organism = synthetic construct	
SEQUENCE: 54 ARWDYGNFAY		10
SEQ ID NO: 55 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 15P17A HC CDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 55 GYTFTNYW		8
SEQ ID NO: 56 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 15P17A HC CDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 56 IHPSDSET		8
SEQ ID NO: 57 FEATURE REGION source	moltype = AA length = 12 Location/Qualifiers 1..12 note = 15P17A HC CDR3 1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 57 AREDGYWYF DV		12
SEQ ID NO: 58 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 15N21A HC CDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 58 GFTFSSYA		8
SEQ ID NO: 59	moltype = AA length = 8	

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FEATURE	Location/Qualifiers	
REGION	1..8	
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SEQUENCE: 59		
INSNGGRN		8
SEQ ID NO: 60	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = 15N21A HC CDR3 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 60		
ARHRGGYYA MDY		13
SEQ ID NO: 61	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
REGION	1..6	
source	note = 13P9A LC CDR1 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 61		
QNINWV		6
SEQ ID NO: 62	moltype = length =	
SEQUENCE: 62		
000		
SEQ ID NO: 63	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 13P9A LC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 63		
QQGQSYPT		9
SEQ ID NO: 64	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
REGION	1..6	
source	note = 5A16A LC CDR1 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 64		
GNIHNY		6
SEQ ID NO: 65	moltype = length =	
SEQUENCE: 65		
000		
SEQ ID NO: 66	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 5A16A LC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 66		
QHFWTTPWT		9
SEQ ID NO: 67	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = 14L22A LC CDR1 1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 67		
QSVLYSSNQK NY		12

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SEQ ID NO: 68	moltype =	length =	
SEQUENCE: 68			
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SEQ ID NO: 69	moltype = AA	length = 8	
FEATURE	Location/Qualifiers		
REGION	1..8		
	note = 14L22A LC CDR3		
source	1..8		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 69			
HQYLSSRT			8
SEQ ID NO: 70	moltype = AA	length = 10	
FEATURE	Location/Qualifiers		
REGION	1..10		
	note = 10P18A LC CDR1		
source	1..10		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 70			
KSVSTSGYSY			10
SEQ ID NO: 71	moltype =	length =	
SEQUENCE: 71			
000			
SEQ ID NO: 72	moltype = AA	length = 9	
FEATURE	Location/Qualifiers		
REGION	1..9		
	note = 10P18A LC CDR3		
source	1..9		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 72			
QHSRELPYT			9
SEQ ID NO: 73	moltype = AA	length = 6	
FEATURE	Location/Qualifiers		
REGION	1..6		
	note = 13P11A LC CDR1		
source	1..6		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 73			
ENVGTY			6
SEQ ID NO: 74	moltype =	length =	
SEQUENCE: 74			
000			
SEQ ID NO: 75	moltype = AA	length = 9	
FEATURE	Location/Qualifiers		
REGION	1..9		
	note = 13P11A LC CDR3		
source	1..9		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 75			
GQSYSYPFT			9
SEQ ID NO: 76	moltype = AA	length = 6	
FEATURE	Location/Qualifiers		
REGION	1..6		
	note = 3C16A LC CDR1		
source	1..6		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 76			
QNVRTA			6
SEQ ID NO: 77	moltype =	length =	
SEQUENCE: 77			
000			

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SEQ ID NO: 78	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 3C16A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 78		
LQHWNYPLT		9
SEQ ID NO: 79	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
REGION	1..6	
source	note = 3I21A LC CDR1	
	1..6	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 79		
DHINNW		6
SEQ ID NO: 80	moltype = length =	
SEQUENCE: 80		
000		
SEQ ID NO: 81	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 3I21A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 81		
QQYWSIPFT		9
SEQ ID NO: 82	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = 8H5A LC CDR1	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 82		
KSLHNSGIT Y		11
SEQ ID NO: 83	moltype = length =	
SEQUENCE: 83		
000		
SEQ ID NO: 84	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 8H5A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 84		
AQNLELPFT		9
SEQ ID NO: 85	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
REGION	1..10	
source	note = 15K2A LC CDR1	
	1..10	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 85		
ESVDIYGNSF		10
SEQ ID NO: 86	moltype = length =	
SEQUENCE: 86		
000		
SEQ ID NO: 87	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	

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source	note = 15K2A LC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 87 QQNNEDPWT		9
SEQ ID NO: 88 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 5A24A LC CDR1	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 88 KSLHNSGIT Y		11
SEQ ID NO: 89 SEQUENCE: 89 000	moltype = length =	
SEQ ID NO: 90 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 5A24A LC CDR3	
source	1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 90 AQNLELPLT		9
SEQ ID NO: 91 FEATURE REGION	moltype = AA length = 10 Location/Qualifiers 1..10 note = 15P17A LC CDR1	
source	1..10 mol_type = protein organism = synthetic construct	
SEQUENCE: 91 ESVDSYGNSF		10
SEQ ID NO: 92 SEQUENCE: 92 000	moltype = length =	
SEQ ID NO: 93 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 15P17A LC CDR3	
source	1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 93 QQNHEDPWT		9
SEQ ID NO: 94 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = 15N21A LC CDR1	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 94 QSLLYSSNQK NY		12
SEQ ID NO: 95 SEQUENCE: 95 000	moltype = length =	
SEQ ID NO: 96 FEATURE REGION	moltype = AA length = 8 Location/Qualifiers 1..8 note = 15N21A LC CDR3	
source	1..8 mol_type = protein organism = synthetic construct	

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SEQUENCE: 96 QQYYTYLT		8
SEQ ID NO: 97 FEATURE REGION source	moltype = AA length = 5 Location/Qualifiers 1..5 note = 13P9A HC CDR1 1..5 mol_type = protein organism = synthetic construct	
SEQUENCE: 97 SYVMH		5
SEQ ID NO: 98 FEATURE REGION source	moltype = AA length = 17 Location/Qualifiers 1..17 note = 13P9A HC CDR2 1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 98 YINPYNDATK YNEKPKG		17
SEQ ID NO: 99 FEATURE REGION source	moltype = AA length = 9 Location/Qualifiers 1..9 note = 13P9A HC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 99 GGYDYDGDY		9
SEQ ID NO: 100 FEATURE REGION source	moltype = AA length = 5 Location/Qualifiers 1..5 note = 5A16A HC CDR1 1..5 mol_type = protein organism = synthetic construct	
SEQUENCE: 100 RYILH		5
SEQ ID NO: 101 FEATURE REGION source	moltype = AA length = 17 Location/Qualifiers 1..17 note = 5A16A HC CDR2 1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 101 YINPYNDGTK YNEKPKG		17
SEQ ID NO: 102 FEATURE REGION source	moltype = AA length = 13 Location/Qualifiers 1..13 note = 5A16A HC CDR3 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 102 DSSGYGGAYA MDF		13
SEQ ID NO: 103 FEATURE REGION source	moltype = AA length = 5 Location/Qualifiers 1..5 note = 14L22A HC CDR1 1..5 mol_type = protein organism = synthetic construct	
SEQUENCE: 103 SYAMS		5
SEQ ID NO: 104 FEATURE REGION	moltype = AA length = 17 Location/Qualifiers 1..17	

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source	note = 14L22A HC CDR2 1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 104 AINSNGGNTY YPDTVKD		17
SEQ ID NO: 105 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 14L22A HC CDR3	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 105 HRGGFYAVD Y		11
SEQ ID NO: 106 FEATURE REGION	moltype = AA length = 5 Location/Qualifiers 1..5 note = 10P18A HC CDR1	
source	1..5 mol_type = protein organism = synthetic construct	
SEQUENCE: 106 GYYID		5
SEQ ID NO: 107 FEATURE REGION	moltype = AA length = 17 Location/Qualifiers 1..17 note = 10P18A HC CDR2	
source	1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 107 YIYPSNGETS YNQKFKG		17
SEQ ID NO: 108 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 10P18A HC CDR3	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 108 ESYAMDY		7
SEQ ID NO: 109 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 13P11A HC CDR1	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 109 NGNHWWS		7
SEQ ID NO: 110 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16 note = 13P11A HC CDR2	
source	1..16 mol_type = protein organism = synthetic construct	
SEQUENCE: 110 YISSSGSTDS NPSLKS		16
SEQ ID NO: 111 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 13P11A HC CDR3	
source	1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 111 TGTWGYFDY		9

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SEQ ID NO: 112	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = 3C16A HC CDR1	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 112		
SYVMH		5
SEQ ID NO: 113	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = 3C16A HC CDR2	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 113		
YVIPYNDGTK YNEKFKG		17
SEQ ID NO: 114	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 3C16A HC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 114		
PSNWDEFDY		9
SEQ ID NO: 115	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = 3I21A HC CDR1	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 115		
NYWMN		5
SEQ ID NO: 116	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = 3I21A HC CDR2	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 116		
RIHPSDSETH YNQKFKT		17
SEQ ID NO: 117	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
source	note = 3I21A HC CDR3	
	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 117		
YDGYFAY		7
SEQ ID NO: 118	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
source	note = 8H5A HC CDR1	
	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 118		
TFGMGVG		7
SEQ ID NO: 119	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = 8H5A HC CDR2	
	1..16	

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SEQUENCE: 119 HIWDDDKYY NPALKS	mol_type = protein organism = synthetic construct	16
SEQ ID NO: 120 FEATURE REGION source	moltype = AA length = 10 Location/Qualifiers 1..10 note = 8H5A HC CDR3 1..10 mol_type = protein organism = synthetic construct	10
SEQUENCE: 120 TYDYDEYFDY		10
SEQ ID NO: 121 FEATURE REGION source	moltype = AA length = 5 Location/Qualifiers 1..5 note = 15K2A HC CDR1 1..5 mol_type = protein organism = synthetic construct	5
SEQUENCE: 121 SYWMN		5
SEQ ID NO: 122 FEATURE REGION source	moltype = AA length = 17 Location/Qualifiers 1..17 note = 15K2A HC CDR2 1..17 mol_type = protein organism = synthetic construct	17
SEQUENCE: 122 RIHPSDSETH YNQKFRT		17
SEQ ID NO: 123 FEATURE REGION source	moltype = AA length = 10 Location/Qualifiers 1..10 note = 15K2A HC CDR3 1..10 mol_type = protein organism = synthetic construct	10
SEQUENCE: 123 EDGYYWYFDV		10
SEQ ID NO: 124 FEATURE REGION source	moltype = AA length = 5 Location/Qualifiers 1..5 note = 5A24A HC CDR1 1..5 mol_type = protein organism = synthetic construct	5
SEQUENCE: 124 DFNMD		5
SEQ ID NO: 125 FEATURE REGION source	moltype = AA length = 17 Location/Qualifiers 1..17 note = 5A24A HC CDR2 1..17 mol_type = protein organism = synthetic construct	17
SEQUENCE: 125 DINPNSGGTI YNQKPKG		17
SEQ ID NO: 126 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 5A24A HC CDR3 1..8 mol_type = protein organism = synthetic construct	8
SEQUENCE: 126 WDYGNFAY		8
SEQ ID NO: 127	moltype = AA length = 5	

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FEATURE	Location/Qualifiers	
REGION	1..5	
	note = 15P17A HC CDR1	
source	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 127		
NYWMN		5
SEQ ID NO: 128	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
	note = 15P17A HC CDR2	
source	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 128		
RIHPSDSETH YNQKFKS		17
SEQ ID NO: 129	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
REGION	1..10	
	note = 15P17A HC CDR3	
source	1..10	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 129		
EDGYWYFDV		10
SEQ ID NO: 130	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
	note = 15N21A HC CDR1	
source	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 130		
SYAMS		5
SEQ ID NO: 131	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
	note = 15N21A HC CDR2	
source	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 131		
AINSGGRNY YPDTVKD		17
SEQ ID NO: 132	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
	note = 15N21A HC CDR3	
source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 132		
HRGGYYAMD Y		11
SEQ ID NO: 133	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
	note = 13P9A LC CDR1	
source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 133		
HASQNINVL S		11
SEQ ID NO: 134	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
	note = 13P9A LC CDR2	
source	1..7	
	mol_type = protein	
	organism = synthetic construct	

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SEQUENCE: 134 KASNLHT		7
SEQ ID NO: 135 FEATURE REGION source	moltype = AA length = 9 Location/Qualifiers 1..9 note = 13P9A LC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 135 QQGQSYPT		9
SEQ ID NO: 136 FEATURE REGION source	moltype = AA length = 11 Location/Qualifiers 1..11 note = 5A16A LC CDR1 1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 136 RASGNIHNYL A		11
SEQ ID NO: 137 FEATURE REGION source	moltype = AA length = 7 Location/Qualifiers 1..7 note = 5A16A LC CDR2 1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 137 NAKTLPY		7
SEQ ID NO: 138 FEATURE REGION source	moltype = AA length = 9 Location/Qualifiers 1..9 note = 5A16A LC CDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 138 QHEWTPWT		9
SEQ ID NO: 139 FEATURE REGION source	moltype = AA length = 17 Location/Qualifiers 1..17 note = 14L22A LC CDR1 1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 139 KSSQSVLYSS NQKNYLA		17
SEQ ID NO: 140 FEATURE REGION source	moltype = AA length = 7 Location/Qualifiers 1..7 note = 14L22A LC CDR2 1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 140 WASTRES		7
SEQ ID NO: 141 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = 14L22A LC CDR3 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 141 HQYLSSRT		8
SEQ ID NO: 142 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15	

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source	note = 10P18A LC CDR1 1..15 mol_type = protein organism = synthetic construct	
SEQUENCE: 142 RASKSVSTSG YSYMH		15
SEQ ID NO: 143 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 10P18A LC CDR2	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 143 LASNLES		7
SEQ ID NO: 144 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 10P18A LC CDR3	
source	1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 144 QHSRELPYT		9
SEQ ID NO: 145 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 13P11A LC CDR1	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 145 KASENVGTIV S		11
SEQ ID NO: 146 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 13P11A LC CDR2	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 146 GASNRFT		7
SEQ ID NO: 147 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 13P11A LC CDR3	
source	1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 147 GQSYSYPFT		9
SEQ ID NO: 148 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = 3C16A LC CDR1	
source	1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 148 KASQNVRTAV A		11
SEQ ID NO: 149 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 3C16A LC CDR2	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 149 LASNRHT		7

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SEQ ID NO: 150	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 3C16A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 150		
LQHWNYPLT		9
SEQ ID NO: 151	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = 3I21A LC CDR1	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 151		
KASDHINNWL A		11
SEQ ID NO: 152	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
source	note = 3I21A LC CDR2	
	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 152		
GATSLET		7
SEQ ID NO: 153	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 3I21A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 153		
QQYWSIPFT		9
SEQ ID NO: 154	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = 8H5A LC CDR1	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 154		
RSSKSLLSN GITYFY		16
SEQ ID NO: 155	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
source	note = 8H5A LC CDR2	
	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 155		
QMSNLAS		7
SEQ ID NO: 156	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = 8H5A LC CDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 156		
AQNLELPFT		9
SEQ ID NO: 157	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
source	note = 15K2A LC CDR1	
	1..15	

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	mol_type = protein organism = synthetic construct	
SEQUENCE: 157 RASESVDIYG NSFMMH		15
SEQ ID NO: 158 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 15K2A LC CDR2 1..7	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 158 LASNLES		7
SEQ ID NO: 159 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 15K2A LC CDR3 1..9	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 159 QQNNEPWT		9
SEQ ID NO: 160 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16 note = 5A24A LC CDR1 1..16	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 160 RSSKSLLSN GITYLY		16
SEQ ID NO: 161 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 5A24A LC CDR2 1..7	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 161 QMSNLAS		7
SEQ ID NO: 162 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9 note = 5A24A LC CDR3 1..9	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 162 AQNLELPLT		9
SEQ ID NO: 163 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15 note = 15P17A LC CDR1 1..15	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 163 RASESVDSYG NSFMMH		15
SEQ ID NO: 164 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = 15P17A LC CDR2 1..7	
source	mol_type = protein organism = synthetic construct	
SEQUENCE: 164 LASNLES		7
SEQ ID NO: 165	moltype = AA length = 9	

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FEATURE	Location/Qualifiers	
REGION	1..9	
	note = 15P17A LC CDR3	
source	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 165		
QQNHEDPWT		9
SEQ ID NO: 166	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
	note = 15N21A LC CDR1	
source	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 166		
KSSQSLLYSS NQKNYLA		17
SEQ ID NO: 167	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
	note = 15N21A LC CDR2	
source	1..7	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 167		
WASTRES		7
SEQ ID NO: 168	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
	note = 15N21A LC CDR3	
source	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 168		
QQYYTYLT		8
SEQ ID NO: 169	moltype = AA length = 618	
FEATURE	Location/Qualifiers	
source	1..618	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 169		
MVSPRMSGLL SQTVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCRLFF		60
RVCLKPGLSE EAAESPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAWPGTF		120
SPIIETWREE LGDQIGGPAW SLLARVAGR RLAAGGPWAR DIQRAGAWEL RFSYRARCEP		180
PAVGTACTRL CRPRSAPSRC GPGLRPCAPL EDECEAPLVC RAGCSPHEGF CEQPGECRCL		240
EGWTGPLCTV PVSTSSCLSP RGPSSATTGC LVPGPGPCDG NPCANGGSCS ETPRSFECTC		300
PRGFYGLRCE VSGVTCADGP CFNGGLCVGG ADPDSAYICH CPPGFQGSNC EKRVDRCSLQ		360
PCRNGGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGCTCVEGG GAHRCSCALG		420
FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP		480
PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPEPSVHAL		540
PDALNNLRTQ EGSGDGPSSS VDWNRPEDVD PQGIYVISAP SIYAREVATP LFPPLHTGRA		600
GQRQHLLFPY PSSILSVK		618
SEQ ID NO: 170	moltype = AA length = 118	
FEATURE	Location/Qualifiers	
REGION	1..118	
	note = H1 Heavy Chain Variable Region	
source	1..118	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 170		
EVRLSQSGGQ MKKPGESMRL SCRASGYTFT SYVMHWVRQA PGRRPEWIGY INPYNDATKY		60
ARKFQGRATL TSDKYSDTAF LELRSLTSD TAVYYCARG YDYGDDYWGR GAPVTVSS		118
SEQ ID NO: 171	moltype = AA length = 107	
FEATURE	Location/Qualifiers	
REGION	1..107	
	note = L1 Light Chain Variable Region	
source	1..107	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 171		

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EIVMTQSPGT	LSLSPGERAT	LSCHASQNIN	VWLSWYQQKP	GQAPRLLIYK	ASNLHTGIPD	60
RFSGSGSGTD	FTLTISRLEP	EDFAVYQCQQ	GQSYPTFTGQ	GTKVEIK		107
SEQ ID NO: 172 moltype = AA length = 107						
FEATURE Location/Qualifiers						
REGION 1..107						
note = L2 Light Chain Variable Region						
source 1..107						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 172						
EIVLTQSPGT	LSLSPGERAT	LSCHASQNIN	VWLSWYQQKP	GQAPRLLIYK	ASNLHTGIPD	60
RFSGSGSGTD	FTLTISRLEP	EDFAVYQCQQ	GQSYPTFTGQ	GTKVEIK		107
SEQ ID NO: 173 moltype = AA length = 107						
FEATURE Location/Qualifiers						
REGION 1..107						
note = L3 Light Chain Variable Region						
source 1..107						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 173						
EIVMTQSPAT	LSLSPGETAI	ISCHASQNIN	VWLSWYQQR	GQAPRLLIYK	ASNLHTGIPD	60
RFSGSGWGT	FNLSISNLES	GDFGVYQCQQ	GQSYPTFTGQ	GTKVEIK		107
SEQ ID NO: 174 moltype = AA length = 107						
FEATURE Location/Qualifiers						
REGION 1..107						
note = L4 Light Chain Variable Region						
source 1..107						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 174						
EIVMTQSPAT	LSLSPGETAI	ISCHASQNIN	VWLSWYQQR	GQAPRLLIYK	ASNLHTGIPD	60
RFSGSGWGT	FNLSISNLES	GDFGVYQCQQ	GQSYPTFTGQ	GTKVEIK		107
SEQ ID NO: 175 moltype = AA length = 114						
FEATURE Location/Qualifiers						
REGION 1..114						
note = KH1 Heavy Chain Variable Region						
source 1..114						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 175						
QVQLVQSGAE	VKKPGSSVKV	SCKASGYTFT	SYWMHWVRQA	PGQGLEWIGN	IDPSDSETHY	60
AQKFQGRATL	TVDKSTSTAY	MELSSLRSED	TAVYYCAGTD	LAYWGQGLTV	TVSS	114
SEQ ID NO: 176 moltype = AA length = 114						
FEATURE Location/Qualifiers						
REGION 1..114						
note = KH2 Heavy Chain Variable Region						
source 1..114						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 176						
QVQLVQSGAE	VKKPGASVKV	SCKASGYTFT	SYWMHWVRQA	PGQGLEWIGN	IDPSDSETHY	60
AQKFQGRVTL	TVDKSTSTVY	MELSSLRSED	TAVYYCAGTD	LAYWGQGLTV	TVSS	114
SEQ ID NO: 177 moltype = AA length = 114						
FEATURE Location/Qualifiers						
REGION 1..114						
note = KH3 Heavy Chain Variable Region						
source 1..114						
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 177						
EVRLSQSGGQ	MKKPGESMRL	SCRASGYTFT	SYWMHWVRQA	PGRRLIEWIGN	IDPSDSETHY	60
ARKFQGRATL	TVDKYSDTAF	LELRSLTSD	TAVYYCAGTD	LAYWGRGAPV	TVSS	114
SEQ ID NO: 178 moltype = AA length = 8						
FEATURE Location/Qualifiers						
REGION 1..8						
note = KH2 HCDR1						
source 1..8						
mol_type = protein						
organism = synthetic construct						

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SEQUENCE: 178 GYTFTSYW		8
SEQ ID NO: 179 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = KH2 HCDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 179 IDPSDSET		8
SEQ ID NO: 180 FEATURE REGION source	moltype = AA length = 7 Location/Qualifiers 1..7 note = KH2 HCDR3 1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 180 AGTDLAY		7
SEQ ID NO: 181 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = H1 HCDR1 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 181 GYTFTSYV		8
SEQ ID NO: 182 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = H1 HCDR2 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 182 INPYNDAT		8
SEQ ID NO: 183 FEATURE REGION source	moltype = AA length = 11 Location/Qualifiers 1..11 note = H1 HCDR3 1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 183 ARGGYDYDGD Y		11
SEQ ID NO: 184 FEATURE REGION source	moltype = AA length = 6 Location/Qualifiers 1..6 note = L2 LCDR1 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 184 QNINVW		6
SEQ ID NO: 185 SEQUENCE: 185 000	moltype = length =	
SEQ ID NO: 186 FEATURE REGION source	moltype = AA length = 9 Location/Qualifiers 1..9 note = L2 LCDR3 1..9 mol_type = protein organism = synthetic construct	
SEQUENCE: 186 QQGQSYPT		9

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SEQ ID NO: 187	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = KH2 HCDR1	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 187		
SYWMH		5
SEQ ID NO: 188	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = KH2 HCDR2	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 188		
NIDPSDSETH YAQKFQG		17
SEQ ID NO: 189	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = KH2 HCDR3	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 189		
TDLAY		5
SEQ ID NO: 190	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = H1 HCDR1	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 190		
SYVMH		5
SEQ ID NO: 191	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = H1 HCDR2	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 191		
YINPYNDATK YARKFQG		17
SEQ ID NO: 192	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = H1 HCDR3	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 192		
GGYDYDGDY		9
SEQ ID NO: 193	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = L2 LCDR1	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 193		
HASQNINVL S		11
SEQ ID NO: 194	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
source	note = L2 LCDR2	
	1..7	

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	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 194		7
KASNLHT		
SEQ ID NO: 195	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
	note = L2 LCDR3	
source	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 195		9
QQGQSYFFT		

1-36. (canceled)

37. An isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof comprising:

- (a) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- (b) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- (d) a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 175, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;
- (e) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- (f) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:176, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173;
- (g) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:171;
- (h) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:172;
- (i) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:177, and a light chain variable region having the polypeptide sequence of SEQ ID NO:173; or
- (j) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:177, and a light chain variable region having the polypeptide sequence of SEQ ID NO: 174.

38. The isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37**, wherein the antibody or antigen-binding fragment thereof is capable of blocking binding of CD47 to SIRP α or inducing macrophage-mediated phagocytosis of cancer cells.

39. An isolated nucleic acid encoding the anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37**.

40. A vector comprising the isolated nucleic acid of claim **39**.

41. A host cell comprising the vector of claim **40**.

42. A pharmaceutical composition comprising the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37** and a pharmaceutically acceptable carrier.

43. A method of blocking binding of CD47 to signal regulatory protein alpha (SIRP α) or inducing macrophage-mediated phagocytosis of cancer cells in a subject in need thereof, comprising administering to the subject in need thereof a pharmaceutical composition comprising the isolated anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37**.

44. A method of treating cancer in a subject in need thereof, comprising administering to the subject the pharmaceutical composition of claim **42**.

45. The method of claim **44**, wherein the cancer is selected from the group consisting of a lung cancer, such as small cell lung cancer (SCLC), large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, and other solid tumors, and a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), an acute myeloid leukemia (AML), and other liquid tumors.

46. A method of producing the anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37**, comprising culturing a cell comprising a nucleic acid encoding the antibody or antigen-binding fragment thereof under conditions to produce the antibody or antigen-binding fragment thereof, and recovering the antibody or antigen-binding fragment thereof from the cell or culture.

47. A method of producing a pharmaceutical composition comprising the anti-CD47 monoclonal antibody or antigen-binding fragment thereof of claim **37**, comprising combining the antibody or antigen-binding fragment thereof with a pharmaceutically acceptable carrier to obtain the pharmaceutical composition.

48. An isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof comprising a heavy chain complementarity determining region 1 (HCDR1), HCDR2,

HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequences of:

- (a) SEQ ID NOs: 28, 29, 30, 64, 65 and 66, respectively, or SEQ ID NOs: 100, 101, 102, 136, 137 and 138, respectively;
- (b) SEQ ID NOs: 31, 32, 33, 67, 68 and 69, respectively, or SEQ ID NOs: 103, 104, 105, 139, 140 and 141, respectively;
- (c) SEQ ID NOs: 34, 35, 36, 70, 71 and 72, respectively, or SEQ ID NOs: 106, 107, 108, 142, 143, and 144, respectively;
- (d) SEQ ID NOs: 37, 38, 39, 73, 74 and 75, respectively, or SEQ ID NOs: 109, 110, 111, 145, 146 and 147, respectively;
- (e) SEQ ID NOs: 43, 44, 45, 79, 80 and 81, respectively, or SEQ ID NOs: 115, 116, 117, 151, 152 and 153 respectively;
- (f) SEQ ID NOs: 49, 50, 51, 85, 86 and 87, respectively, or SEQ ID NOs: 121, 122, 123, 157, 158 and 159, respectively; or
- (g) SEQ ID NOs: 55, 56, 57, 91, 92 and 93, respectively, or SEQ ID NOs: 127, 128, 129, 163, 164 and 165, respectively;

wherein the antibody or antigen-binding fragment thereof specifically binds DLL3.

49. The isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of claim **48**, comprising a heavy chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO: 3, 5, 7, 9, 13, 17, or 21, or a light chain variable region having a polypeptide sequence at least 95% identical to SEQ ID NO: 4, 6, 8, 10, 14, 18, or 22.

50. The isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of claim **49**, comprising:

- (a) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:3, and a light chain variable region having the polypeptide sequence of SEQ ID NO:4;
- (b) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:5, and a light chain variable region having the polypeptide sequence of SEQ ID NO:6;
- (c) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:7, and a light chain variable region having the polypeptide sequence of SEQ ID NO:8;

- (d) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:9, and a light chain variable region having the polypeptide sequence of SEQ ID NO:10;

- (e) a heavy chain variable region having the polypeptide sequence of SEQ ID NO: 13, and a light chain variable region having the polypeptide sequence of SEQ ID NO:14;

- (f) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:17, and a light chain variable region having the polypeptide sequence of SEQ ID NO: 18; or

- (g) a heavy chain variable region having the polypeptide sequence of SEQ ID NO:21, and a light chain variable region having the polypeptide sequence of SEQ ID NO:22.

51. The isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of claim **48**, wherein the monoclonal antibody or antigen-binding fragment thereof is capable of inducing effector-mediated tumor cell lysis, mediating the recruitment of conjugated drugs, and/or forming a bispecific antibody.

52. A pharmaceutical composition comprising the isolated anti-DLL3 monoclonal antibody or antigen-binding fragment thereof of claim **48** and a pharmaceutically acceptable carrier.

53. A method of targeting DLL3 on a cancer cell surface or a method of treating cancer in a subject in need thereof, comprising administering to the subject in need thereof the pharmaceutical composition of claim **52**.

54. The method of claim **53**, wherein the cancer is selected from the group consisting of a lung cancer, a small cell lung cancer (SCLC), a large cell neuroendocrine carcinoma (LCNEC), a gastric cancer, a colon cancer, a hepatocellular carcinoma, a renal cell carcinoma, a bladder urothelial carcinoma, a metastatic melanoma, a breast cancer, an ovarian cancer, a cervical cancer, a head and neck cancer, a pancreatic cancer, a glioma, a glioblastoma, a non-Hodgkin's lymphoma (NHL), an acute lymphocytic leukemia (ALL), a chronic lymphocytic leukemia (CLL), a chronic myelogenous leukemia (CML), a multiple myeloma (MM), and an acute myeloid leukemia (AML).

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